



AMS Manual

Amsterdam Modeling Suite 2023.1

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1.1 Overview

AMS is the new driver program introduced in the 2018 release of the Amsterdam Modeling Suite. The job of AMS is to handle all changes in the simulated system's geometry, e.g. during a geometry optimization or molecular dynamics calculation, using the so-called "engines" like ADF, BAND or DFTB for the calculation of energies and forces. In summary, one might say that the AMS driver steers the engines across the potential energy surface.

Prior to the 2018 release of the Amsterdam Modeling Suite, what we now call engines used to be separate programs, each with their own input and output files and formats. Starting with the 2018 release, the engines are only accessible through the AMS driver program, that provides a unified interface to all of them.

1.2 What's new in the AMS driver?

1.2.1 New in AMS2023.1

- A new *Conformers tool* (page 326) tool allows conformer generation with any *AMS engine* (page 250).
- *Molecular orbitals energies and occupations* (page 248) can now be requested from the `Properties` block in the driver input and are printed in an engine independent manner.
- The *AMSbatch* (page 367) utility program allows executing the same AMS job for multiple systems.
- A Martinez style *Nanoreactor* (page 133) was added to the MD driver.
- The *PES scan* (page 68) task can now use all *geometry optimizers* (page 55). Previously it was limited to using the Quasi-Newton optimizer. This will make pure *lattice PES scans* (page 70) (e.g. energy-volume scans) with fast *engines* (page 250) and large cells much faster.
- The `GeometryOptimization%Convergence%Quality` keyword can now be used to *easily tighten or relax all convergence thresholds* (page 49) for geometry optimizations at once.
- The calculation of normal modes now also calculates and prints the reduced masses and force constants of the individual modes.
- The *PES point characterization* (page 180) now uses the force constants instead of the vibrational frequencies to identify transition states, making it more reliable in the presence of numerical noise.
- Environment variables in the input will now be *expanded* (page 11).
- The default value of `VibrationalAnalysis%Displacement` has been changed to 0.005 Bohr, related to precision issues with derivatives of polarizability.

- Various improvements to the *OLED workflows* (page 303), see the *changelog* (page 304) on the respective manual page.
- The calculation of the *vibronic density of states* (page 233) for transfer phenomena using the Adiabatic-Hessian Franck-Condon formalism has been added.
- Calculation of *vibrational polarizabilities* (page 224) under the harmonic approximation.

1.2.2 New in AMS2022.1

- The MD driver now supports Rattle/Shake methods for *constrained molecular dynamics simulations* (page 97). The *FIRE optimizer* (page 59) now supports *distance constraints* (page 52).
- The *PES scan* (page 68) task now allows the *scanning of lattice degrees of freedom* (page 70).
- The *molecule gun* (page 113) now supports the *generation of molecule mixtures* (page 117) through the `Mole-Fraction` keyword.
- The *Replay task* (page 142) for recomputing properties for trajectory frames with a different engine.
- The *PES exploration* (page 152) can now include *fragmented states* (page 166) in the energy landscape when studying adsorption processes.
- A new option allows *Geometry optimizations* (page 47) with *PES point characterization* (page 180) and no *symmetry* (page 35) to converge more reliably to minima instead of transition states or higher order saddle points: in case a geometry optimization converges to a TS, it can will now *automatically restart* (page 51) after displacing all atoms along the imaginary mode.
- The calculation of Franck-Condon factors with the *FCF program* (page 225) has been improved regarding precision, speed, and memory requirements.

1.2.3 New in AMS2021.1

- *PES exploration* (page 152) tasks for the automated discovery of stationary points on the potential energy surface.
 1. *Process Search* (page 160): a composite method for finding escape mechanisms from a state. This will find both local minima and their connecting saddle points.
 2. *Basin Hopping* (page 164): a Monte Carlo method for finding local minima.
 3. *Saddle Search* (page 161): a single-ended method for finding nearby saddle points.
- *Force bias Monte Carlo* (page 130) is now available in AMS, enabling pure MC or mixed MD/MC simulations with any engine.
- The *molecule gun* (page 113) can now generate random shooting directions in a given cone.
- A new *wall potential* (page 266) engine add-on can be used to simulate spherical nanoreactors.
- The *D4 dispersion add-on* (page 258) can now also be used for calculations on periodic systems.
- Graceful interactive termination of running jobs through the *interactive input file* (page 15).
- *Geometry optimizations* (page 47) write the optimized geometry to the results directory as an *extended XYZ file* (page 477).

1.2.4 New in AMS2020.1

- ADF has been fully integrated as an AMS engine.
- New engines: *MLPotential* implementing several different type of machine learning (ML) potentials. A *Hybrid engine* for combining other engines in QM/MM calculations. Enhanced *ForceField* engine (formerly UFF).
- Improvements to the *Quasi-Newton geometry optimizer* (page 57): Periodic systems can now be optimized in delocalized coordinates. Better performance for systems made up of disconnected fragments.
- Geometry optimization can now be performed with *frozen and equal strain constraints* (page 55) for the lattice degrees of freedom. This option is currently only available with the *FIRE optimizer* (page 59).
- Support for *external electric fields* (page 38): Homogeneous as well as multipole charges.
- Enhanced support for *vibrational spectroscopy* (page 187): (resonance) Raman, (resonance) vibrational Raman optical activity, vibrational circular dichroism.
- The MD driver now supports time-dependent *lattice deformations* (page 110) as well as a method for accelerating bonding reactions (*Bond Boost method* (page 128)).
- Reactive MD calculations with the AMS driver can now be analyzed with *ChemTraYzer* (page 269).
- It is now possible to selectively disable writing some parts of a *MD trajectory* (page 105) to save space.
- More *trajectory analysis* (page 279) options: *autocorrelation functions* (page 284) and *diffusion coefficient* (page 299)
- The *molecular composition analysis* (page 246) can now be done with respect to an adsorption support region.
- The *transition state search* (page 65) task now allows the users to specify an approximate reaction coordinate (TSRC).
- For the calculation of normal modes, the *Mobile Block Hessian* (page 193) method now allows to treat parts of the system as rigid blocks.
- New coordinates for *constrained geometry optimizations* (page 52) and *PES scans* (page 68): Sum of distances and difference of distances.
- Added the ability to include additional potential terms (i.e. springs) through the *Restrains engine add-on* (page 264).
- A running AMS driver process can be used from Python through the new *AMSWorker class* in the *PLAMS* library. The communication between PLAMS and the AMS driver happens via the new *Pipe interface* (page 25) protocol.
- Introduced *Regions* (page 36) to simplify the input syntax for options that apply to a subset of atoms only.
- Symmetrization of systems from the input and the option to input a Z-matrix.
- Low frequencies contribution to *thermodynamics properties* (page 209) can be corrected using a free rotor interpolation method.

1.2.5 New in AMS2019.3

- The *Nudged elastic band method (NEB)* (page 75) for finding minimum energy paths of transitions has been added.
- The new *PES point character property* (page 180) can be used to quickly calculate a few of the lowest vibrational modes of a system and to verify the success of a geometry optimization or transitions state search.
- *Driver level parallelism* (page 21) is now enabled and managed automatically, improving the performance and scalability of many applications.
- A *Mode Scanning* (page 195) calculation can now be *started automatically* (page 191) for all modes within a specific frequency range.

- Methods for the quick calculation of the *vibrationally resolved electronic spectra* (page 224): *Vibronic-Structure Refinement* (page 237) and *Vibronic-Structure Tracking* (page 236).
- New geometry optimizer available: *Limited-memory BFGS* (page 63)
- Input keywords that expect lists of numbers can now be specified as *ranges using a Python slice-like notation* (page 12). Input keywords that expect a single real number now also accept fractions (of integers).
- New option to include a *non-isotropic external stress* (page 262) for 1D,2D and 3D periodic systems. This can be used to study structural deformation and mechanical properties of materials under non-isotropic stress.
- New *add-on system* (page 258) for manipulating and augmenting the results returned from the *engines* (page 250):
 1. Grimme's D4 and D3 dispersion corrections can be used with any engine through the *D4Dispersion and D3Dispersion add-ons* (page 258).

1.2.6 New in AMS2019.1

- *Intrinsic Reaction Coordinate (IRC) Scan* (page 83) is now available in the AMS driver for molecular and periodic systems.
- Support for the *Grand Canonical Monte Carlo (GCMC)* (page 144) method has been added in the AMS driver.
- Molecular composition analysis for molecular dynamics simulations (see [tutorial](#))
- *Collective Variable-driven Hyperdynamics (CVHD)* (page 123)
- *Molecule gun* (page 113) and *molecule sink* (page 117) for molecular dynamics
- *PLUMED library support* (page 120) for MD analysis and a wide variety of free energy methods
- The initial symmetry of a system is enforced during geometry optimizations with the Quasi-Newton optimizer.
- *Thermodynamic properties* (page 209) (assuming an ideal gas) are automatically computed after normal modes calculations.
- *Partial vibrational density of states (PVDOS)* (page 213) for normal modes.
- The system's symmetry is used to accelerate numerical nuclear derivatives and to provide symmetry labels for normal modes.
- The AMS driver starts up much faster, significantly speeding up scripting applications that launch AMS many times.
- New tools for mode selective vibrational analysis:
 1. *Mode Scanning* (page 195) (aka ADF's ScanFreq)
 2. *Mode Refinement* (page 196) (aka "Frequency range selection")
 3. *Mode Tracking* (page 199)

1.3 Motivation and progress

The Amsterdam Modeling Suite has grown substantially over the last decade, and in the 2017 release included programs implementing methods all the way from accurate density functional theory, through semi-empirical methods, to fast reactive force fields. Many of these programs have originally been developed by academic groups and are now maintained and expanded by SCM in collaboration with the original authors.

This rapid growth of the Amsterdam Modeling Suite had, however, led to a certain degree of unnecessary inhomogeneity within the suite: The input for the same task, e.g. a geometry optimization, differed quite a lot between the different

programs in the suite. While this problem was mostly hidden for users of the graphical interface, it constituted a barrier for users of the new scripting frameworks such as PLAMS. Furthermore, the different programs produced rather different output files for the same task, making the automated extraction of results unnecessarily difficult. Finally, and most importantly, the rapid growth of the AMS suite had also led to a certain level of feature fragmentation, where some features were available in one program but not the other: ADF, for example, was able to do a linear transit calculation, while BAND was not. Constrained geometry optimization was supported in DFTB, but not in UFF. ReaxFF could be used for Grand Canonical Monte Carlo simulations, but DFTB could not.

In order to overcome these issues and make the Amsterdam Modeling Suite more powerful and user friendly, we introduced the AMS driver program with the 2018 release of the suite. The idea of this reorganization is to have only a single program called the AMS driver that under the hood uses the so-called “engines” like ADF, BAND and DFTB for the calculation of energies and gradients, where the engines are technically no longer separate programs but just libraries used by the AMS driver. In this way much of the input and output of AMS is the same, no matter which particular engine is used for a calculation. It also avoids the feature fragmentation, since any new feature in the AMS driver can immediately be used with all engines in the suite. Furthermore, the AMS driver also allows running *external programs as an engine* (page 254) providing energies and gradients, allowing end-users to perform all calculations supported by AMS with virtually any atomistic modeling program they have access to and to visualize the results in the graphical user interface of the Amsterdam Modeling Suite.

Converting all the programs of the Amsterdam Modeling Suite into engine libraries that are used by the AMS driver was a big reorganization of the entire suite, which was spread out over multiple releases between 2018 and 2020. As of the AMS2020 release, ADF itself has been integrated into the AMS driver, making the integration of all engines into the AMS driver finally complete. (The only exception is QuantumEspresso, which is integrated into the GUI, but has no connection to the AMS driver in the 2020 release.)

As with any large reorganization, it is unavoidable that some things change. For GUI users this should not create any issues, but users familiar with the existing command line and scripting interfaces will notice these changes and their existing workflows might need to be adjusted to the new setup. We know that these kind of changes can be disrupting for existing users, and where possible we try to keep backwards compatibility with previous versions, but unfortunately this is not always possible. However, overall AMS provides a much more consistent and convenient interface to command line and scripting users, and we believe that the new simplicity and expanded feature set of AMS make transitioning to the new framework well worth the effort.

1.4 Input, execution and output

With the introduction of AMS in the 2018 release of the Amsterdam Modeling Suite, there were some changes in the input and output files and formats used by our software. Users of the graphical interface should not notice these changes, but people using the software from the command line or through the scripting frameworks need to be aware of them.

This section contains the main changes. For a more complete description see:

- The extended *Input, execution and output section* (page 9).

Generally the input for AMS has the block and keyword structure that most programs in the Amsterdam Modeling Suite have already been using. See the *General remarks on input structure and parsing* (page 11) section for more details. The only new construct in the AMS input is a special *Engine* block, that selects which engine is used for the simulation and also contains all the details of its configuration. This is probably best illustrated by an example. Let us look at the following AMS input, which optimizes the geometry of the methane molecule and calculates its normal modes of vibration at the optimized geometry:

```

$AMSBIN/ams << EOF
Task GeometryOptimization

GeometryOptimization
Convergence

```

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```

      Gradients 1.0e-4
    End
  End

  Properties
    NormalModes true
  End

  System
    Atoms
      C      0.00000000    0.00000000    0.00000000
      H      0.63294000   -0.63294000   -0.63294000
      H     -0.63294000    0.63294000   -0.63294000
      H      0.63294000    0.63294000    0.63294000
      H     -0.63294000   -0.63294000    0.63294000
    End
  End

  Engine DFTB
    Model DFTB3
    ResourcesDir DFTB.org/3ob-3-1
  EndEngine
EOF

```

Note how DFTB is selected as the engine in the `Engine DFTB` line that opens the Engine block. All DFTB specific configuration is contained within this engine block, which is terminated by `EndEngine`. The fact that we want to run a geometry optimization with normal modes for methane and things like convergence criteria for the optimization are of course completely independent from which engine is actually used to perform this calculation. Therefore they are all found *outside* of the Engine block. In this sense, the AMS input is split up into the driver level input (everything outside of the engine block) and the engine input, which is just a single Engine block. This separation makes it easy to perform the same calculation at a different level of theory, by simply switching out the Engine block in the input. We could, for example, repeat the same calculation at the DFT-GGA level using the Band engine:

```

Engine BAND
  XC
  GGA PBE
End
EndEngine

```

Engines like ADF and BAND that have many options and can calculate many properties, consequently also have a large number of possible keywords in their input. In order to have a better structured documentation we have split off the description of the engine inputs into separate *engine specific manuals* (page 250), while this AMS manual only documents the driver level keywords outside of the Engine block. All the engine specific options are found in the respective engine's manual, which documents the keywords in its Engine block. In general all engines can be used with all tasks in AMS. There are only a few rather obvious restrictions, for example that only engines which can handle periodic systems can be used for the calculation of phonons.

The introduction of the Engine block is the only real change AMS brings to the input side of things. On the output side there are a few more changes.

The first change to the output is that AMS does not put any of its output files into the present working directory, as virtually all of the standalone programs in the suite did. Instead AMS creates a `*.results` directory, which collects all result file associated with a job. Here `*` is replaced by the jobname, which is set with the `AMS_JOBNAME` environment variable:


```
AMS_JOBNAME=methane $AMSBIN/ams << EOF

... see above ...

EOF
```

This would put all results related to our geometry optimization of methane into the newly created folder `methane.results`. (The default name of the results folder is `ams.results` if `AMS_JOBNAME` is not set, see the *environment variables* (page 20) section of this manual for documentation of all environment variables used by AMS.) In this way users can easily run multiple jobs in the same directory without danger of clashing output files, which was a common problem before the introduction of AMS. This new setup is also more consistent with the graphical user interface, which already collected all files associated with a specific job into a dedicated results directory. Note that AMS will by default **not overwrite** results directories if a job is rerun or another job is run with the same jobname.

Inside of the results directory users will always find the logfile `ams.log`, which is written during a running calculation and can be used to monitor its progress. Furthermore the results directory contains binary result files in the KF format, which can be opened and inspected with the KFBrowser GUI component.

- The main `ams.rkf` written by the AMS driver. It contains high level information about the trajectory that the AMS driver took over the potential energy surface. For example, for a molecular dynamics simulation it would contain the full trajectory. The format in which this information is written is independent from which engine was used for a calculation.
- The engine specific main binary output file written by the engine (and partly by the AMS driver). This file is kept for only one special point, e.g. the final geometry in a geometry optimization. For example, for ADF this engine file is called `adf.rkf` (instead of `TAPE21` in ADF<=2019), for BAND `band.rkf`, for DFTB `dftb.rkf`. If a property, like vibrational modes, is tied to the special point on the potential energy surface, it is stored in this file. Also all engine specific properties are written to this file, like orbitals in case of a quantum mechanical engine.
- Additionally there might be a binary output file for every point on the potential energy surface that was visited during the calculation.
- Other engine specific binary (and ASCII) output files written by the engine.

Having multiple different binary output files could be confusing for people that are used to the single result file that was written by the standalone programs in ADF<=2017. After all, it brings up the question in which file the desired property is stored. The general rule is: if the property is tied to a particular point on the potential energy surface, it is stored in the engine output file belonging to that particular point. If the information depends on the entire trajectory over the PES, it is found in the main `ams.rkf` written by the AMS driver.

INPUT, EXECUTION AND OUTPUT

2.1 Input

The input for AMS has a block and keyword structure. See the *General remarks on input structure and parsing* (page 11) section for more details.

The input keys *System* (page 31), *Task* (page 10), and *Engine* (page 250), are obligatory. Most other input keys in AMS are optional, like *Properties* (page 10). In the rest of this manual one can find all input keys for AMS.

The Engine specific input can be found in the respective Engine Manuals, for example, the manual for *ADF*, *BAND*, *DFTB*, *ForceField*, *MOPAC*, and *ReaxFF*.

2.1.1 Example

The AMS input has a special *Engine* block, that selects which engine is used for the simulation and also contains all the details of its configuration. This is probably best illustrated by an example. Let us look at the following AMS input, which optimizes the geometry of the methane molecule and calculates its normal modes of vibration at the optimized geometry:

```

$AMSBIN/ams << EOF
  Task GeometryOptimization

  GeometryOptimization
    Convergence
      Gradients 1.0e-4
    End
  End

  Properties
    NormalModes true
  End

  System
    Atoms
      C      0.00000000    0.00000000    0.00000000
      H      0.63294000   -0.63294000   -0.63294000
      H     -0.63294000    0.63294000   -0.63294000
      H      0.63294000    0.63294000    0.63294000
      H     -0.63294000   -0.63294000    0.63294000
    End
  End

  Engine DFTB
    Model DFTB3

```

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```
ResourcesDir DFTB.org/3ob-3-1
EndEngine
EOF
```

Note how DFTB is selected as the engine in the `Engine DFTB` line that opens the `Engine` block. All DFTB specific configuration is contained within this engine block, which is terminated by `EndEngine`. The fact that we want to run a geometry optimization with normal modes for methane and things like convergence criteria for the optimization are of course completely independent from which engine is actually used to perform this calculation. Therefore they are all found *outside* of the `Engine` block. In this sense, the AMS input is split up into the driver level input (everything outside of the engine block) and the engine input, which is just a single `Engine` block. This separation makes it easy to perform the same calculation at a different level of theory, by simply switching out the `Engine` block in the input. We could, for example, repeat the same calculation at the DFT-GGA level using the `Band` engine:

```
Engine BAND
  XC
    GGA PBE
  End
EndEngine
```

Engines like `ADF` or `BAND` that have many options and can calculate many properties, consequently also have a large number of possible keywords in their input. In order to have a better structured documentation we have split off the description of the engine inputs into separate *engine specific manuals* (page 250), while this AMS manual only documents the driver level keywords outside of the `Engine` block. All the engine specific options are found in the respective engine's manual, which documents the keywords in its `Engine` block. In general all engines can be used with all tasks in AMS. There are only a few rather obvious restrictions, for example that only engines which can handle periodic systems can be used for the calculation of phonons.

2.1.2 Tasks

The key `Task` is described in more detail in the section *Structure, Reactivity, and Molecular Dynamics* (page 45). The `Task VibrationalAnalysis` is described in more detail in the section *Vibrational Spectroscopy* (page 187) (Mode Scanning, Mode Refinement, Mode Tracking, VG-FC Resonance Raman) and in the section *Vibrationally resolved electronic spectra* (page 224) (VG-FC: Vertical Gradient Franck-Condon).

Below the possible arguments for `Task` are given.

```
Task [GCMC | GeometryOptimization | IRC | MolecularDynamics | NEB | PESExploration | ↵
↵PESScan |
    Replay | SinglePoint | TransitionStateSearch | VibrationalAnalysis]
```

2.1.3 Properties

The block key `Properties` is described in more detail in the section *Gradients, Hessian, Stress tensor, Elasticity* (page 178), in the section *Vibrational Spectroscopy* (page 187), and in the section *Dipole moment, Polarizability, Bond orders* (page 244).

Below the possible `Properties` are summarized.

```
Properties
  BondOrders Yes/No
  Charges Yes/No
  DipoleGradients Yes/No
```

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```

DipoleMoment Yes/No
ElasticTensor Yes/No
GSES Yes/No
Gradients Yes/No
Hessian Yes/No
Molecules Yes/No
NormalModes Yes/No
OrbitalsInfo Yes/No
Other Yes/No
PESPointCharacter Yes/No
Phonons Yes/No
Polarizability Yes/No
Raman Yes/No
SelectedRegionForHessian string
StressTensor Yes/No
VCD Yes/No
VROA Yes/No
End

```

2.1.4 General remarks on input structure and parsing

- Most keys are optional. Defaults values will be used for keys that are not specified in the input
- Keys/blocks can either be *unique* (i.e. they can appear in the input only once) or *non-unique*. (i.e. they can appear multiple times in the input)
- The order in which keys or blocks are specified in the input does not matter. Possible exceptions to this rule are a) the content of non-standard blocks b) some non-unique keys/blocks)
- Comments in the input file start with one of the following characters: #, !, :::

```

# this is a comment
! this is also a comment
:: yet another comment

```

- Empty lines are ignored
- The input parsing is **case insensitive** (except for string values):

```

# this:
UseSymmetry false
# is equivalent to this:
USESMMETRY FALSE

```

- Indentation does not matter and multiple spaces are treaded as a single space (except for string values):

```

# this:
    UseSymmetry    false
# is equivalent to this:
UseSymmetry false

```

- Environment variables in the input will be replaced by their value. We only support simple substitution of variables (optionally surrounded by {}). All other [parameter expansion features of the POSIX shell](https://pubs.opengroup.org/onlinepubs/9699919799/utilities/V3_chap02.html#tag_18_06_02) (e.g. default values) are **not** supported. Expansion of a variable can be prevented by prefixing the leading dollar (\$) with a backslash (\). Note that variables which are not set will expand to an empty string, just like in a shell:

```
File $SOME_DIRECTORY/file.txt
File ${SOME_DIRECTORY}_BACKUP/file.txt
Key \ $WILL_NOT_EXPAND
```

2.1.5 Keys

Key-value pairs have the following structure:

```
KeyName Value
```

Possible types of keys:

bool key The value is a single Boolean (logical) value. The value can be `True` (equivalently `Yes`) or `False` (equivalently `No`). Not specifying any value is equivalent to specifying `True`. Example:

```
KeyName Yes
```

integer key The value is a single integer number. Example:

```
KeyName 3
```

float key The value is a single float number. For scientific notation, the E-notation is used (e.g. -2.5×10^{-3} can be expressed as `-2.5E-3`). The decimal separator should be a dot (`.`), and **not** a comma (`,`). Example:

```
KeyName -2.5E-3
```

Note that fractions (of integers) can also be used:

```
KeyName 1/3 (equivalent to: 0.333333333333...)
```

string key The value is a string, which can include white spaces. Only ASCII characters are allowed. Example:

```
KeyName Lorem ipsum dolor sit amet
```

multiple_choice key The value should be a single word among the list options for that key (the options are listed in the documentation of the key). Example:

```
KeyName SomeOption
```

integer_list key The value is list of integer numbers. Example:

```
KeyName 1 6 0 9 -10
```

Note that one can also specify ranges of integers by specifying the interval and (optionally) the step size separated by colons:

```
KeyName 1:5 (equivalent to: 1 2 3 4 5)
KeyName 2:10:2 (equivalent to: 2 4 6 8 10)
KeyName 20:10:-2 (equivalent to: 20 18 16 14 12 10)
```

Note also that ranges can be freely combined with individual numbers:

```
KeyName 1:5 10 20 (equivalent to: 1 2 3 4 5 10 20)
```

float_list key The value is list of float numbers. The convention for float numbers is the same as for Float keys. Example:

```
KeyName 0.1 1.0E-2 1.3
```

Float lists can also be specified as a range with equidistant points, by specifying the interval's boundaries (inclusive) as well as the number of desired subintervals separated by colons:

```
KeyName 1.0:1.5:5 (equivalent to: 1.0 1.1 1.2 1.3 1.4 1.5)
```

Range specifications can be freely combined with each other and single numbers:

```
KeyName 0.0 1.0:1.5:5 2.0:3.0:10
```

2.1.6 Blocks

Blocks give a hierarchical structure to the input, grouping together related keys (and possibly sub-blocks). In the input, blocks generally span multiple lines, and have the following structure:

```
BlockName
  KeyName1 value1
  KeyName2 value2
  ...
End
```

Headers

For some blocks it is possible (or necessary) to specify a *header* next to the block name:

```
BlockName someHeader
  KeyName1 value1
  KeyName2 value2
  ...
End
```

Compact notation

It is possible to specify multiple key-value pairs of a block on a single line using the following notation:

```
# This:
BlockName KeyName1=value1 KeyName2=value2

# is equivalent to this:
BlockName
  KeyName1 value1
  KeyName2 value2
End
```

Notes on compact notation:

- The compact notation cannot be used for blocks with headers.
- Spaces (blanks) between the key, the equal sign and the value are ignored. However, if a value itself needs to contain spaces (e.g. because it is a list, or a number followed by a unit), the entire value must be put in either single or double quotes:

```
# This is OK:
BlockName Key1=value Key2 = "5.6 [eV]" Key3='5 7 3 2'
# ... and equivalent to:
```

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```

BlockName
  Key1  value
  Key2  5.6 [eV]
  Key3  5 7 3 2
End

# This is NOT OK:
BlockName Key1=value Key2 = 5.6 [eV] Key3=5 7 3 2

```

Non-standard Blocks

A special type of block is the *non-standard block*. These blocks are used for parts of the input that do not follow the usual key-value paradigm.

A notable example of a non-standard block is the `Atoms` block (in which the atomic coordinates and atom types are defined).

2.1.7 Including an external file

You can include an external ASCII file in the input with the `@include` directive:

```

@include FileName.in
@include "file name with spaces.in"

```

The file name should include the path, either absolute or relative to the run-directory. The content of the file is included in the input at the point where the `@include` directive occurs. The `@include` directive may occur any number of times in the input.

The `@include` feature makes it easy to pack your preferred settings in one file and use them in every run with minimum input-typing effort.

2.1.8 Units

Some keys have a default unit associated (not all keys have units). For such keys, the default unit is mentioned in the key documentation. One can specify a different unit within square brackets at the end of the line:

```

KeyName value [unit]

```

For example, assuming the key `EnergyThreshold` has as default unit `Hartree`, then the following definitions are equivalent:

```

# Use defaults unit:
EnergyThreshold 1.0

# use eV as unit:
EnergyThreshold 27.211 [eV]

# use kcal/mol as unit:
EnergyThreshold 627.5 [kcal/mol]

# Hartree is the atomic unit of energy:
EnergyThreshold 1.0 [Hartree]

```

Available units:

- **Energy:** Hartree, Joule, eV, kJ/mol, kcal/mol, cm¹, MHz
- **Forces:** Hartree/Bohr, eV/Bohr, Hartree/Angstrom, eV/Angstrom, kcal/mol/Angstrom, kJ/mol/Angstrom
- **Length:** Bohr, Angstrom, meter
- **Angles:** radian, degree
- **Mass:** el, proton, atomic, kg
- **Pressure:** atm, Pascal, GPa, a.u., bar, kbar
- **Electric field:** V/Angstrom, V/meter, a.u.

2.2 Execution

2.2.1 Shell script

The AMS driver reads its input from standard input, i.e. what is called `STDIN` on Unix-like systems. Technically it is possible to run AMS and type the input file in interactively. This is however highly impractical and most people run AMS from a small shell script that contains the AMS text input and sends it directly to the AMS executable. For example, the content of the file ‘example.run’ could be like:

```
#!/bin/sh

$AMSBIN/ams << EOF

... AMS text input goes here:

Block
  Keyword value
  OtherKeyword value
End

EOF
```

The shell script ‘example.run’ needs to be executable, if it isn’t you will need to make it executable, e.g. `chmod u+x example.run`. The ‘example.run’ file needs to be executed as a shell script, not as input to AMS.

```
./example.run > example.out
```

2.2.2 Interactive input file

As of the 2021.1 version the AMS driver has the concept of an interactive input file. The interactive input file is a second input file, that users may create in the *results directory* (page 18) of an already running job to interact with it. The name of the interactive input file is `interactive.in`. Note that the file does not exist by default, but has to be created by the user wanting to interact with the running AMS job.

In AMS2021.1 the interactive input file may be used to request the graceful and orderly termination of a job.

```
echo "Stop" > ams.results/interactive.in
```

Stop

Type Bool

Default value No

Description Makes the AMS driver stop execution in an ordered manner at the next opportunity. This will not interrupt the execution in the middle of the numerical calculation of a PES point property (e.g. a Hessian).

It is generally preferable to request the termination through the interactive input file over killing a job at the operating system level. This makes sure that the job stops at a logical point and still has time to write intermediate results to disk, making restarting from such jobs easier and more reliable. From the graphical user interface, the stopping can be requested in AMSjobs by selecting the running job and clicking **Job → Request Early Stop** in the menu bar.

As of AMS2021.1, the tasks that can be stopped through the interactive input file are:

- *Molecular dynamics* (page 90) simulations will stop at the next sampling or checkpoint as if the maximum number of steps had been reached.
- *Geometry optimizations* (page 47) will stop after the current iteration and be considered converged. This can be used if a geometry optimization does not make progress anymore, e.g. because the convergence thresholds are set tighter than the noise level of the used engine.
- *Nudged elastic band* (page 75) calculations will stop after the current iteration (i.e. the calculations for all images) is complete.
- *PES scans* (page 68) will interrupt the currently running geometry optimization and skip the optimization for all further PES points.
- *PES explorations* (page 152) will terminate after the currently running expedition. No new explorers will be dispatched, but currently active explorers will be allowed to finish.

Note that the `Stop` keyword in the interactive input file will not interrupt the job in the middle of the numerical calculation of a *PES point property* (page 244), such as a Hessian or stress tensor. It will also never stop a job that is currently running an engine, and will hence not stop an engine that is calculating these properties analytically. It is possible to interrupt the numerical calculation of *PES point properties* (page 244) using the `StopProperties` keyword. We advise users to be careful with this keyword and always combine it with the `Stop` keyword, as it is generally not possible to skip the evaluation of properties, but continue with a task as the AMS driver level. (After all, the driver may need the properties that we interrupt.)

```
echo "Stop" > ams.results/interactive.in  
echo "StopProperties" >> ams.results/interactive.in
```

StopProperties

Type Bool

Default value No

Description Makes the AMS driver stop execution during the evaluation of PES point properties. This may for example be used to interrupt the numerical calculation of a Hessian. Note that this just works at the level of the loops used for the `**numerical**` calculation of the properties, so engines which calculate a property analytically may not be interruptible using this keyword. It is recommended to use this keyword in combination with the generic `Stop` keyword.

As of AMS2021.1 it is not possible to restart the calculation of properties that were interrupted like this. Hence the use of the `StopProperties` keyword is limited.

2.2.3 Running AMS on compute clusters

AMS is parallelized with MPI and can therefore be run in parallel on distributed memory machines, aka compute clusters. See the [installation manual](#) for general documentation on how to set up and run all the programs from the Amsterdam Modeling Suite on compute clusters. In this section we give some more advice that is specific to the AMS driver and its engines.

Normally users use the login node to prepare their jobs and input files somewhere in their home directory, and also want the results of their jobs to end up there. Quite often, compute clusters are set up such that the user's home directory is also mounted on the compute nodes, usually via NFS (Network File System). Before the introduction of the AMS driver it was not recommended to `cd` to the home directory in the submission script and have the compute nodes execute the job directly there. This was simply due to the fact that a lot of file I/O was done on temporary files in the present working directory, which in this case would be on a slow network-mounted file system.

On the other hand, with AMS, switching to the home directory is the preferred way of running on a cluster where the home directory is mounted on the compute nodes. Running in the home directory mounted over NFS does not come with a performance penalty for AMS, but has many advantages. This is because AMS and its engines are already built under the assumption that access to this directory is slow. Basically there are three directories that are used by the AMS driver and its engines:

1. The **starting directory**, i.e. the present working directory at the time the AMS driver is started. This folder is generally read-only for AMS, except for creating the results directory there at the beginning of a calculation. Note that all relative paths in the AMS input, e.g. for loading results from previous calculations, are relative to the starting directory. The starting directory is assumed to be on a slow filesystem, but since data is normally only read once from there in the beginning of a calculation, this is in practice not a problem.
2. The **results directory**, where the results of a calculation as well as important intermediate steps (e.g. restart files) are collected. It also contains the log file which can be used to monitor a running calculations. The results directory is assumed to be on a slow filesystem, so AMS and its engines will be very careful not to do much disk I/O there. Generally something is only written to the results directory when AMS is sure that it should remain on disk when the calculation finishes. The results directory can also contain some intermediate restart files, so the contents of the result directory should be all that is needed in case the calculation crashes or is killed before it finishes normally.
3. The **scratch directory**, the location of which is set with the `$SCM_TMPDIR` environment variable, see also the [installation manual](#). This directory should be put on a fast disk, e.g. an SSD in the compute node, as it will be used to store temporary results on disk. Users do not really need to care or know about the temporary files in the scratch directory. Normally, any files and directories created in the scratch directory are cleaned up at the end of the calculation. In case of errors, AMS tries to copy anything useful (e.g. the text output of all the different ranks) to the results directory in order to make finding the problem easier. However, for some kinds of crashes (or if the `SIGKILL` signal is sent to AMS), the cleanup of the scratch directory might not be performed, in which case users might want to manually check or remove the `amstmp_*` folders in the scratch directory.

With this setup there is no performance penalty for running directly on a network mounted home directory: Results will just be put there immediately, instead of being copied there at the end of a calculation.

Normally all batch systems provide an environment variable that is set to the directory from which the job was submitted, which is then where one should `cd` in the run script:

```
#!/bin/sh

if [ -z "$PBS_O_WORKDIR" ]; then
  # PBS batch system
  cd "$PBS_O_WORKDIR"
elif [ -z "$SLURM_SUBMIT_DIR" ]; then
  # Slurm batch system
  cd "$SLURM_SUBMIT_DIR"
elif [ -z "..." ]; then
  # add other batch systems as necessary ...
```

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```
cd "..."  
fi  
export AMS_JOBNAME=myJob  
  
$AMSBIN/ams << EOF  
  
# Normal AMS text input, but with all paths  
# relative to where the job was submitted from, e.g.:  
LoadSystem previousJob.results/ams.rkf  
  
EOF
```

With this runsript the AMS driver would make a `myJob.results` folder in the directory where the job was submitted from, and there is no need to copy results around manually in the run script. Furthermore this runsript always produces exactly the same files in the same locations, no matter if it is run interactively or submitted to a compute node through the batch system. Furthermore all paths in the input file can be specified relative to the location from where the runsript is submitted (normally the folder in which the runsript is located). This removes the need to copy or specify absolute paths to previous results, e.g. when restarting calculations. Finally, files useful for monitoring the running calculation are also conveniently there and not hidden somewhere on the compute node.

2.3 Output

AMS produces two ASCII files: standard output and the `ams.log` file, and produces several binary output data files. The `ams.log` file is a very concise summary of the calculation's progress during the run. The binary output data files contain job characteristics and computational results produced by AMS and the Engine. Part of what is written to the binary output files is also written in a human readable form to standard output.

2.3.1 Results directory

Note that AMS does not put any of its binary output files and the `ams.log` file into the present working directory, as virtually all of the standalone programs in the suite did. Instead AMS creates a `*.results` directory, which collects all result file associated with a job. Here `*` is replaced by the jobname, which is set with the `AMS_JOBNAME` environment variable:

```
AMS_JOBNAME=methane $AMSBIN/ams << EOF  
  
... see Input example before ...  
  
EOF
```

This would put all results related to our geometry optimization of methane into the newly created folder `methane.results`. (The default name of the results folder is `ams.results` if `AMS_JOBNAME` is not set, see the *environment variables* (page 20) section of this manual for documentation of all environment variables used by AMS.) In this way users can easily run multiple jobs in the same directory without danger of clashing output files, which was a common problem before the introduction of AMS. This new setup is also more consistent with the graphical user interface, which already collected all files associated with a specific job into a dedicated results directory. Note that AMS will by default **not overwrite** results directories if a job is rerun or another job is run with the same jobname.

2.3.2 Logfile `ams.log`

Inside of the results directory users will always find the logfile `ams.log`, which is written during a running calculation and can be used to monitor its progress.

The logfile `ams.log` is generated during the calculation and flushed after (almost) each message that is sent to it by the program. Consequently, the user can inspect it and see what is going on without being delayed by potentially large system I/O buffers. Each message contains date and time of the message plus additional info.

Be alert on error messages. Take them seriously: inspect the standard output carefully and try to understand what has gone wrong. Be also alert to warnings. They are not necessarily fatal but you should understand what they are about before being satisfied with the results of the calculation. Do not ignore them just because the program has not aborted: in some cases the program may not be able to determine whether or not you really want to do what appears to be wrong or suspicious. If you believe that the program displays erratic behavior, then the standard output file may contain more detailed information. Therefore, in such case save the complete standard output file, together with the logfile `ams.log`, in case we need these files for further analysis.

2.3.3 Binary output files

The results directory contains binary result files in the KF format, which can be opened and inspected with the KFBrowser GUI component. KF stands for Keyed File: KF files are keyword oriented, which makes them easy to process by simple procedures. KF files are Direct Access binary files.

- The main `ams.rkf` written by the AMS driver. It contains high level information about the trajectory that the AMS driver took over the potential energy surface. For a geometry optimization it would for example contains the history of how the systems geometry changed during the optimization as well as the final optimized geometry. For a molecular dynamics simulation it would contain the full trajectory. The format in which this information is written is independent from which engine was used for a calculation.
- The engine specific main binary output file written by the engine (and partly by the AMS driver). This file is kept for only one special point, e.g. the final geometry in a geometry optimization. The ADF engine writes `adf.rkf` (instead of `TAPE21` in older versions). The BAND engine writes `band.rkf` (instead of `RUNKF` in older versions). The DFTB engine writes `dftb.rkf`. If a property, like vibrational modes, is tied to this special point on the potential energy surface, it is stored in this file. Also all engine specific properties are written to the main binary output file, like orbitals in case of a quantum mechanical engine.

Table 2.1: Engine specific main binary output file

Engine	main file
ADF	<code>adf.rkf</code>
BAND	<code>band.rkf</code>
DFTB	<code>dftb.rkf</code>
ForceField	<code>forcefield.rkf</code>
MOPAC	<code>mopac.rkf</code>
ReaxFF	<code>reaxff.rkf</code>
External	<code>external.rkf</code>

- Additionally there might be an engine specific binary output file for every point on the potential energy surface that was visited during the calculation. Like the engine specific main binary output file they contain information tied to a specific point on the potential energy surface. These engine output files all have the extension `.rkf`, but their filename is usually somehow descriptive of the point on the PES that they correspond to. Note that one does not always get an engine output file for every PES point that was visited during the calculation. For most applications this would just be too much data.
- Other engine specific binary (and ASCII) output files written by the engine.

Having multiple different binary output files could be confusing for people that are used to the single result file that was written by the standalone programs in ADF<=2017. After all, it brings up the question in which file the desired property is stored. The general rule is: If the property is tied to a particular point on the potential energy surface, it is stored in the engine output file belonging to that particular point. This includes the Hessian, stress tensor, elastic tensor, normal modes of vibration, phonons, Raman intensities and other vibrational properties. If the information depends on the entire trajectory over the PES, it is found in the main `ams.rkf` written by the AMS driver.

2.3.4 Standard output

The standard output file contains in a human readable form part of the job characteristics and computational results produced by AMS and the Engine.

2.3.5 Optimized geometry in xyz format

In case of *Geometry Optimizations* (page 47), the optimized geometry is saved as an *extended XYZ file* (page 477) in the results directory with the name `output.xyz`.

Note that the optimized geometry is also stored in the binary file `ams.rkf` and is printed to the standard output.

2.3.6 AMS environment variables

The behavior of AMS related to the output can be modified through a number of environment variables.

AMS_JOBNAME Sets the name of a job. This name is used to determine the name of the results folder AMS creates, which is `$AMS_JOBNAME.results` or `ams.results` if this environment variable is not set.

AMS_RESULTSDIR If this environment variable is set, instead of creating a new results folder, AMS will use the set directory as the results folder. Note that the directory set here will *not* be created by AMS and therefore has to exist before starting AMS. Note that this environment variable can be used to prevent AMS from creating result folders, by setting `AMS_RESULTSDIR=.` This reproduces the pre-AMS behavior of putting all result files into the directory from which a job is started.

AMS_SWITCH_LOGFILE_AND_STDOUT If this environment variable is set, AMS will redirect what is normally printed on standard output to a file (`ams.out`) in the results directory. Instead the contents of the log file (`ams.log`) will be printed to standard output while a job is running, allowing users to easily monitor the jobs progress. Note that the log file will still be created normally as if this environment variable was not set. This environment variable is just a convenience feature for users that would always redirect their output into a file and then use `tail -f` on the log file to monitor the running calculation.

This is an example run-script using the `AMS_SWITCH_LOGFILE_AND_STDOUT` and `AMS_JOBNAME` environment variables:

```
#!/bin/sh

# By setting AMS_SWITCH_LOGFILE_AND_STDOUT, the (more compact)
# logfile will be printed to standard output while the full
# text output of the calculation is redirected to the file
# ams.out in the ams results folder

export AMS_SWITCH_LOGFILE_AND_STDOUT=true

# By default ams creates a folder 'ams.results' and puts the
# results of the calculation there. If we set AMS_JOBNAME, the
# results folder will instead be called $AMS_JOBNAME.results
```

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```
# (in this case, 'H2_optimization.results')
AMS_JOBNAME=H2_optimization $AMSBIN/ams <<eor
  System
    Atoms
      H 0 0 0
      H 0 0 1
    End
  End
  Task GeometryOptimization
  Engine DFTB
    Model GFN1-xTB
  EndEngine
eor
```

2.4 Driver level parallelism

See also:

See also the [GUI tutorial](#) on the parallel scalability of the calculation of elastic tensors.

AMS is a parallel program using MPI for efficient execution on distributed memory machines, aka compute clusters. For most jobs, the AMS driver part of a calculation is computationally not particularly costly and most of the execution time is spent inside of the *compute engines* (page 250). Therefore the main parallelization of AMS is inside of the engines, making sure that a good performance is obtained for *tasks* (page 45) such as *molecular dynamics* (page 90) or *geometry optimizations* (page 47), which consist of a series of interdependent engine invocations: We need to have completed step n before we can continue with step $n + 1$.

However, not all workloads are of this sequentially dependent type. Some jobs have a lot of independent work, that can be done in parallel. This kind of trivial parallelizability can be exploited at the AMS driver level: Instead of having all cores collaborate on a single PES point and then doing all needed PES points sequentially, we can just distribute the available PES points over the all the available cores. Normally this leads to a better parallel scaling than the default parallelization inside of the engines: Parallelizing the engines is relatively complicated and often requires a lot of communication between cores. Parallelizing on the driver level on the other hand is very easy, and often the only communication required is at the very end of the calculation, when results are collected.

Note that it is perfectly possible to combine both the in-engine parallelization and the driver level parallelism: At the driver level we could split our e.g. in total 32 cores into 4 groups of 8 cores, and then have each group of 8 use the in-engine parallelization to collaborate on a specific calculation. This is especially useful if the total number of cores is larger than then number of independent calculations we have to do. It might also be that we have a very large number of calculations to do, but not enough memory to let every core work alone on its own calculation, as would be ideal from a parallel scaling point of view.

Because of the two levels of parallelism – both at the driver and the engine level – we call this setup **double parallelization**.

Starting with the AMS2019.3 release, driver level parallelism is used and configured automatically. That means that the AMS driver will automatically parallelize at the driver level when it is possible and considered advantageous. As such it should normally not be necessary for users to explicitly configure the driver level parallelism.

Driver level parallelism can be used for the calculation of the *PES point properties* (page 178) which are derivatives, if these need to be done numerically:

- Numerical calculation of *forces / nuclear gradients* (page 179). With a double sided derivative this requires $6 \times n_{\text{atoms}}$ independent calculations on geometries with one atom displaced along a cartesian coordinate.

- Numerical calculation of the *stress tensor* (page 183) for periodic systems. This requires up to 12 calculations for a double sided derivative along the 6 strain directions, but might require less in case some of the strains are symmetry equivalent.
- Numerical calculation of the *Hessian* (page 180) and normal modes of vibration. This is currently only supported for engines that calculate nuclear gradients analytically and done by numerically differentiating this first (analytic) derivative. As such it requires $6 \times n_{\text{atoms}}$ independent calculations on geometries with one atom displaced along a cartesian coordinate.
- Numerical calculation of the *elastic tensor* (page 184). This requires 84 independent geometry optimizations on systems with differently strained lattices, with each optimization having a variable number of steps.
- Numerical calculation of *phonons* (page 213). This requires at most $6 \times n_{\text{atoms}}$ displacements, but might require less in case some of the displacements are symmetry equivalent. Note that the displacements are done in a super cell system, which for many engines will increase the memory requirements, but also improve the in-engine parallel scalability.
- The forward and backward displacements along normal modes for the *Mode Scanning* (page 195), *Mode Refinement* (page 196), and *Mode Tracking* (page 199).

There are also tasks using driver level parallelism, e.g. *Nudged Elastic Band* (page 75), for which the calculations of all the images is trivially parallel.

Details of the driver level parallelism, i.e. how much to parallelize at the driver level, are generally configured for the above mentioned cases on an individual basis, because one might want a different grouping strategy for each case. For each case there is a separate `Parallel` block somewhere in the input (e.g. `ElasticTensor%Parallel` for the calculation of the elastic tensor), which has the following keywords:

```
Parallel
  nGroups integer
  nCoresPerGroup integer
  nNodesPerGroup integer
End
```

Note that only one of them should be specified in the input, depending of course on what is the desired strategy for parallelization.

nGroups n Splits all cores evenly into *n* groups. We recommend choosing *n* such that it divides the total number of cores without a remainder.

nCoresPerGroup n Each group consists of *n* cores. As such `nCoresPerGroup 1` results in the maximum possible parallelism at the driver level. We recommend choosing *n* such that it divides the total number of cores without a remainder.

nNodesPerGroup n Makes groups from all cores within *n* nodes, e.g. `nNodesPerGroup 1` would make every cluster node into a separate group. Note that this option should *only be used on homogeneous compute clusters*, where all used nodes have the same number of cores. Otherwise cores from different nodes will be grouped together in very surprising and unintended ways, probably resulting in suboptimal performance.

The optimal grouping strategy and number of groups depends on the total number of cores used in the calculation, the amount of independent tasks to be done in parallel, as well as the parallel scalability of the engine itself. In practice it can be a bit tricky, which is why the grouping strategy is determined automatically since AMS2019.3.

However, sometimes it can be useful to configure the groups manually. Suppose, as an example, that we want to calculate the elastic properties of a bulk material on a 32 core machine. The calculation of the *elastic tensor* (page 184) should be done on a relaxed geometry, including relaxed lattice degrees of freedom. We therefore first perform a geometry optimization, before calculating the elastic tensor. In AMS this can easily be done with the following input:

```
Task GeometryOptimization
```

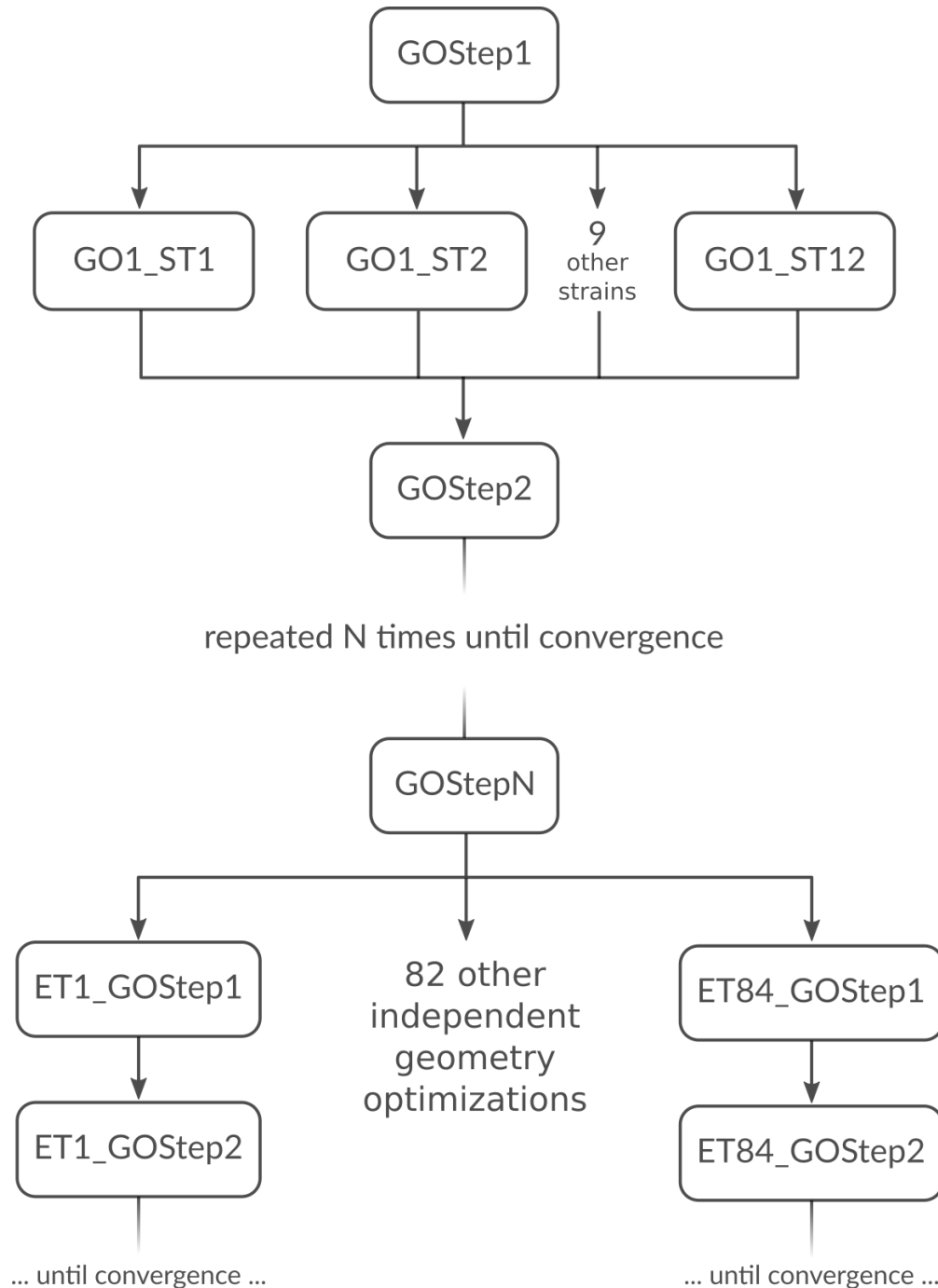
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```
GeometryOptimization
  OptimizeLattice True
End

Properties
  ElasticTensor True
End
```

But what is the most optimal parallel setup for this calculation? First we recognize that performing a lattice optimization requires the calculation of the *stress tensor* (page 183) at every step of the optimization. Assuming that our bulk system does not have any symmetries AMS can exploit, the numerical calculation of the stress tensor (assuming the engine can not calculate it analytically) would require 12 independent strained calculations for every step in the geometry optimization. Once the geometry optimization is converged, we have to perform 84 independent geometry optimizations to determine the elements of the elastic tensor. In summary, the graph of dependencies between all these tasks looks like this:



How do we best parallelize this? For the main steps, e.g. `GOSTep1` there is no question: We have nothing to do in parallel and all 32 cores work on it together to finish it as quickly as possible. For the numerical calculation of the stress tensor we have 12 tasks that can be done in parallel by the 32 cores in our machine. Now 12 obviously does not divide 32 without a remainder, so there is no way to split into equally sized groups and do all 12 strains in parallel. The greatest common divisor of 12 and 32 is 4, so it's probably best to split into 4 groups of 8 cores each. This is done with `nGroups 4`. Each group would then do 3 of the 12 strained calculations sequentially, using the in-engine parallelization to speed up the individual calculations. Once the stress tensor is computed in this way all groups merge and all 32 cores work together on `GOSTep2`. This splitting and merging now continues until the geometry optimization is converged. For the elastic tensor we now have 84 tasks to perform in parallel, where each task is a completely separate geometry optimization (without optimizing the lattice) of a strained system. 84 tasks is more than double the number of cores we have. In this

case it is probably not too bad to just run as parallel as possible at the driver level and make 32 “groups” of just one core to throw the 84 tasks at. This is easily done by setting `nCoresPerGroup 1` in the `ElasticTensor` block. Putting everything together we should add the following to our input file in order to optimally utilize our machine for this example calculation:

```
NumericalDifferentiation
  Parallel
    nGroups 4
  End
End

ElasticTensor
  Parallel
    nCoresPerGroup 1
  End
End
```

2.5 Python interface

There is a complete Python interface to AMS, which allows users to set up and run arbitrary AMS jobs, and to conveniently analyze the calculation results directly from Python. In this way AMS jobs can be automatized and complex multi-stage workflows implemented.

The scripting framework is called **PLAMS** as in “Python Library for Automating Molecular Simulation”, which conveniently can also be read as “Python Layer for AMS”. It is documented in a separate manual:

- [PLAMS introduction](#)
- [Running AMS through PLAMS](#)

2.6 Pipe interface

AMS can interact with other programs using a *custom communication protocol* (page 25). This enables two independent processes to communicate over a pair of data pipes (FIFOs), exchanging data in a highly efficient manner. One of the processes is the “pipe master”, driving the calculation and sending the atoms, coordinates etc. to the other process to perform calculations. The other process is the “pipe worker”, receiving requests from the master, performing the requested calculations and returning the results such as energies and gradients.

For technical details on the AMSPipe protocol see:

2.6.1 AMSPipe protocol specification

The AMSPipe protocol is a remote procedure call protocol used for communication between two processes on the same computer. One of these processes is the “pipe master”, submitting geometries and requests for calculations and receiving the results. The other process is the “pipe worker”, which listens for calls from the master, executes the requested calculations and returns their results.

Communication takes place over a pair of pipes, a “call pipe” (master to worker) and a “reply pipe” (worker to master). Each pipe carries a sequence of messages, which are processed in order. Each message is an associative object (like a JSON object or a Python dict) containing a single item. The key of this item denotes the name of the message, while the value of this item is another object containing the payload.

Each message sent over the call pipe constitutes a method call. The name of the message is equal to the name of the method being called, while the payload object contains any arguments. For methods without arguments, the payload is an empty object.

Once the worker receives a call message, it will execute the specified method and potentially write a sequence of zero or more messages to the reply pipe, containing the results of the calculation. After the execution of the method is completed, the worker will write a “return” messages to the reply pipe, denoting the success or failure of the method call.

Any method whose name starts with “Set” doesn’t send a “return” message. Instead, errors encountered during the execution of a Set method are buffered by the worker to be returned the next time a “return” message is generated. While an error is buffered, any further method calls are ignored by the worker and are not executed. Once a non-Set call is seen by the worker, such a call will also be discarded without being executed, but a “return” message will be immediately generated with the buffered error data. The buffered error will then be cleared and normal processing of calls resumes.

As a special case, the “Exit” method may be called at any time and will be immediately executed by the worker, terminating the protocol session. The “Exit” method never returns a “return” message, discarding any potentially buffered error.

All values are always in atomic units: Hartree for energies, Bohr for distances, Hartree/Bohr for gradients etc.

Low-level message encoding

All messages are encoded using Universal Binary JSON. AMSPipe implementations MAY encode messages using the UBJSON optimized container format (with explicit length and/or strong typing). Implementations MUST support decoding UBJSON containers whether or not they’re written using optimized format.

UBJSON arrays in messages MUST NOT contain other arrays or objects. Multi-dimensional arrays MUST be flattened on encoding (and unflattened on decoding as necessary). Flattening SHOULD preserve the original order of elements in memory. All arrays MUST be accompanied by an additional integer array holding the original dimensions before flattening. The name of this auxiliary array is equal to the name of the main array with a `_dim_` suffix. The dimensions are written in Fortran (column-major) order, so that the first value in the `_dim_` array corresponds to the index that changes the fastest when iterating over consecutive elements of the flattened array.

Arrays also MUST NOT contain elements of incompatible types. The elements of an array MUST be either all integers, all real numbers, all Boolean, or all strings. UBJSON type “char” is equivalent to a UBJSON “string” of length 1 (elements of type “char” and “string” MAY thus be mixed in an array). An empty array is equivalent to an array that is not present at all.

When sending messages over stream transport mechanisms (such as UNIX pipes), each message MUST be prefixed with a 32-bit native endian integer length.

Return messages and error handling

The “return” message consists of the following fields:

- “status” (integer): Zero for success or one of the error codes listed below.
- “method” (string, optional): Name of the method in which the error occurred.
- “argument” (string, optional): Name of the argument in error.
- “message” (string, optional): Human-readable error message.

The “status” field can have one of the following values:

0: success No error, method executed successfully.

1: decode_error Message could not be decoded correctly (invalid UBJSON encoding or a violation of one of the constraints above).

2: logic_error Programmer error, such as methods called in an incorrect sequence or with an invalid worker state.

- 3: runtime_error** An error occurred during the execution of a method (outside of the AMSPipe protocol).
- 4: unknown_version** (Only returned from “Hello”.) Requested protocol version is not supported by the worker.
- 5: unknown_method** A method of the requested name is not supported by the worker.
- 6: unknown_argument** The argument in “argument” is not known to the worker and couldn’t be processed. If multiple arguments to given single call are unknown, “argument” will be set to the one at the lowest nesting depth (if an argument contains nested objects). If multiple fields at the same nesting depth are unknown, the first one in ASCII sort order will be returned.
- 7: invalid_argument** An argument doesn’t have the correct type or dimensions, or it has an invalid value.

Methods

Hello(version)

- “version” (integer):

Attempt to activate a given version of the AMSPipe protocol. Only version 1 is defined at the moment.

Other methods (with the exception of “Hello” and “Exit”) MUST NOT be called until a Hello has completed successfully. Pipe masters SHOULD attempt a Hello with the highest supported protocol version and iterate downwards if an unknown_version error is returned. Once a Hello has succeeded, it MUST NOT be called again during the lifetime of a pipe session.

Exit()

Terminate the worker and disconnect both pipes. This method never returns.

The worker MAY also discard any remembered calculations.

SetCoords(coords)

- “coords” (real(3,:)):

Replace the Cartesian coordinates in the current chemical system. The number of atoms must match.

SetLattice(vectors)

- “vectors” (real(:,,:)):

Replace the lattice matrix of the current chemical system. If “vectors” is absent or of dimensions (0,0), make the system non-periodic.

SetSystem(atomSymbols, coords, totalCharge)

- “atomSymbols” (string(:)):
- “coords” (real(3,:)):
- “totalCharge” (real):

Define a new chemical system.

Solve(request, keepResults, prevTitle)

- **“request” (object):**
 - “title” (string): Unique string key identifying this calculation.
 - “quiet” (bool): If true, the worker SHOULD keep any standard output from the calculation to a minimum.
 - “gradients” (bool): Calculate gradients on atoms.
 - “stressTensor” (bool): Calculate the stress tensor.
 - “elasticTensor” (bool):
 - “hessian” (bool):
 - “dipoleMoment” (bool):
 - “dipoleGradients” (bool):
- “keepResults” (bool, default false): Remember worker state for future restart.
- “prevTitle” (string, optional): Title of a previously stored calculation to restart from.

Run a single point calculation on the current chemical system and return a “results” object if successful. If the calculation fails with a runtime error, a “results” object MAY still be returned (possibly with just some of the requested properties).

All Boolean fields in “request” default to false if not present. All non-Boolean fields in “request” except for “title” are optional and their default values are worker-dependent. The master SHOULD NOT explicitly set any Boolean fields in “request” to False. The worker MAY raise an unknown argument error if an unknown Boolean is set to False. The worker SHOULD raise an unknown argument error as usual if an unknown Boolean is set to True or if an unknown non-Boolean is set. Workers SHOULD raise these errors before performing any time-consuming calculations so that the master can efficiently retry the call.

If “keepResults” is not specified or set to false, the worker will discard all data from the calculation after returning a “results” object. If “keepResults” is set to true, the worker will remember any internal state related to the calculation. This internal state can later be reused for restart by passing the “title” of the stored calculation as “prevTitle”. The pipe master SHOULD call DeleteResults to discard the stored state as soon as it is no longer needed.

A “results” object consists of the following fields. Workers MAY include additional fields not listed here. A master MUST NOT signal an error due to any fields it does not expect or understand.

- **“results” (object):**
 - “messages” (string(:)): Runtime error or warning messages generated by the calculation.
 - “energy” (real):
 - “gradients” (real(3,:)):
 - “stressTensor” (real(:,,:)):
 - “elasticTensor” (real(:,,:)):
 - “hessian” (real(:,,:)):

- “dipoleMoment” (real(,:)):
- “dipoleGradients” (real(,:)):
- “charges” (real(:)):

DeleteResults(title)

- “title” (string): Title of a previously remembered calculation.

Discard any worker state corresponding to a previously remembered calculation.

Forward and backward compatibility considerations

The AMSPipe protocol is designed to support combining new masters with old workers and vice versa. Major, incompatible changes in the protocol will be handled by increasing the protocol version number. Negotiating a suitable protocol version is then handled by call(s) to Hello at the beginning of a pipe session.

The following requirements are in place to ensure that the protocol stays extensible within a single protocol version:

- Workers MUST raise an `unknown_method` error on any call to a method they don’t implement. If the method name starts with Set, such an error will be buffered to be returned later. If the method name doesn’t start with Set, a “return” message will be generated immediately.
- Workers MUST raise `unknown_argument` errors any time they encounter an argument to a known method that they don’t know how to handle. The master SHOULD then retry the call without such an argument or choose an alternative sequence of calls if possible.
- The master SHOULD ignore unexpected messages of unsupported type on the reply pipe.

Namely, the following changes are permitted without increasing the protocol version number:

- Adding new methods to the protocol.
- Adding new optional arguments to existing methods.
- Adding new fields to returned objects.
- Adding new reply message types.

2.6.2 AMS as a pipe master

The AMS driver can play the role of a pipe master, allowing users to combine the features of the AMS driver with potentials implemented in external programs. Unlike a *traditional external engine* (page 254), the overhead introduced by the pipe interface is entirely negligible, because the external program is only started once at the beginning of the run and all communication is handled by an efficient binary protocol instead of text files. This mode is enabled by using `Engine Pipe` in the input for the master.

```
Engine Pipe
  WorkerCommand /path/to/pipe/worker
EndEngine
```

WorkerCommand

Type String

Description The command to execute to run the external worker. The command is executed in a subdirectory of the results directory.

All calculations requested by the driver will then be forwarded over the pipe to the worker for processing.

Note: AMS currently must be run in serial (NSCM=1) when serving as a pipe master.

A Python module implementing the worker side of the AMSPipe protocol is available in `scm.ampipe`. To facilitate interfacing with various existing computational engines, this module provides the `ASEPipeWorker` class. This class can wrap any ASE calculator object and make it serve as a pipe worker.

```
calculator = ase.calculators.lj.LennardJones()
# calculator.parameters = ...

engine = scm.ampipe.ASEPipeWorker(calculator=calculator)
engine.run()
```

See also:

Example: ASE calculator as a pipe worker (page 474)

2.6.3 AMS as a pipe worker

AMS can also serve as a pipe worker, allowing external drivers to take advantage of its *engines* (page 250). This mode is enabled by using `Task Pipe`. No *Geometry, System definition* (page 31) is required on the input because the system will be supplied by the pipe master.

Hint: For most users it will easiest to use this functionality through the new `AMSWorker` class in the `PLAMS` library. This class hides all the details of the underlying AMSPipe protocol and provides users an easy way to get very fast access to energies, gradients and other properties from any of the engines in the AMS driver. See the [respective page](#) in the PLAMS manual for details.

See also:

Example: AMS as a pipe worker (page 476)

Additionally AMS can also be driven through the `FlexMD` library using `AMSPipeForceJob`:

```
forcejob = AMSPipeForceJob(mdmol)
forcejob.settings.engine = 'ReaxFF'
forcejob.settings.engineSettings = { 'ForceField': 'Glycine.ff' }
```


GEOMETRY, SYSTEM DEFINITION

The definition of the system to simulate, i.e. the positions and types of the nuclei, the total charge, and potentially lattice vectors, is enclosed in the `System` block:

```
System header
  Atoms header # Non-standard block. See details.
  ...
End
  Lattice header # Non-standard block. See details.
  ...
End
  FractionalCoords Yes/No
  AllowCloseAtoms Yes/No
  GeometryFile string
  Symmetrize Yes/No
  LatticeStrain float_list
  SuperCell integer_list
  Charge float
  BondOrders # Non-standard block. See details.
  ...
End
End
```

3.1 Geometry, Lattice

The geometry of the system is specified with the `Atoms` and `Lattice` blocks.

System

Type Block

Recurring True

Description Specification of the chemical system. For some applications more than one system may be present in the input. In this case, all systems except one must have a non-empty string ID specified after the `System` keyword. The system without an ID is considered the main one.

Atoms

Type Non-standard block

Description The atom types and coordinates. Unit can be specified in the header. Default unit is Angstrom.

Lattice

Type Non-standard block

Description Up to three lattice vectors. Unit can be specified in the header. Default unit is Angstrom.

FractionalCoords

Type Bool

Default value No

Description Whether the atomic coordinates in the Atoms block are given in fractional coordinates of the lattice vectors. Requires the presence of the Lattice block.

The `Atoms` block contains one line per atoms, similar to the lines found in an `.xyz` file: First the name of the element, then three real numbers representing the coordinates of that atom in Angstrom. The following `Atoms` block shows how one would define a water molecule:

```
System
  Atoms
    O  0.0  0.0  0.59372
    H  0.0  0.76544 -0.00836
    H  0.0 -0.76544 -0.00836
  End
End
```

Note that it is possible to specify a different unit of length in the header of the block (that is in the line after the keyword opening the block) by putting the name of the unit in [and] brackets. So the same water molecule could also be specified as follows:

```
System
  Atoms [Bohr]
    O  0.0  0.0  1.12197
    H  0.0  1.44647 -0.01580
    H  0.0 -1.44647 -0.01580
  End
End
```

It is also possible to specify the input geometry as a Z-Matrix, by putting the string `Z-Matrix` in the header of the block:

```
System
  Atoms Z-Matrix
    C
    H  1  1.089000
    H  1  1.089000  2  109.4710
    H  1  1.089000  2  109.4710  3  120.0000
    H  1  1.089000  2  109.4710  3 -120.0000
  End
End
```

Periodic systems require the specification of 1 (for chains), 2 (for slabs) or 3 (for bulk) lattice vectors in addition to the nuclear coordinates. Every lattice vector is specified on a separate line of three numbers, representing the vectors x,y and z-component. Note that for chain systems, the single lattice vector **must** point along the x-axis, while for slab systems the two lattice vectors **must** be in the xy-plane. Consider the following input for graphene:

```
System
  Atoms
    C  0.0  0.0  0.0
    C  1.23  0.71014  0.0
```

(continues on next page)

(continued from previous page)

```

End
Lattice
  2.46  0.0    0.0
  1.23  2.13042 0.0
End
End

```

As with the `Atoms` block, the length unit in which the lattice vectors are given can be changed by specifying the desired unit in the header of the block (enclosed in `[]`). It is also possible to define a system given the fractional coordinates of the atoms using the `FractionalCoords` keyword. The numbers in the `Atoms` block are then interpreted as fractional coordinates according to the lattice vectors in the `Lattice` block. Note that for chain and slab systems, the coordinates perpendicular to the periodic direction (z and y for chains, z for slabs) are of course still in Angstrom (or alternatively the unit set in the header of the `Atoms` block). Using the `FractionalCoords` keyword we could specify the geometry of table salt (NaCl) as follows:

```

System
  Lattice
    0.0  2.75  2.75
    2.75 0.0  2.75
    2.75 2.75 0.0
  End
  FractionalCoords True
  Atoms
    Na  0.0  0.0  0.0
    Cl  0.5  0.5  0.5
  End
End

```

Instead of specifying the geometry of the system directly in the input file it can also be read from an external file.

System

GeometryFile

Type String

Description Read the geometry from a file (instead of from `Atoms` and `Lattice` blocks). Supported formats: `.xyz`

Note that the `GeometryFile` key replaces both the `Atoms` and the `Lattice` blocks in the input. So if you specify the `GeometryFile` keyword in the input, the `Atoms` and `Lattice` blocks must not appear there. At the moment only the *extended XYZ file format* (page 477) is supported.

3.1.1 Modifying the geometry

Finally there are a number of keywords that *modify* the system geometry:

System

Symmetrize

Type Bool

Default value No

Description Whether to symmetrize the input structure. This might also rototranslate the structure into a standard orientation. This will symmetrize the atomic coordinates to machine precision. Useful if the system is almost symmetric or to rototranslate a symmetric molecule into a standard orientation.

LatticeStrain**Type** Float List**Description** Deform the input system by the specified strain. The strain elements are in Voigt notation, so one should specify 6 numbers for 3D periodic system (order: xx,yy,zz,yz,xz,xy), 3 numbers for 2D periodic systems (order: xx,yy,xy) or 1 number for 1D periodic systems.**SuperCell****Type** Integer List**Description** Create a supercell of the input system (only possible for periodic systems). The integer numbers represent the diagonal elements of the supercell transformation; you should specify as many numbers as lattice vectors (i.e. 1 number for 1D, 2 numbers for 2D and 3 numbers for 3D periodic systems).**SuperCellTrafo****Type** Integer List**Description** Create a supercell of the input system (only possible for periodic systems) $\vec{a}'_i = \sum_j T_{ij} \vec{a}_j$. The integer numbers represent the supercell transformation T_{ij} : 1 number for 1D PBC, 4 numbers for 2D PBC corresponding to a 2x2 matrix (order: (1,1),(1,2),(2,1),(2,2)) and 9 numbers for 3D PBC corresponding to a 3x3 matrix (order: (1,1),(1,2),(1,3),(2,1),(2,2),(2,3),(3,1),(3,2),(3,3)).**PerturbCoordinates****Type** Float**Default value** 0.0**Unit** Angstrom**Description** Perturb the atomic coordinates by adding random numbers between [-PerturbCoordinates,PerturbCoordinates] to each Cartesian component. This can be useful if you want to break the symmetry of your system (e.g. for a geometry optimization).**PerturbLattice****Type** Float**Default value** 0.0**Description** Perturb the lattice vectors by applying random strain with matrix elements between [-PerturbLattice,PerturbLattice]. This can be useful if you want to deviate from an ideal symmetric geometry, for example if you look for a phase change due to high pressure.**MapAtomsToUnitCell****Type** Bool**Default value** No**Description** For periodic systems the atoms will be moved to the central cell.

These modifications are applied immediately after the system block is read. To the rest of AMS (and the input) it looks exactly as if the modified system was specified explicitly in the `System` block input. That means that the `SuperCell` keyword is not easily usable with input options that require the specification of atom indices, e.g. the *constraints* (page 52) block. Note that the randomization of the coordinates is applied after a potential supercell creation.

3.2 Symmetry

Symmetry can be used in AMS optimizations of molecules and of periodic structures.

In case of molecules at the start of an AMS calculation one can symmetrize an almost symmetric structure. In the *Appendix Symmetry* (page 481) one can find molecular orientation requirements that AMS needs such that AMS can use the (sub)symmetry of a molecule. If the system is symmetrized (and no symmetry is given in the System block key) the molecular structure is rotranslated into this standard orientation. In the *Appendix Symmetry* (page 480) one can also find Schönflies symbols for molecular point groups and symmetry labels that are used in AMS for molecules to label normal modes.

```
System header
  Symmetrize Yes/No
  Symmetry [...]
End
```

```
Symmetry
  SymmetrizeTolerance float
  Tolerance float
End
```

```
UseSymmetry Yes/No
```

System

Symmetrize

Type Bool

Default value No

Description Whether to symmetrize the input structure. This might also rototranslate the structure into a standard orientation. This will symmetrize the atomic coordinates to machine precision. Useful if the system is almost symmetric or to rototranslate a symmetric molecule into a standard orientation.

Symmetry

Type Multiple Choice

Default value AUTO

Options [AUTO, NOSYM, C(LIN), D(LIN), C(I), C(S), C(2), C(3), C(4), C(5), C(6), C(7), C(8), C(2V), C(3V), C(4V), C(5V), C(6V), C(7V), C(8V), C(2H), C(3H), C(4H), C(5H), C(6H), C(7H), C(8H), D(2), D(3), D(4), D(5), D(6), D(7), D(8), D(2D), D(3D), D(4D), D(5D), D(6D), D(7D), D(8D), D(2H), D(3H), D(4H), D(5H), D(6H), D(7H), D(8H), I, I(H), O, O(H), T, T(D), T(H), S(4), S(6), S(8)]

Description Use (sub)symmetry with this Schoenflies symbol. Can only be used for molecules. Orientation should be correct for the (sub)symmetry. If used icw Symmetrize, the symmetrization will not reorient the molecule.

Symmetry

SymmetrizeTolerance

Type Float

Default value 0.05

Description Tolerance used to detect symmetry in case symmetrize is requested.

Tolerance**Type** Float**Default value** 1e-07**Description** Tolerance used to detect symmetry in the system.**UseSymmetry****Type** Bool**Default value** Yes**Description** Whether to use the system's symmetry in AMS. Symmetry is recognized within a tolerance as given in the Symmetry key.

3.3 Regions

Some options of the AMS driver and its engines require specifying a subset of a system's atoms. For example one might want to freeze part of the system in a molecular dynamics calculation. We refer to these subsets of atoms as "regions". Atoms are assigned to regions by specifying the region names behind the atomic coordinates in the `Atoms` block of the input:

```
System
  Atoms
    C      1.22110608      -0.00000000      1.65928963      region=ring_1
    C      0.37734253      -1.16134090      1.65928963      region=ring_1
    C      0.37734253      1.16134090      1.65928963      region=ring_1
    C     -0.98789557      -0.71774815      1.65928963      region=ring_1
    C     -0.98789557      0.71774815      1.65928963      region=ring_1
    H      2.30849293      -0.00000000      1.64874914      region=ring_1
    H      0.71336355      -2.19550724      1.64874914      region=ring_1
    H      0.71336355      2.19550724      1.64874914      region=ring_1
    H     -1.86761001      -1.35689810      1.64874914      region=ring_1
    H     -1.86761001      1.35689810      1.64874914      region=ring_1
    Fe     0.00000000      0.00000000      0.00000000
    H      0.71336355      2.19550724     -1.64874914      region=ring_2
    H      0.71336355      -2.19550724     -1.64874914      region=ring_2
    C      1.22110608      -0.00000000     -1.65928963      region=ring_2
    C      0.37734253      1.16134090     -1.65928963      region=ring_2
    C      0.37734253     -1.16134090     -1.65928963      region=ring_2
    C     -0.98789557      0.71774815     -1.65928963      region=ring_2
    C     -0.98789557     -0.71774815     -1.65928963      region=ring_2
    H      2.30849293      -0.00000000     -1.64874914      region=ring_2
    H     -1.86761001      1.35689810     -1.64874914      region=ring_2
    H     -1.86761001     -1.35689810     -1.64874914      region=ring_2
  End
End
```

In the above example of a ferrocene molecule, we have created two separate regions for the two cyclopentadienyl rings. The region names (`ring_1` and `ring_2` in the example above) can be freely chosen by the user. Note that an atom can be in more than one region, in which case the region names should be separated by commas:

```
System
  Atoms
    ...
    Mg  0.0  0.0  0.0  region=metal_centers,mol_1
```

(continues on next page)

(continued from previous page)

```

    ...
End
End

```

Technically the region is handled as an *atomic attribute* (page 41).

3.4 Charge, atomic masses, input bond orders

AMS allows to set user-defined masses for particular atoms. This can be used to simulate isotopes of different atoms. Masses are specified by adding the desired mass (in Dalton) at the end of the atom's line. The following input shows the system specification for a heavy water molecule:

```

System
  Atoms
    O  0.0  0.0  0.59372
    H  0.0  0.76544 -0.00836  mass=2.014
    H  0.0 -0.76544 -0.00836  mass=2.014
  End
End

```

(Observe that the mass specified this way is an example of the *atomic attributes* (page 41) system.)

Finally the `System` block also contains the specification of the system's total charge as well as optionally defined bond orders.

System

Charge

Type Float

Default value 0.0

GUI name Total charge

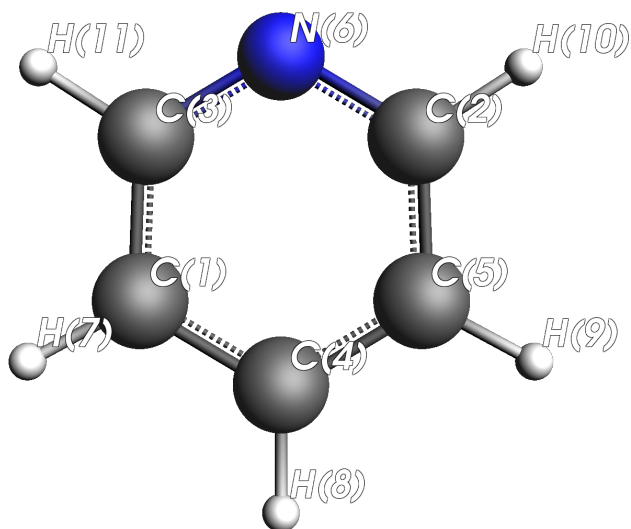
Description The system's total charge in atomic units.

BondOrders

Type Non-standard block

Description Defined bond orders. Each line should contain two atom indices, followed by the bond order (1, 1.5, 2, 3 for single, aromatic, double and triple bonds) and (optionally) the cell shifts for periodic systems. May be used by MM engines and for defining constraints. If the system is periodic and none of the bonds have the cell shift defined then AMS will attempt to determine them following the minimum image convention.

The following example shows the `System` block with defined bond orders for pyridine:



```

System
Atoms
  C  0.0  -1.19129014  -0.47777633
  C  0.0   1.1420834   0.90885782
  C  0.0  -1.1420834   0.90885782
  C  0.0   0.0         -1.18887601
  C  0.0   1.19129014  -0.47777633
  N  0.0   0.0         1.5894377
  H  0.0  -2.14522862  -0.99205897
  H  0.0   0.0        -2.27338592
  H  0.0   2.14522862  -0.99205897
  H  0.0   2.05492975   1.4973896
  H  0.0  -2.05492975   1.4973896
End
BondOrders
  1 3  1.5
  1 4  1.5
  1 7  1.0
  2 5  1.5
  2 6  1.5
  2 10 1.0
  3 6  1.5
  3 11 1.0
  4 5  1.5
  4 8  1.0
  5 9  1.0
End
End

```

Note that the specified bond orders are currently only used by the ForceField engine and for generating distance constraints via the All bonds option in the constraints block.

3.5 Homogeneous electric field and multipole charges

A homogeneous electric field and multipole charges can be requested at the AMS level. Currently this option is supported by the engines ADF, BAND, DFTB, and MOPAC.

Homogeneous electric field:

```
System
  ElectrostaticEmbedding
    ElectricField ex ey ez
  End
End
```

ElectrostaticEmbedding

ElectricField

Type Float List

Unit V/Angstrom

Description External homogeneous electric field with three Cartesian components: ex, ey, ez, the default unit being V/Å.

In atomic units: Hartree/(e bohr) = 14.39964 V/Angstrom; the relation to SI units is: 1 Hartree/(e bohr) = 5.14 ... e11 V/m.

Supported by the engines adf, band, dftb and mopac.

For periodic systems the field may only have nonzero components orthogonal to the direction(s) of periodicity (i.e. for 1D periodic system the x-component of the electric field should be zero, while for 2D periodic systems both the x and y components should be zero. This options cannot be used for 3D periodic systems.

Point and multipole charges:

```
System
  ElectrostaticEmbedding
    MultipolePotential
      Coordinates
        x y z q py pz px
        x y z q py pz px
        ...
      End
    End
  End
End
```

ElectrostaticEmbedding

MultipolePotential

Type Block

Description External point charges (and dipoles).

ChargeModel

Type Multiple Choice

Default value Point

Options [Point, Gaussian]

Description A multipole may be represented by a point (with a singular potential at its location) or by a spherical Gaussian distribution.

ChargeWidth

Type Float

Default value -1.0

Description The width parameter in a.u. in case a Gaussian charge model is chosen. A negative value means that the width will be chosen automatically.

Coordinates

Type Non-standard block

Description Positions and values of the multipoles, one per line. Each line has the following format:

x y z q, or x y z q μ_x μ_y μ_z .

Here x, y, z are the coordinates in Å, q is the charge (in atomic units of charge) and μ_x , μ_y , μ_z are the (optional) dipole moment components (in atomic units, i.e. e*Bohr).

Periodic systems are not supported.

Note: When running geometry optimizations (or other similar tasks) in combination with point charges, you should be aware that the system might end up on top of the point charge(s), resulting in non-physical situations. You should consider using *constraints* (page 52), *restraints* (page 264) or explicitly setting *rigid motions* (page 580) options.

3.6 Load a System from file

Instead of specifying the system to simulate in the `System` block of the input, it is also possible to read the system used in a previous calculation from the binary `.rkf` result files of AMS. This is done with the `LoadSystem` block in the input:

```
LoadSystem header
  File string
  Section string
End
```

LoadSystem

Type Block

Recurring True

Description Block that controls reading the chemical system from a KF file instead of the [System] block.

File

Type String

Description The path of the KF file from which to load the system. It may also be the results directory containing it.

Section

Type String

Default value Molecule

Description The section on the KF file from which to load the system.

Note that the `LoadSystem` block is mutually exclusive with the `System` block: The system *either* needs to be specified in the input, *or* loaded from a previous results file.

Any `.rkf` file written by AMS should be suitable to load a system from. For *engine output files* (page 19) the loaded geometry is just the one for which the engine was invoked when it wrote this file. For the *main result file* (page 19) `ams.rkf` written by the AMS driver, which geometry is loaded depends on the *task* (page 45) that AMS was performing when this file was written. Generally the `ams.rkf` file contains two systems:

- The input system corresponding just to the `System` block that was read in by AMS. This system is written to the `InputMolecule` section on the `ams.rkf`, and can be loaded from there using the `LoadSystem%Section` keyword. This can be useful in order to repeat a previous AMS calculation for the same system, but with different settings, e.g. a different engine.
- The system which was the result of a previous AMS calculation, e.g. a geometry optimization or transition state search. This system is written to the `Molecule` section on the `ams.rkf`. What exactly is considered the resulting geometry of a calculation depends in the *task* (page 45) of the previous calculation. (For tasks that do not change the geometry (like a single point calculation) or where no configuration is particularly special (e.g. a PES scan), the result system is normally just the same as the input system.)

3.7 Atom attributes

There is in general the possibility to add text after the coordinates of an atom, we call these atomic attributes. The text should be of the form `key=value`, separated by spaces:

```
System
  Atoms
    O  0.0  0.0      0.59372  key1=1 key2=y
    H  0.0  0.76544 -0.00836  file=ams.rkf
    H  0.0 -0.76544 -0.00836
  End
End
```

You can enter any arbitrary key/value list, but that will have no effect in general. Although there is one important effect that atoms with different atomic attributes (even unrecognized ones) are considered different elements during the symmetry detection.

The order in which keys are specified has no effect.

Examples of atomic attributes are the region, and mass.

3.8 Force field related extensions

For forcefield there are two dedicated *atomic attributes* (page 41), the `ForceField.Type` and `ForceField.Charge`. Obviously these attributes are ignored by all other engines, although it can reduce the symmetry of the system:

```
System
  Atoms
    O  0.0  0.0      0.59372  ForceField.Type=O ForceField.Charge=-0.1
    H  0.0  0.76544 -0.00836  ForceField.Type=H ForceField.Charge=+0.05
    H  0.0 -0.76544 -0.00836  ForceField.Type=H ForceField.Charge=+0.05
```

(continues on next page)

End End

3.8.1 Load charges for a forcefield into regions

When you want to use a forcefield, the charges obtained by a previous calculation can be loaded into a specific region (with the same molecule). Currently the order of the atoms has to be the same for this to work.

Once loaded, it is as if the user had typed in the ForceField.Charge attributes.

System

LoadForceFieldCharges

Type Block

Recurring True

Description This is a mechanism to set the ForceField.Charge attribute in the input. This information is currently only used by the ForceField engine.

CheckGeometryRMSD

Type Bool

Default value No

Description Whether the geometry RMSD test should be performed, see MaxGeometryRMSD. Otherwise only basic tests are performed, such as number and atom types. Not doing the RMSD test allows you to load molecular charges in a periodic system.

File

Type String

Description Name of the (kf) file

MaxGeometryRMSD

Type Float

Default value 0.1

Unit Angstrom

Description The geometry of the charge producing calculation is compared to the one of the region, and need to be the same within this tolerance.

Region

Type String

Default value *

Description Region for which the charges should be loaded

Section

Type String

Default value AMSResults

Description Section name of the kf file

Variable

Type String

Default value Charges

Description Variable name of the kf file

3.8.2 Load forcefield atom types

After you have done a forcefield calculation the atom types are stored. You can load those for a next calculation.

Once loaded, it is as if the user had typed in the ForceField.Type atom attributes.

System

LoadForceFieldAtomTypes

Type Block

Description This is a mechanism to set the ForceField.Type attribute in the input. This information is currently only used by the ForceField engine.

File

Type String

Description Name of the (kf) file. It needs to be the result of a forcefield calculation.

STRUCTURE AND REACTIVITY, MOLECULAR DYNAMICS

4.1 Single point calculations

A single point calculation is the simplest task available in the AMS driver. It simply runs the *engine* (page 250) once for the given geometry. In other words, the AMS driver does not explore the potential energy surface (PES), but simply samples a “single point” of it.

A single point calculation is performed by selecting it with the `Task` keyword:

```
Task SinglePoint
```

Note that a single point calculation in AMS includes the calculation of *PES point properties* (page 178). Many of these, such as the nuclear gradients and the Hessian, are derivatives at this PES point with respect to nuclear displacements. These derivatives might be done numerically by the AMS driver, in which case it would technically run the engine multiple times and sample PES points around the initial point. However, in AMS this is still considered a single point calculation. Take for example the calculation of the normal modes of vibration of a molecule. This used to be a separate task in the 2017 release of the DFTB program, but in AMS is just a single point calculation with a request for normal modes:

```
Task SinglePoint

Properties
  NormalModes True
End
```

See the manual section on *PES point properties* (page 178) for an overview of which properties can be calculated with the `SinglePoint` task in AMS.

4.2 Bond energy calculations

The way to calculate bonding energies is always the same, regardless of the engine. It is about combining ground state energies for several systems.

4.2.1 Ground state energy

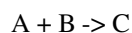
Let system A have a ground state energy $E(A)$

The ground state energy of a system is obtained by a full relaxation with respect to the geometry coordinates and (if relevant) to the electronic degrees of freedom. In case of periodic materials the lattice vectors need relaxation as well.

Electronic degrees of freedom are specific for the method underpinning the engine. A simple force field may have a charge equilibration scheme, whereas more advanced engines such DFT- and DFTB-based ones have orbitals. The electronic relaxation can become a non-trivial problem in case of *open shell* (page 47) systems.

4.2.2 Formation energy

Say we have a reaction of two molecules (A and B) forming a new one (C).



The interaction energy follows from three *ground state* (page 46) calculations

$$E(\text{bond}) = E(C) - E(A) - E(B)$$

Let us look at a slightly more complicated reaction. The (metastable) material Octanitrocubane with the formula $C_8(NO_2)_8$ can be formed from 8 CO_2 molecules and four N_2 molecules. The formation energy is

$$E(\text{bond}) = E(\text{Octanitrocubane}) - 8 E(CO_2) - 4 E(N_2)$$

the result being positive as this reaction is highly endothermic.

4.2.3 Atomization energies

Let us now look at atomization energies. For instance, the cohesive energy the NaCl crystal is

$$E(\text{cohesive energy}) = E(\text{NaCl-crystal}) - E(\text{Na-atom}) - E(\text{Cl-atom})$$

(Atomization energies can also be calculated for molecules.)

For engines with electronic degrees of freedom, the tricky part here is how to calculate the atomic energies, in particular $E(\text{Cl-atom})$, because they are open shell systems. See the notes on a *atomic corrections* (page 47).

Of course you need to weigh the atomic energies by how often they occur in the system (molecule or crystal).

4.2.4 Chemisorption energies

What is the adsorption energy of a molecule on a surface?

The main thing here is whether the “real” system has translational symmetry. For instance in an experiment this may be the case and correspond to a certain coverage. This can be perfectly modeled in a periodic calculation

$$E(\text{chemisorption}) = E(\text{mol@surface}) - E(\text{mol}) - E(\text{bare surface})$$

You need to choose the right super cell to get the correct coverage (how many adsorbed atoms per unit cell).

If the experiment is about the adsorption of a single molecule you need to try to converge the result with progressively larger super cells.

The other main issue is that almost always in the experimental setup the surface is macroscopically thick. Therefore the slab thickness is an issue to be tested. Fortunately, often less than 10 layers are needed.

4.2.5 Atomic corrections

Sometimes we need to calculate the ground state energy of a single atom. As there are no geometric variables, the only degrees of freedom are electronic. In general atoms are *open shell* (page 47) systems. The idea is to let the engine run without any restrictions imposed on the spin-polarization, or the symmetry of the orbitals.

One possible trick is to run two atoms quite far away (10-20 angstrom), thus reducing the exact spherical symmetry.

Calculating atomic corrections can be very tricky, as there may be many nearly degenerate orbitals near the fermi level. Also SCF convergence can be very difficult. There is not a single solution for all atoms.

4.2.6 Open shell systems

The idea is to let the engine run without any restrictions imposed on the spin-polarization, or the symmetry of the orbitals.

Calculating open shell systems can be very tricky, as there may be many close lying states (of which the lowest is searched for). Also SCF convergence can be very difficult.

From a theoretical point of view these states should ultimately be described by multi-determinantal wave functions, lacking from methods such as DFT.

There may be no automatic way to find the absolute minimum. If possible try to avoid the need to do such calculations.

4.2.7 Impurities

Let's say that we want to introduce a single impurity in a crystal. Currently we do not support such a method. But using periodic boundary conditions (PBCs) we can approximate this.

Say we want to introduce a single Li atom in an Al crystal. This can be done by considering progressively larger super cells.

First we make a 2x2x2 super cell, with 8 Al atoms, then we insert one Li, thus modeling an "impurity", with a 1/8 Li/Al ratio, rather than a 1/infinity. With bigger super cells this approximation becomes better.

The insertion energy is then

$$E(8Al+Li) - E(8Al) - E(Li\text{-atom})$$

See also the comments for Atomization energies.

4.3 Geometry optimization

A geometry optimization is the process of changing the system's geometry (the nuclear coordinates and potentially the lattice vectors) to minimize the total energy of the systems. This is typically a local optimization, i.e. the optimization converges to the next local minimum on the potential energy surface (PES), given the initial system geometry specified in the `System` block. In other words: The geometry optimizer moves "downhill" on the PES into the local minimum.

See also:

[Examples](#) (page 371) and [silicon lattice optimization and phonons tutorial](#)

Geometry optimizations are performed by selecting them as the `Task`. The details of the optimization can be configured in the corresponding block:

```
Task GeometryOptimization
```

```

GeometryOptimization
  Convergence
    Energy float
    Gradients float
    Quality [VeryBasic | Basic | Normal | Good | VeryGood | Custom]
    Step float
    StressEnergyPerAtom float
  End
  MaxIterations integer
  CalcPropertiesOnlyIfConverged Yes/No
  OptimizeLattice Yes/No
  KeepIntermediateResults Yes/No
  PretendConverged Yes/No
  MaxRestarts integer
  RestartDisplacement float
End

```

4.3.1 Convergence criteria

GeometryOptimization

Type Block

Description Configures details of the geometry optimization and transition state searches.

Convergence

Type Block

Description Convergence is monitored for up to 4 quantities: the energy change, the Cartesian gradients, the Cartesian step size, and for lattice optimizations the stress energy per atom. Convergence criteria can be specified separately for each of these items.

Energy

Type Float

Default value 1e-05

Unit Hartree

GUI name Energy convergence

Description The criterion for changes in the energy. The energy is considered converged when the change in energy is smaller than this threshold times the number of atoms.

Gradients

Type Float

Default value 0.001

Unit Hartree/Angstrom

GUI name Gradient convergence

Description Threshold for nuclear gradients.

Quality

Type Multiple Choice

Default value Custom

Options [VeryBasic, Basic, Normal, Good, VeryGood, Custom]

GUI name Convergence

Description A quick way to change convergence thresholds: 'Good' will reduce all thresholds by an order of magnitude from their default value. 'VeryGood' will tighten them by two orders of magnitude. 'Basic' and 'VeryBasic' will increase the thresholds by one or two orders of magnitude respectively.

Step

Type Float

Default value 0.01

Unit Angstrom

GUI name Step convergence

Description The maximum Cartesian step allowed for a converged geometry.

StressEnergyPerAtom

Type Float

Default value 0.0005

Unit Hartree

Description Threshold used when optimizing the lattice vectors. The stress is considered 'converged' when the maximum value of $\text{stress_tensor} * \text{cell_volume} / \text{number_of_atoms}$ is smaller than this threshold (for 2D and 1D systems, the cell_volume is replaced by the cell_area and cell_length respectively).

A geometry optimization is considered converged when all the following criteria are met:

1. The difference between the bond energy at the current geometry and at the previous geometry step is smaller than $\text{Convergence}\% \text{Energy}$ times the number of atoms in the system.
2. The maximum Cartesian nuclear gradient is smaller than $\text{Convergence}\% \text{Gradient}$.
3. The root mean square (RMS) of the Cartesian nuclear gradients is smaller than $2/3 \text{Convergence}\% \text{Gradient}$.
4. The maximum Cartesian step is smaller than $\text{Convergence}\% \text{Step}$.
5. The root mean square (RMS) of the Cartesian steps is smaller than $2/3 \text{Convergence}\% \text{Step}$.

Note: If the maximum and RMS gradients are 10 times smaller than the convergence criterion, then criteria 4 and 5 are ignored.

The $\text{Convergence}\% \text{Quality}$ sets the criteria as follows:

Quality	Energy (Ha)	Gradients (Ha/Å)	Step (Å)	StressEnergyPerAtom (Ha)
VeryBasic	10^{-3}	10^{-1}	1	5×10^{-2}
Basic	10^{-4}	10^{-2}	0.1	5×10^{-3}
Normal	10^{-5}	10^{-3}	0.01	5×10^{-4}
Good	10^{-6}	10^{-4}	0.001	5×10^{-5}
VeryGood	10^{-7}	10^{-5}	0.0001	5×10^{-6}

Some remarks on the choice of the convergence thresholds:

- Molecules may differ very much in the stiffness around the energy minimum. Using the standard convergence thresholds without second thought is therefore not recommended. Strict criteria may require a large number of steps, while a loose threshold may yield geometries that are far from the minimum (with respect to atom-atom

distances, bond-angles etc...) even when the total energy of the molecule might be very close to the value at the minimum. It is good practice to consider first what the objectives of the calculation are. The default settings in AMS are intended to be reasonable for most applications, but inevitably situations may arise where they are inadequate.

- The convergence threshold for the coordinates (`Convergence%Step`) is not a reliable measure for the precision of the final coordinates. Usually it yields a reasonable estimate (order of magnitude), but to get accurate results one should tighten the criterion on the gradients, rather than on the steps (coordinates). (The reason for this is that with the Quasi-Newton based optimizers the estimated uncertainty in the coordinates is related to the used Hessian, which is updated during the optimization. Quite often it stays rather far from an accurate representation of the true Hessian. This does usually not prevent the program from converging nicely, but it does imply a possibly incorrect calculation of the uncertainty in the coordinates.)
- Note that tight convergence criteria for the geometry optimization require accurate and noise-free gradients from the engine. For some engines this might mean that their numerical accuracy has to be increased for geometry optimization with tight convergence criteria, see e.g. the `NumericalQuality` keyword in the BAND manual.

The maximum number of geometry iterations allowed to locate the desired structure is specified with the `MaxIterations` keyword:

GeometryOptimization

MaxIterations

Type Integer

GUI name Maximum number of iterations

Description The maximum number of geometry iterations allowed to converge to the desired structure.

CalcPropertiesOnlyIfConverged

Type Bool

Default value Yes

Description Compute the properties requested in the 'Properties' block, e.g. Frequencies or Phonons, only if the optimization (or transition state search) converged. If False, the properties will be computed even if the optimization did not converge.

PretendConverged

Type Bool

Default value No

Description Normally a non-converged geometry optimization is considered an error. If this keyword is set to True, the optimizer will only produce a warning and still claim that the optimization is converged. (This is mostly useful for scripting applications, where one might want to consider non-converged optimizations still successful jobs.)

If the geometry optimization does not converge within this many steps it is considered failed and the iteration aborted, i.e. *PES point properties* (page 178) block will not be calculated at the last geometry. The default maximum number of steps is chosen automatically based on the used optimizer and the number of degrees of freedom to be optimized. The default is a fairly large number already, so if the geometry has not converged (at least to a reasonable extent) within that many iterations you should step back and consider the underlying cause rather than simply increase the allowed number of iterations and try again.

4.3.2 Automatic restarts

While a geometry optimization aims to find a (local) PES minimum, it may occur that it ends up finding a saddle point instead. The `PESPointCharacter` property keyword can be used to quickly calculate the lowest few Hessian eigenvalues to determine what kind of stationary PES point the optimization found. More information on this feature can be found on its [Documentation Page](#) (page 180). Since AMS2022.1, geometry optimizations with enabled PES point characterization can automatically restart when a transition state (or higher order saddle point) is found: the geometry is distorted along the lowest frequency mode and the optimizer run again. The applied distortion is often symmetry breaking in this case, so this automatic restarting is only enabled if the system does not have any symmetry operators or the use of symmetry is explicitly disabled using the `UseSymmetry` keyword. Furthermore the automatic restarting must be explicitly enabled by setting the `MaxRestarts` option to a value >0. Of course the PES point characterization needs to be enabled too:

```
GeometryOptimization
  MaxRestarts 5
End

UseSymmetry False

Properties
  PESPointCharacter True
End
```

Details of the automatic restarting can configured with the following keywords:

GeometryOptimization

MaxRestarts

Type Integer

Default value 0

Description If a geometry optimization of a system with no symmetry operators (or with explicitly disabled symmetry: `UseSymmetry False`) and enabled PES point characterization converges to a transition state (or higher order saddle point), it can be restarted automatically after a small displacement along the imaginary vibrational mode. In case the restarted optimization again does not find a minimum, this can happen multiple times in succession. This keyword sets the maximum number of restarts. The default value is 0, so the automatic restarting is disabled by default.

RestartDisplacement

Type Float

Default value 0.05

Unit Angstrom

Description If a geometry optimization of a system with no symmetry operators (or with explicitly disabled symmetry: `UseSymmetry False`) and enabled PES point characterization converges to a transition state (or higher order saddle point), it can be restarted automatically after a small displacement along the imaginary vibrational mode. This keywords sets the size of the displacement for the furthest moving atom.

4.3.3 Lattice optimization

For periodic systems the lattice degrees of freedom can be optimized in addition to the nuclear positions.

GeometryOptimization

OptimizeLattice

Type Bool

Default value No

Description Whether to also optimize the lattice for periodic structures. This is currently only supported with the Quasi-Newton, FIRE, L-BFGS and SCMGO optimizers.

See also *Constrained optimization* (page 52) for constrained lattice optimizations.

4.3.4 Keep all results files

The GeometryOptimization block also contains some technical options:

GeometryOptimization

KeepIntermediateResults

Type Bool

Default value No

Description Whether the full engine result files of all intermediate steps are stored on disk. By default only the last step is kept, and only if the geometry optimization converged. This can easily lead to huge amounts of data being stored on disk, but it can sometimes be convenient to closely monitor a tricky optimization, e.g. excited state optimizations going through conical intersections, etc. ...

4.3.5 Constrained optimization

The AMS driver also allows to perform constrained optimizations, where a number of specified degrees of freedom are fixed to particular values.

See also:

Example demonstrating all supported constraints (page 379)

The desired constraints are specified in the Constraints block at the root level of the AMS input file:

```
Constraints
  Atom integer
  AtomList integer_list
  FixedRegion string
  Coordinate integer [x|y|z] float?
  Distance (integer){2} float
  All ... [Bonds|Triangles] ...
  Angle (integer){3} float
  Dihedral (integer){4} float
  SumDist (integer){4} float
  DifDist (integer){4} float
  BlockAtoms integer_list
  Block string
```

(continues on next page)

(continued from previous page)

```

FreezeStrain [xx] [xy] [xz] [yy] [yz] [zz]
EqualStrain  [xx] [xy] [xz] [yy] [yz] [zz]
End

```

Constraints

Type Block

Description The Constraints block allows geometry optimizations and potential energy surface scans with constraints. The constraints do not have to be satisfied at the start of the calculation.

The different types constraints are described with examples below.

Note that in principle an arbitrary number of constraints can be specified and thus combined. However, it is the user's responsibility to ensure that the specified constraints are actually *compatible with each other*, meaning that it is theoretically possible to satisfy all of them at the same time. The AMS driver does **not** detect this kind of problems, but the optimization will show very unexpected results. Furthermore, for calculations involving block constraints the following restrictions apply:

- There should be no other constrained coordinates used together with block constraints although this may work in many situation.
- The user should absolutely avoid specifying other constraints that include atoms of a frozen block.

Fixed atoms

The following constraints can be used to fix atoms in space.

Atom atomIdx Fix the atom with index `atomIdx` at the initial position, as given in the `System%Atoms` block.

AtomList [atomIdx1 .. atomIdxN] Fix all atoms in the list at the initial position, as given in the `System%Atoms` block.

FixedRegion regionName Fix all atoms in a *region* (page 36) to their initial positions.

Coordinate atomIdx [x|y|z] coordValue? Constrain the atom with index `atomIdx` (following the order in the `System%Atoms` block) to have a cartesian coordinate (x, y or z) of `coordValue` (given in Angstrom). If the `coordValue` is missing, the coordinate will be fixed to its initial value.

Internal degrees of freedom

The following options allow constraints of internal degrees of freedom, such as distances, angles and dihedral angles.

Distance atomIdx1 atomIdx2 distValue Constrain the distance between the atoms with index `atomIdx1` and `atomIdx2` (following the order in the `System%Atoms` block) to `distValue`, given in Angstrom.

Angle atomIdx1 atomIdx2 atomIdx3 angleValue Constrain the angle (1)–(2)–(3) between the atoms with indices `atomIdx1–3` (as given by their order in the `System%Atoms` block) to `angleValue`, given in degrees.

Dihedral atomIdx1 atomIdx2 atomIdx3 atomIdx4 dihedValue Constrain the dihedral angle (1)–(2)–(3)–(4) between the atoms with indices `atomIdx1–4` (as given by their order in the `System%Atoms` block) to `dihedValue`, given in degrees.

SumDist atomIdx1 atomIdx2 atomIdx3 atomIdx4 sumDistValue Constrain the sum of the distances $R(1,2)+R(3,4)$ between the atoms with indices `atomIdx1–4` (as given by their order in the `System%Atoms` block) to `sumDistValue`, given in Angstrom.

DifDist atomIdx1 atomIdx2 atomIdx3 atomIdx4 difDistValue Constrain the difference between the distances R(1,2)-R(3,4) of the atoms with indices atomIdx1-4 (as given by their order in the System%Atoms block) to difDistValue, given in Angstrom.

Note that the above constraints do **not** need to be satisfied at the beginning of the optimization.

The Distance keyword described above can be used to set up constraints for specific pairs of atoms in the system. For some applications, this input can be cumbersome and one would rather specify a constraint for **all** bonds of a particular type. Since the AMS2022.1 release, there is a simplified input for this using the All keyword. The All keyword allows generating distance constraints for matching *bonds defined in the System block* (page 37). The bonds for which distance constraints will be generated can be selected based on the elements of the bonded atoms, as well as the bond order defined in the System block. The following example would constrain all carbon-carbon single bonds to a distance of 1.4 Angstrom, and all bonds with hydrogen atoms to their initial distance:

```
Constraints
  All single bonds C C to 1.4
  All bonds H *
End
```

It is also possible to constrain neighboring bonds and the angle between them using the combination All triangles. This is mostly useful for water molecules, which can then easily be made entirely rigid:

```
All triangles H O H
```

Warning: It is very easy to generate a large number of interdependent distance constraints using the All triangles keyword. Interdependent distance constraints can impair optimizer performance and should be avoided. Consider for example the input All triangles H C H for methane: there are 6 triangles matching this description in CH₄, generating 18 interdependent distance constraints. A rigid CH₄ would be better set up using a block constraint.

See below for a full description of the Constraints%All keyword.

Constraints

All

Type String

Recurring True

Description Fix multiple distances using one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 as well as the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then any bond between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk "*" denoting any atom. If the distance is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at the start of the simulation can be constrained, which means that the bonds may need to be specified in the System block.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

Block constraints

Block constraints can be used to treat parts of the System as a rigid unit in the optimization.

BlockAtoms [*atomIdx1* ... *atomIdxN*] Creates a block constraint (freezes all internal degrees of freedom) for a set of atoms identified by the list of integers [*atomIdx1* ... *atomIdxN*]. These atom indices refer to the order of the atoms in the `System%Atoms` block.

Block *regionName* Creates a block constraint (freezes all internal degrees of freedom) for all atoms in a *region* (page 36) defined in the `System%Atoms` block. Example:

```
System
  Atoms
    C  0.0  0.0  0.0   region=myblock
    C  0.0  0.0  1.0   region=myblock
    C  0.0  1.0  0.0
  End
End
Constraints
  Block myblock
End
```

Lattice constraints

For lattice optimizations, the following constraints can be used on the lattice degrees of freedom:

FreezeStrain [*xx*] [*xy*] [*xz*] [*yy*] [*yz*] [*zz*] Exclusively for lattice optimizations: Freezes any lattice deformation corresponding to a particular component of the strain tensor. Accepts a set of strain components [*xx*, *xy*, *xz*, *yy*, *yz*, *zz*] to be frozen.

EqualStrain [*xx*] [*xy*] [*xz*] [*yy*] [*yz*] [*zz*] Exclusively for lattice optimizations: Accepts a set of strain components [*xx*, *xy*, *xz*, *yy*, *yz*, *zz*] which are to be kept equal. The applied strain will be determined by the average of the corresponding stress tensors components.

Restraints

Not all optimizers support constraints. An alternative is to use so-called restraints. These are not exact constraints, but rather a number of springs that pull the system towards the preferred constraints, see *Restraints* (page 264).

4.3.6 Optimization under pressure / external stress

Pressure (page 261) or *non-isotropic external stress* (page 262) can be included in your simulation via the corresponding *engine addons* (page 258).

4.3.7 Optimization methods

The AMS driver implements a few different geometry optimization algorithms. It also allows to choose the coordinate space in which the optimization is performed:

```
GeometryOptimization
  Method [Auto | Quasi-Newton | SCMGO | FIRE | L-BFGS | ConjugateGradients]
  CoordinateType [Auto | Delocalized | Cartesian]
End
```

GeometryOptimization

Method

Type Multiple Choice

Default value Auto

Options [Auto, Quasi-Newton, SCMGO, FIRE, L-BFGS, ConjugateGradients]

GUI name Optimization method

Description Select the optimization algorithm employed for the geometry relaxation. Currently supported are:

the Hessian-based Quasi-Newton-type BFGS algorithm,

the experimental SCMGO optimizer,

the fast inertial relaxation method (FIRE),

the limited-memory BFGS method,

and the conjugate gradients method. The default is to choose an appropriate method automatically based on the engine's speed, the system size and the supported optimization options.

CoordinateType

Type Multiple Choice

Default value Auto

Options [Auto, Delocalized, Cartesian]

GUI name Optimization space

Description Select the type of coordinates in which to perform the optimization. 'Auto' automatically selects the most appropriate CoordinateType for a given Method.

If 'Auto' is selected, Delocalized coordinates will be used for the Quasi-Newton and SCMGO methods, while Cartesian coordinates will be used for all other methods.

We **strongly** advise leaving both the Method as well as the Coordinate type on the Auto setting. There are many restrictions as to which optimizer and coordinate type can be used together with which kind of optimization. The following (roughly) sketches the compatibility of the different optimizers and options:

Optimizer	Constraints	Lattice opt.	Coordinate types
Quasi-Newton	All, except strain	Yes	All
FIRE	Fixed coordinates, distances, strain	Yes	Cartesian
SCMGO	No	Yes	Delocalized
L-BFGS	No	Yes	Cartesian
Conjugate gradients	No	No	Cartesian

Furthermore for optimal performance the optimizer should be chosen with the speed of the engine: a faster engine in combination should use an optimizer with little overhead (FIRE), while slower engines should use optimizers that strictly minimize the number of steps (Quasi-Newton, SCMGO). This is all handled automatically by default, and we recommend changing `Method` and `Coordinate` only in case there are problems with the automatic choice.

The following subsections list the strengths and weaknesses of the individual optimizers in some more detail, motivating why which optimizer is chosen automatically under which circumstances.

Quasi-Newton

This optimizer implements a quasi Newton approach¹²³, using the Hessian for computing changes in the geometry so as to reach a local minimum. The Hessian itself is typically *approximated* (page 58) in the beginning and updated in the process of optimization. It uses delocalized coordinates by default both for molecules and periodic systems. The molecular part is based mainly on the work by Marcel Swart⁴. Cartesian coordinates are used in the presence of an external electric field and/or frozen atom constraints.

The Quasi-Newton (QN) optimizer supports all types of constraints and can be used for both molecular and periodic systems, including lattice optimizations. For cases where the optimization can be performed in delocalized coordinates, the number of steps taken to reach the local minimum is usually smaller than when optimizing in Cartesian ones. For fast compute *engines* (page 250), the overhead of the QN optimizer can become a bottleneck of the calculation, thus a more light-weight optimizer such as *FIRE* (page 59) may give an better overall performance. In principle, a QN optimization in delocalized coordinates may run out of memory for a very large system (say over 1000 atoms) because of the SVD step. However, since it is going to be used for a moderate-to-slow engine we still recommend sticking to it for the benefit of fewer steps. Because of these properties the QN optimizer is the default in AMS for all kinds of optimizations with moderate and slow engines, such DFTB and ADF. It is also used as the optimizer back-end for the *PES scan task* (page 68), the *transition state search* (page 65) as well as the calculation of the *elastic tensor* (page 184).

Details of the Quasi-Newton optimizer are configured in a dedicated block:

```
GeometryOptimization
  Quasi-Newton
    MaxGDIISVectors integer
    Step
      TrustRadius float
      VaryTrustRadius Yes/No
    End
    UpdateTSVectorEveryStep Yes/No
  End
End
```

GeometryOptimization

Quasi-Newton

Type Block

Description Configures details of the Quasi-Newton geometry optimizer.

MaxGDIISVectors

Type Integer

¹ L. Versluis and T. Ziegler, *The determination of Molecular Structure by Density Functional Theory*, Journal of Chemical Physics 88, 322 (1988) (<https://doi.org/10.1063/1.454603>)

² L. Versluis, *The determination of molecular structures by the HFS method*, PhD thesis, University of Calgary, 1989

³ L. Fan and T. Ziegler, *Optimization of molecular structures by self consistent and non-local density functional theory*, Journal of Chemical Physics 95, 7401 (1991) (<https://doi.org/10.1063/1.461366>)

⁴ M. Swart and F.M. Bickelhaupt, *Optimization of strong and weak coordinates*, International Journal of Quantum Chemistry 106, 2536 (2006) (<https://doi.org/10.1002/qua.21049>)

Default value 0

Description Sets the maximum number of GDIIS vectors. Setting this to a number >0 enables the GDIIS method.

Step

Type Block

Description

TrustRadius

Type Float

Description Initial value of the trust radius.

VaryTrustRadius

Type Bool

Description Whether to allow the trust radius to change during optimization. By default True during energy minimization and False during transition state search.

UpdateTSVectorEveryStep

Type Bool

Default value Yes

GUI name Update TSRC vector every step

Description Whether to update the TS reaction coordinate at each step with the current eigenvector.

The Quasi-Newton optimizer uses the Hessian to compute the step of the geometry optimization. The Hessian is typically approximated in the beginning and then updated during the optimization. A very good initial Hessian can therefore increase the performance of the optimizer and lead to faster and more stable convergence. The choice of the initial Hessian can be configured in a dedicated block:

```
GeometryOptimization
  InitialHessian
    File string
      Type [Auto | UnitMatrix | Swart | FromFile | Calculate | ↵
↵CalculateWithFastEngine]
    End
  End
End
```

GeometryOptimization

InitialHessian

Type Block

Description Options for initial model Hessian when optimizing systems with either the Quasi-Newton or the SCMGO method.

File

Type String

GUI name Initial Hessian from

Description KF file containing the initial Hessian (or the results dir. containing it). This can be used to load a Hessian calculated in a previously with the [Properties%Hessian] keyword.

Type

Type Multiple Choice**Default value** Auto**Options** [Auto, UnitMatrix, Swart, FromFile, Calculate, CalculateWithFastEngine]**GUI name** Initial Hessian

Description Select the type of initial Hessian. Auto: let the program pick an initial model Hessian. UnitMatrix: simplest initial model Hessian, just a unit matrix in the optimization coordinates. Swart: model Hessian from M. Swart. FromFile: load the Hessian from the results of a previous calculation (see InitialHessian%File). Calculate: compute the initial Hessian (this may be computationally expensive and it is mostly recommended for TransitionStateSearch calculations). CalculateWithFastEngine: compute the initial Hessian with a faster engine.

While there are some options for the construction of approximate model Hessians, the best initial Hessians are often those calculated explicitly at a lower level of theory, e.g. the real DFTB Hessian can be used the initial Hessian for an optimization with the more accurate BAND engine. Using the CalculateWithFasterEngine keyword can be used to automatically chose a fast engine at a lower level of theory. What the lower level of theory is depends on the main engine used in the calculation: DFTB with the GFN1-xTB model is used as the lower level of theory for relatively slow engines, e.g. DFT based engines. For semi-empirical engines like DFTB or MOPAC, the lower level of theory is currently UFF. If more control over the lower level engine is needed, the initial Hessian can be calculated with a user defined engine and then loaded from file, see [this example](#) (page 371).

FIRE

The Fast Inertial Relaxation Engine⁵ based optimizer has basically no overhead per step, so that the speed of the optimization purely depends on the performance of the used compute *engine* (page 250). As such it is a good option for large systems or fast compute engines, where the overhead of the Quasi-Newton optimizer would be significant. Note that it also supports *fixed atom constraints* (page 53) and *coordinate constraints* (page 53) (as long as the value of the constrained coordinate is already satisfied in the input geometry), distance constraints, as well as lattice optimizations (with strain constraints).

FIRE is selected as the default optimizer for fast compute engines if it is compatible with all other settings of the optimization (i.e. no unsupported constraints or coordinate types).

Note: FIRE is a very robust optimizer. In case of convergence problems with the other methods, it is a good idea to see if the optimization converges with FIRE. If it does not, it is very likely that the problem is not the optimizer but the shape of the potential energy surface ...

The details of the FIRE optimizer are configured in a dedicated block. It is quite easy to make the optimization numerically unstable when tweaking these settings, so we strongly recommend leaving everything at the default values.

```
GeometryOptimization
  FIRE
    AllowOverallRotation Yes/No
    AllowOverallTranslation Yes/No
    MapAtomsToUnitCell Yes/No
    NMin integer
    alphaStart float
    dtMax float
    dtStart float
```

(continues on next page)

⁵ E. Bitzek, P. Koskinen, F. Gähler, M. Moseler and P. Gumbusch, *Structural Relaxation Made Simple*, Physical Review Letters 97, 170201 (2006) (<https://doi.org/10.1103/PhysRevLett.97.170201>)

```
fAlpha float
fDec float
fInc float
strainMass float
End
End
```

GeometryOptimization

FIRE

Type Block

Description This block configures the details of the FIRE optimizer. The keywords name correspond to the symbols used in the article describing the method, see PRL 97, 170201 (2006).

AllowOverallRotation

Type Bool

Default value Yes

Description Whether or not the system is allowed to freely rotate during the optimization. This is relevant when optimizing structures in the presence of external fields.

AllowOverallTranslation

Type Bool

Default value No

Description Whether or not the system is allowed to translate during the optimization. This is relevant when optimizing structures in the presence of external fields.

MapAtomsToUnitCell

Type Bool

Default value No

Description Map the atoms to the central cell at each geometry step.

NMin

Type Integer

Default value 5

Description Number of steps after stopping before increasing the time step again.

alphaStart

Type Float

Default value 0.1

Description Steering coefficient.

dtMax

Type Float

Default value 1.0

Unit Femtoseconds

Description Maximum time step used for the integration. For ReaxFF and APPLE&P, this value is reduced by 50%.

dtStart

Type Float

Default value 0.25

Unit Femtoseconds

Description Initial time step for the integration.

fAlpha

Type Float

Default value 0.99

Description Reduction factor for the steering coefficient.

fDec

Type Float

Default value 0.5

Description Reduction factor for reducing the time step in case of uphill movement.

fInc

Type Float

Default value 1.1

Description Growth factor for the integration time step.

strainMass

Type Float

Default value 0.5

Description Fictitious relative mass of the lattice degrees of freedom. This controls the stiffness of the lattice degrees of freedom relative to the atomic degrees of freedom, with smaller values resulting in a more aggressive optimization of the lattice.

SCMGO

The SCMGO optimizer is a new implementation of a Quasi-Newton style optimizer working in delocalized coordinates. In the 2020 release of the Amsterdam Modeling Suite it is still considered experimental and therefore never selected automatically. However, for molecules and fully connected periodic systems it already shows a quite good performance, and could be a reasonable alternative to the classic *Quasi-Newton* (page 57) optimizer.

```

GeometryOptimization
  SCMGO
    ContractPrimitives Yes/No
    NumericalBMatrix Yes/No
    Step
      TrustRadius float
      VariableTrustRadius Yes/No
    End
  logSCMGO Yes/No
  testSCMGO Yes/No

```

(continues on next page)

```
End
End
```

GeometryOptimization**SCMGO****Type** Block**Description** Configures details SCMGO.**ContractPrimitives****Type** Bool**Default value** Yes**Description** Form non-redundant linear combinations of primitive coordinates sharing the same central atom**NumericalBMatrix****Type** Bool**Default value** No**Description** Calculation of the B-matrix, i.e. Jacobian of internal coordinates in terms of numerical differentiations**Step****Type** Block**Description****TrustRadius****Type** Float**Default value** 0.2**Description** Initial value of the trust radius.**VariableTrustRadius****Type** Bool**Default value** Yes**Description** Whether or not the trust radius can be updated during the optimization.**logSCMGO****Type** Bool**Default value** No**Description** Verbose output of SCMGO internal data**testSCMGO****Type** Bool**Default value** No**Description** Run SCMGO in test mode.

Note that SCMGO also supports different initial Hessians, and uses the same options for the initial Hessian as the Quasi-Newton optimizer, see *above* (page 58).

Limited-memory BFGS

AMS also offers an L-BFGS based geometry optimizer. It usually converges faster than *FIRE* (page 59), but does not support constrained optimizations. For periodic systems it can be quite good for lattice optimizations. The new implementation has not been thoroughly tested yet, therefore never selected automatically. For large systems and fast engines you may want to disable symmetry: simply the detection of (non-existing) symmetry may be a huge overhead.

```

GeometryOptimization
  HessianFree
    Step
      MaxCartesianStep float
      MinRadius float
      TrialStep float
      TrustRadius float
    End
  End
End

```

GeometryOptimization

HessianFree

Type Block

Description Configures details of the Hessian-free (conjugate gradients or L-BFGS) geometry optimizer.

Step

Type Block

Description

MaxCartesianStep

Type Float

Default value 0.1

Unit Angstrom

Description Limit on a single Cartesian component of the step.

MinRadius

Type Float

Default value 0.0

Unit Angstrom

Description Minimum value for the trust radius.

TrialStep

Type Float

Default value 0.0005

Unit Angstrom

Description Length of the finite-difference step when determining curvature. Should be smaller than the step convergence criterion.

TrustRadius

Type Float

Default value 0.2

Unit Angstrom

Description Initial value of the trust radius.

Conjugate gradients

AMS also offers a conjugate gradients based geometry optimizer, as it was also implemented in the pre-2018 releases of the DFTB program. However, it is usually slightly slower than *FIRE* (page 59), and supports neither lattice nor constrained optimizations. It is therefore never selected automatically, and we do not recommend using it. Like L-BFGS, the conjugate gradients optimizer is also configured in the `HessianFree` block, see L-BFGS section above for details.

4.3.8 Troubleshooting

Failure to converge

First of all one should look how the energy changed during the latest ten or so iterations. If the energy is decreasing more or less consistently, possibly with occasional jumps, then there is probably nothing wrong with the optimization. This behavior is typical in the cases when the starting geometry was far away from the minimum and the optimization has a long way to go. Just increase the allowed number of iterations, restart from the latest geometry and see if the optimization converges.

If the energy oscillates around some value and the energy gradient hardly changes then you may need to look at the calculation setup.

The success of geometry optimization depends on the accuracy of the calculated forces. The default accuracy settings are sufficient in most cases. There are, however, cases when one has to increase the accuracy in order to get geometry optimization converged. First of all, this may be necessary if you tighten the optimization convergence criteria. In some cases it may be necessary to increase the accuracy also for the default criteria. Please refer to the *engine manuals* (page 250) for instructions on how to increase the accuracy of an engine's energies and gradients. Often this is done with the `NumericalQuality` keyword in the engine input.

A geometry optimization can also fail to converge because the underlying potential energy surface is problematic, e.g. it might be discontinuous or not have a minimum at which the gradients vanish. This often indicates real problems in the calculation setup, e.g. an electronic structure that changes fundamentally between subsequent steps in the optimization. In these cases it is advisable to run a single point calculation at the problematic geometries and carefully check if the results are physically actually sensible.

Finally it can also be a technical problem with the specific *optimization method* (page 55) used. In these cases switching to another method could help with convergence problems. We recommend first trying the *FIRE* (page 59) optimizer, as it is internally relatively simple and stable.

Converged, but did not find a minimum on the PES

If *Normal Modes* (page 187) or *PES point characterization* (page 180) were requested, the *PES character* (page 180) of the final optimized geometry is checked.

While you would generally expect the final optimized geometry to be a local minimum (i.e. no imaginary frequencies), it can happen for the optimization procedure to converge to a saddle point instead (i.e. a stationary point on the PES with one or more imaginary frequency). In that case you will get the following error message:

```
ERROR: Geometry optimization failed! (Converged, but did not find a minimum on the
↳PES.)
```

Depending on your application, (small) imaginary frequencies might not be a problem. But if you want to get rid of all imaginary frequencies, these are a few recommendations:

- Try using a tighter *gradient convergence threshold* (page 48) (`GeometryOptimization%Convergence%Gradient`). E.g. 1.0E-4 (instead of the default 1.0E-3).
- Try using the *MaxRestart* (page 51) option. Reasonable values for `MaxRestart` range from 2 to 20 (if there are many imaginary frequencies, a larger value might be needed). When using the `MaxRestart` option, you might try increasing `RestartDisplacement`.
- Open the results with the **AMSSpectra** GUI module and visually inspect the negative/imaginary vibrational modes. You can then manually perturb the input geometry along those modes and re-run the optimization.
- If the system is symmetric and *symmetry* (page 35) is enabled, the optimizer will try not to break the symmetry of the system. It might be that in order to reach the local minimum, symmetry must be broken. Try disabling symmetry (`UseSymmetry False`) and slightly perturb the atomic coordinates in order to break the symmetry (or use the *PerturbCoordinates* (page 33) option.)

Restarting a geometry optimization

During a running optimization the system's geometry is written out to the AMS driver's output file `ams.rkf` after every step (in the `Molecule` section). This means that crashed or otherwise canceled geometry optimizations can be restarted by simply loading the last frame from there using the `LoadSystem` keyword, see *its documentation* (page 40) in the system definition section of this manual:

```
LoadSystem File=my_crashed_GO.results/ams.rkf
```

This can of course also be used to continue an optimization but e.g. with tighter convergence criteria or a different optimizer, as it essentially starts a new geometry optimization from the previous geometry, and does not propagate any information internal to the optimizer (e.g. the approximate Hessian for the Quasi-Newton optimizer or the FIRE velocities) to the new job. As such it might take a few more steps to convergence than if the original job had continued, but allows for additional flexibility.

4.4 Transition state search

A transition state (TS) search is very much like a *geometry optimization* (page 47): the purpose is to find a stationary point on the potential energy surface, primarily by monitoring the energy gradients, which should vanish. The difference between a transition state and a minimum is that at the transition state the Hessian has a negative eigenvalue: We are at a saddle point, not a minimum, with the "negative" mode connecting the two basins on the potential energy surface.

See also:

- *Examples* (page 371)

- Tutorial Transition state search and characterization of a Ziegler Natta Catalyst
- Tutorial Tips and Tricks for Transition State Searches for Click Reactions

A transition state search in AMS is performed by selecting the corresponding task:

```
Task TransitionStateSearch
```

Due to the similarities between energy minimization and transition state search, the `TransitionStateSearch` task in AMS is actually implemented as a special kind of geometry optimization using the *quasi-Newton* (page 57) optimizer. As such all the settings and keywords described on the *geometry optimization manual page* (page 47) also apply to transition state searches.

In a geometry optimization with a quasi-Newton based optimizer the Hessian is used to make a reasonably sized step in the “downhill” direction on the potential energy surface, as the goal is simply to minimize the energy. A transition state search is a bit different: In the first step a normal mode is picked along which the energy is to be *maximized*, while it is *minimized* along all other directions. Normally the mode with the lowest eigenvalue is picked, since we know that there should be exactly one negative eigenvalue at the TS geometry, but one can also choose an approximate reaction coordinate, either by setting the `ReactionCoordinate` or by adding another `System` block named `final`, similar to how it’s done for NEB. If the initial geometry is sufficiently close to the transition state, i.e. we are close to the saddle, the lowest mode is normally the correct one to follow in order to get to the ridge of the saddle. Alternatively a different mode can also be selected manually.

```
TransitionStateSearch
  ModeToFollow integer
  ReactionCoordinate
    Angle string
    Coordinate string
    Dihedral string
    Distance string
  End
End
```

TransitionStateSearch

Type Block

Description Configures some details of the transition state search.

ModeToFollow

Type Integer

Default value 1

Description In case of Transition State Search, here you can specify the index of the normal mode to follow (1 is the mode with the lowest frequency).

ReactionCoordinate

Type Block

Description Specify components of the transition state reaction coordinate (TSRC) as a linear combination of internal coordinates (distances or angles).

Angle

Type String

Recurring True

Description The TSRC contains the valence angle between the given atoms. Three atom indices followed by the weight.

Coordinate**Type** String**Recurring** True**Description** The TSRC contains Cartesian displacement of an atom: atom index followed by [x|y|z] and the weight.**Dihedral****Type** String**Recurring** True**Description** The TSRC contains the dihedral angle between the given atoms. Four atom indices followed by the weight.**Distance****Type** String**Recurring** True**Description** The TSRC contains the distance between the given atoms. Two atom indices followed by the weight.

This selection happens only in the first step. Subsequent steps will attempt to maximize along the mode that resembles most (by overlap) the previous maximization direction.

Practice shows that a transition state are much harder to find than a minimum. For a large part this is due to the much stronger anharmonicities that usually occur near the TS, which threaten to invalidate the quasi-Newton methods to find the stationary point. For this reason it is good advice to be more cautious in the optimization strategy when approaching a transition state:

- We recommend starting the transition state search with an initial geometry that is already close to the transition state. One can use a *potential energy surface scan* (page 68) along something resembling the reaction coordinate to get a rough idea where the transition state is. This geometry can then be used as an initial geometry for the transition state search.
- It is strongly recommended to provide a good initial Hessian for the transition state search. Otherwise the first step of the search may not be taken in the correct direction and subsequent steps may keep steering in the wrong direction. In AMS this is easily possible by loading a Hessian from a previous calculation, see the *initial Hessian section* (page 58) of this manual. A good way to obtain a reasonable Hessian is to compute it explicitly with one of the fast engines (i.e. at a lower level of theory) and read that Hessian as the initial Hessian for the transition state search at a higher level of theory.
- When no accurate initial Hessian is available, it may be a good idea to specify an approximate normal mode vector using the `ReactionCoordinate` input block. A reaction coordinate (RC) is a linear combination of distances and/or valence and dihedral angles:

```

TransitionStateSearch
  ReactionCoordinate
    Distance  i j      fac
    Distance  i j      fac
    Angle     i j k    fac
    Dihedral  i j k l  fac
  End
End

```

Here, *i*, *j*, *k*, and *l* are atom indices, and the *fac* is the factor with which the internal coordinate enters the linear combination.

One should be careful when specifying more than one bond or angle as the reaction coordinate. For example, suppose atom 2 is located between atoms 1 and 3. Then the following ReactionCoordinate block:

```
TransitionStateSearch
  ReactionCoordinate
    Distance 1 2 1.0
    Distance 2 3 -1.0
  End
End
```

means that the RC consists of two distances: R(1-2) and R(2-3). The positive direction of the RC is defined as an increase of the R(1-2) and a decrease of the R(2-3). In other words, this RC corresponds to atom 2 moving along the R(1-3) axis.

- As an alternative to `ReactionCoordinate` one can add a second System to the input and call it `final`. The difference between the initial and the `final` geometry will be used as the reaction coordinate. For non-periodic systems, the difference is computed in the internal coordinates and only coordinates that differ significantly (by more than about 0.1 Bohr or radian) are included. For this reason, the `final` geometry should not be too close to the initial. For periodic systems, the difference in the Cartesian coordinates is used. In this case, only coordinates that differ by more than 0.5 Bohr are included.
- When the method converges it is usually a good idea to verify that the found geometry is indeed a transition state. This can be done by performing a frequency analysis and checking whether the Hessian has exactly one negative eigenvalue (represented by a mode with a negative frequency). Doing so is expensive however. Since we are really only interested in the lowest two normal modes calculating the full Hessian is however not necessary and one can use the faster PES point characterization instead. This uses a Davidson-type algorithm to obtain the lowest few normal modes without constructing the full Hessian. The user is referred to the *PES point characterization* (page 180) documentation page for further details.

4.5 Linear Transit, PES scan

The PES scan task in AMS allows users to scan the potential energy surface of a system along one or multiple degrees of freedom, while relaxing all other degrees of freedom. If only one coordinate is scanned, this kind of calculation is usually just called a linear transit. However, since AMS allows scanning of multiple coordinates, and linear transit is just a special case of such a calculation, the task is always called a PES scan in AMS.

A linear transit may be used for instance to sketch an approximate path over the transition states between reactants and products. From this a reasonable guess for the Transition State can be obtained which may serve as starting point for a true transition state search for instance.

See also:

- [Examples](#) (page 371)
- [Tutorial Transition state search and characterization of a Ziegler Natta Catalyst](#)

The PES scan task is enabled by selecting it with the `Task` keyword:

```
Task PESScan
```

The `PESScan` block configures all details of the scan:

```
PESScan
  CalcPropertiesAtPESPoints [True | False]
  FillUnconvergedGaps [True | False]
  ScanCoordinate
```

(continues on next page)

(continued from previous page)

```

nPoints integer
Coordinate integer [x|y|z] (float){2}
Distance (integer){2} (float){2}
Angle (integer){3} (float){2}
Dihedral (integer){4} (float){2}
SumDist (integer){4} (float){2}
DifDist (integer){4} (float){2}
FromLattice
    ...
End
ToLattice
    ...
End
FromStrainVoigt (float){6}
ToStrainVoigt (float){6}
CellVolumeRange (float){2}
CellVolumeScalingRange (float){2}
LatticeARange (float){2}
LatticeBRange (float){2}
LatticeCRange (float){2}
End
End

```

The PESScan block needs to contain at least one ScanCoordinate block specifying which coordinate to scan, and how many points (keyword nPoints) to sample along this coordinate. By default, 10 points are sampled along each scanned coordinate (including the start and end point of the scan).

4.5.1 Distance, angle, and dihedral angle coordinates

The coordinate descriptors are very similar to the *constraint descriptors* (page 52) in the Constraints block used by the geometry optimization task, but are followed by two values delimiting the start and end of the coordinates, instead of just a single value:

Coordinate atomIdx [x|y|z] startValue endValue Moves the atom with index atomIdx (following the order in the System block) along the a cartesian coordinate (x, y or z), starting at startValue and ending at endValue (given in Angstrom).

Distance atomIdx1 atomIdx2 startDist endDist Scans the distance between the atoms with index atomIdx1 and atomIdx2, starting from startDist and ending at endDist, both given in Angstrom.

Angle atomIdx1 atomIdx2 atomIdx3 startAngle endAngle Scans the angle (1)–(2)–(3) between the atoms with indices atomIdx1–3, as given by their order in the System%Atoms block. The scanned angle starts at startAngle and ends at endAngle, given in degrees.

Dihedral atomIdx1 atomIdx2 atomIdx3 atomIdx4 startAngle endAngle Scans the dihedral angle (1)–(2)–(3)–(4) between the atoms with indices atomIdx1–4, as given by their order in the System%Atoms block. The scanned dihedral starts at startAngle and ends at endAngle, given in degrees.

SumDist atomIdx1 atomIdx2 atomIdx3 atomIdx4 start end Scans the sum of the distances $R(1,2)+R(3,4)$ between the atoms with indices atomIdx1–4, as given by their order in the System%Atoms block. The values to be scanned start at start and end at end, given in Angstrom.

DifDist atomIdx1 atomIdx2 atomIdx3 atomIdx4 start end Scans the difference between the distances $R(1,2)-R(3,4)$ of the atoms with indices atomIdx1–4, as given by their order in the System%Atoms block. The values to be scanned start at start and end at end, given in Angstrom.

4.5.2 Joint scan coordinates

Note that multiple of these coordinate descriptors can be combined within a single `ScanCoordinate` block. This combines the individual coordinates into one compound coordinate, i.e. all coordinates will transit together through their respective ranges. In this way the symmetric stretch in water could be scanned by specifying the following single `ScanCoordinate` block (assuming that the oxygen atom is the first in the `System%Atoms` block):

```
ScanCoordinate
  Distance 1 2 0.8 1.1
  Distance 1 3 0.8 1.1
End
```

4.5.3 Multidimensional PES scan

A multidimensional PES scan can be performed by specifying multiple `ScanCoordinate` blocks in the input. To scan the space spanned by the bending and symmetric stretch modes in water, one would use the following scan coordinates:

```
ScanCoordinate
  Distance 1 2 0.8 1.1
  Distance 1 3 0.8 1.1
End
ScanCoordinate
  Angle 2 1 3 90 130
End
```

In principle an arbitrary number of `ScanCoordinate` blocks can be combined to specify the scanned configuration space. However, the total number of sample points is the product of the number of points along all coordinates, and hence grows quickly with the number of dimensions. Furthermore, only 1D (linear transit) and 2D PES scans can be visualized in the GUI. We therefore suggest sticking with ≤ 2 dimensional PES scans. (Note that it is possible to constrain additional degrees of freedom through the `Constraints` block. This could be used to sample a few points along a third dimension “manually”, while still being able to see the surfaces in the GUI.)

4.5.4 Lattice scan coordinates for periodic systems

Several ways to scan lattice degrees of freedom were added to the AMS2022.1 release. **Note that for each unit cell, a geometry optimization is performed.** To keep the fractional coordinates fixed during the PES Scan, set `GeometryOptimization%MaxIterations` to 0.

There can be only one scan coordinate for lattice degrees of freedom in a single PES scan job. Also note that scan coordinates for lattice degrees of freedom may not contain other coordinate descriptors within the same scan coordinate. It is for example *not* possible to have a *joint scan coordinate* (page 70) for a concerted lattice and bond length stretch.

It is, however, perfectly fine to combine a lattice scan coordinate with another scan coordinate for a *two-dimensional PES scan* (page 70).

See also:

Example input files (page 412) for PES scan jobs with lattice degrees of freedom.

Important: If you use k-space sampling (e.g., with BAND or DFTB), then the k-space grid is determined for the **input structure**, which is not necessarily any of the sampled points.

Isotropic scaling of the unit cell volume or area

CellVolumeScalingRange startValue endValue Isotropic scaling of the unit cell. Example: `CellVolumeScalingRange 0.9 1.1` will scale the volume between 90% and 110% of the original unit cell. For 2D-periodic crystals, the area will be scaled instead.

CellVolumeRange startValue endValue Isotropic scaling of the unit cell. Example: `CellVolumeRange 300 500` will scale the volume between 300 Å³ and 500 Å³ for a 3d-periodic system. For 2D-periodic systems, the area will be scaled between 300 Å² and 500 Å².

Scaling of the lattice vector lengths

These options keep the angles between lattice vectors fixed.

LatticeARange startValue endValue Scans the length of the **first** lattice vector. Can be combined with the `LatticeBRange` and `LatticeCRange` keywords, but no other coordinates within the same `ScanCoordinate`. Unit: angstrom.

LatticeBRange startValue endValue Scans the length of the **second** lattice vector. Can be combined with the `LatticeARange` and `LatticeCRange` keywords, but no other coordinates within the same `ScanCoordinate`. Unit: angstrom.

LatticeCRange startValue endValue Scans the length of the **third** lattice vector. Can be combined with the `LatticeARange` and `LatticeBRange` keywords, but no other coordinates within the same `ScanCoordinate`. Unit: angstrom.

Strain matrix in Voigt notation

3D crystal: FromStrainVoigt xx yy zz yz xz xy, ToStrainVoigt xx yy zz yz xz xy The `FromStrainVoigt` and `ToStrainVoigt` keywords need to be applied together. Example: `FromStrainVoigt -0.1 -0.1 -0.1 -0.1 -0.1 -0.1, ToStrainVoigt 0.1 0.1 0.1 0.1 0.1 0.1`

2D crystal: FromStrainVoigt xx yy xy, ToStrainVoigt xx yy xy The `FromStrainVoigt` and `ToStrainVoigt` keywords need to be applied together. Example: `FromStrainVoigt -0.1 -0.1 -0.1, ToStrainVoigt 0.1 0.1 0.1`

1D crystal: FromStrainVoigt xx, ToStrainVoigt xx The `FromStrainVoigt` and `ToStrainVoigt` keywords need to be applied together. Example: `FromStrainVoigt -0.1, ToStrainVoigt 0.1`

Scan arbitrary lattices

Scan arbitrary lattices specifying the initial and final lattice vectors, using the same format as in the *System%Lattice* (page 32) block. The PES scan will then interpolate the lattice vectors linearly between these two values:

```
ScanCoordinate
  FromLattice
    ! lattice vectors as in System%Lattice
  End
  ToLattice
    ! ...
  End
End
```

4.5.5 Calculate properties for all PES points

By default the engine result files for the individual PES points are not saved on disk, as this can easily lead to huge amounts of data to be stored. This behavior can be changed with the `PESScan%CalcPropertiesAtPESPoints` keyword:

PESScan

CalcPropertiesAtPESPoints

Type Bool

Default value No

Description Whether to perform an additional calculation with properties on all the sampled points of the PES. If this option is enabled AMS will produce a separate engine output file for every sampled PES point.

Note that this performs a full single point calculation on every sampled PES point, including the calculation of any *PES point properties* (page 178) selected in `Properties` block.

4.5.6 Troubleshooting

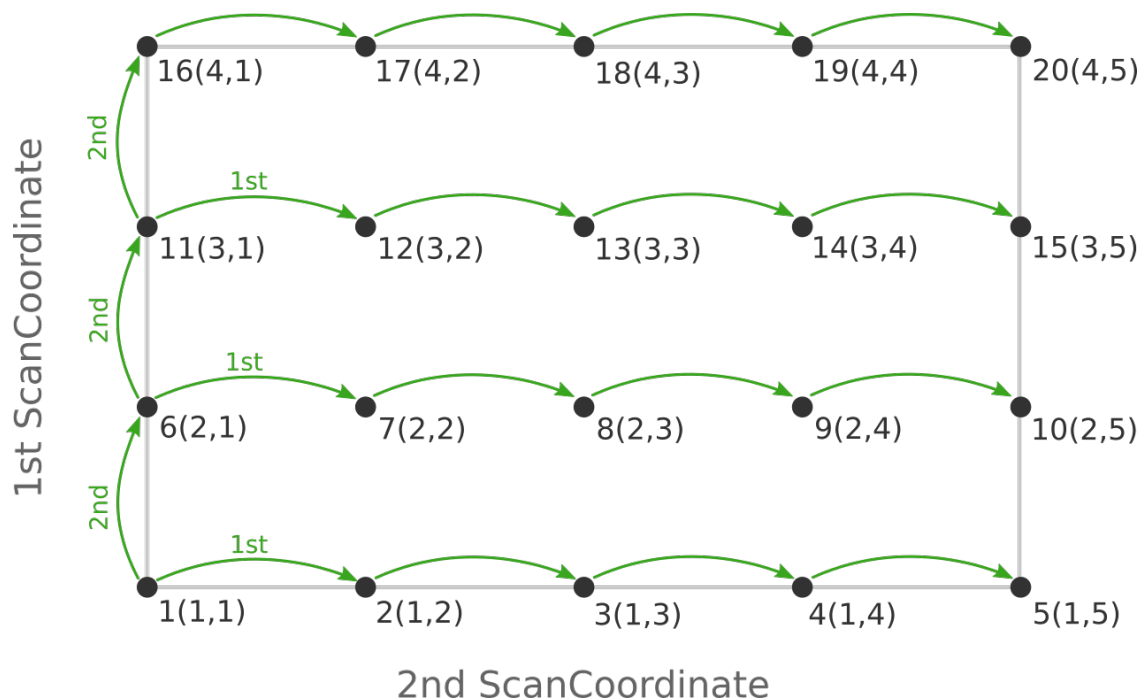
Technically all PES scan calculations are conducted as a series of geometry optimizations with constraints for the scanned coordinates, where the value of the constraint varies slowly through the scanned range. In this way every sampled point on the potential energy surface corresponds to a particular set of constraints. As with any geometry optimization, it can happen that an optimization towards a particular point on the potential energy surface does not converge. This is the most common problem encountered during PES scan calculations.

Since PES scans are implemented as a series of geometry optimizations, they are influenced by the settings used for the geometry optimizer, e.g. its convergence thresholds and the maximum number of steps before an optimization is considered to have failed. The optimizer is configured in the `GeometryOptimization` block, see the page on *geometry optimization* (page 47) in the AMS manual.

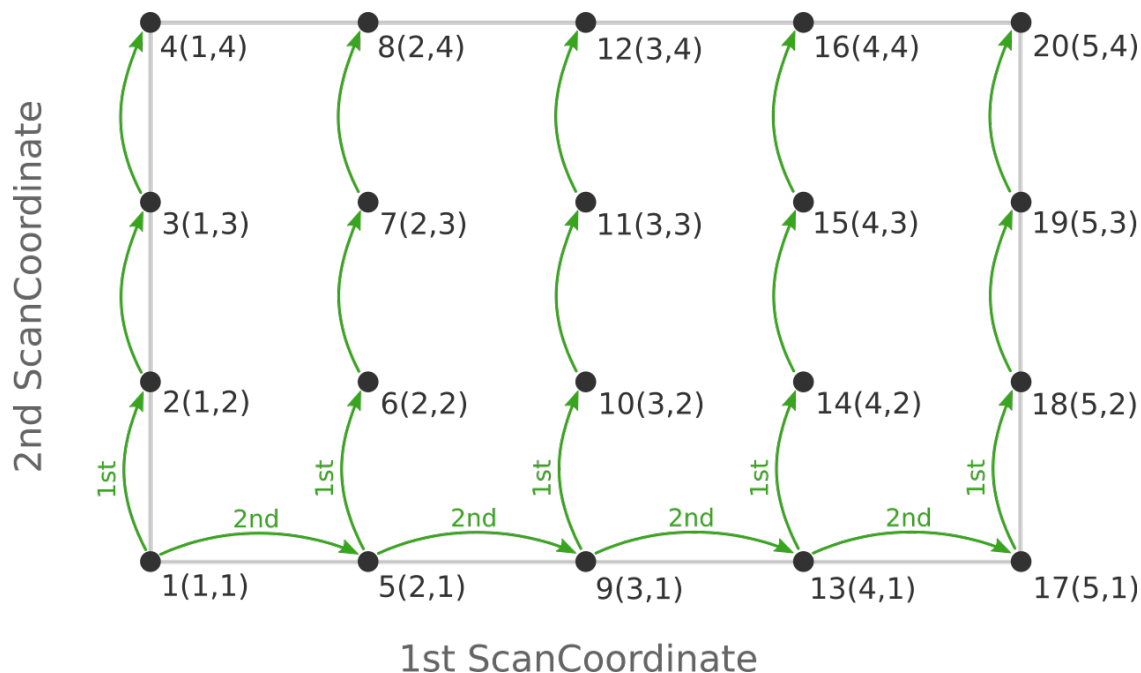
While tweaking the geometry optimizer's settings can sometimes help with convergence problems, these problems can also be easily caused by errors in the user input.

A very common problem is that the geometry in the input, i.e. the `System` block, is incompatible with the starting values of the scanned coordinates. This would for example be the case if one wants to scan a dihedral angle from 0 to 90 degrees, but the actual angle on the input geometry is close to 90 degrees. In this case it would be better to flip the scanned range from 90 to 0 degrees, so that the input geometry already close to the first sampled point on the PES. Otherwise the optimization for the first point has to cross a very long distance on the PES, making convergence much harder. AMS automatically detects this and prints a warning. We generally advise preparing the input geometry for a PES scan by first running a geometry optimization with constraints set to lower bound of the scanned coordinate intervals.

For multidimensional PES scans the order in which the PES points are visited depends on the order in which the scanned coordinates are specified, i.e. the order of the `ScanCoordinate` blocks in the input. Generally, the order in which the PES points are visited is such that the coordinate which was specified in the first `ScanCoordinate` block varies **slowest**. This is illustrated in the following figure:



Here the scan starts at point 1 (1, 1) at the bottom left corner of the PES and first moves along the entire range of the 2nd scan coordinate, before taking a step along the 1st coordinate to point 6 (2, 1). The same PES points could be visited in a different order (and under different names) if the order of the two `ScanCoordinate` blocks is reversed in the AMS input:



Depending on the shape of the scanned potential energy surface a particular order of visiting the PES points might be easier or harder for the optimizer, and convergence problems can sometimes be fixed by simply changing the order of the scanned coordinates. In the example above, it might be that scanning along the “vertical” direction is “harder” than scanning along the “horizontal” direction. In this case one should use the scan order from the first picture, which has only three “vertical” steps (whereas the other scan order has 15).

Note that AMS has a little safe-guard built in to help with PES scan convergence issues: If the optimization towards a particular PES point did not succeed in the initial attempt, AMS will later try again, but starting from a different (converged) point close to unconverged one. This “PES gap filling” happens at the very end of the calculation, after the initial scan has been completed. This gap filling step is enabled by default, but can be controlled with the `PESScan%FillUnconvergedGaps` keyword:

PESScan**FillUnconvergedGaps**

Type Bool

Default value Yes

Description After the initial pass over the PES, restart the unconverged points from converged neighboring points.

4.5.7 Output

Results are printed to the text output and stored in the binary result file `ams.rkf`. Most information is found in the `PESScan` section, which references the corresponding geometries from the `History` section via the `PESScan%HistoryIndices` entry.

PESScan Section content: Data related to the Potential Energy Surface (PES) Scan procedure.

PESScan%GOConverged

Type bool_array

Description Whether the (constrained) optimization at the various PES scan points converged.

Shape [nPoints]

PESScan%HistoryIndices

Type int_array

Description The indices of the frames in the History section corresponding to the PES point values.

Shape [nPoints]

PESScan%nPoints

Type int

Description The total number of scanned PES points. This is the product of all `nPoints(#)` values.

PESScan%nPoints (#)

Type int

Description Number of points along the corresponding scan coordinate.

PESScan%nScanCoord

Type int

Description Number of (independent) coordinates along which the PES scan is performed.

PESScan%PES

Type float_array

Description The total energy at each particular PES point.

Unit Hartree

Shape [nPoints]

PESScan%PESCoords

Type float_array

Description The values of all coordinates for each particular PES point.

Shape[:, nPoints]

PESScan%RangeEnd (#)

Type float_array

Description The final value(s) for the corresponding scan coordinate.

PESScan%RangeStart (#)

Type float_array

Description The starting value(s) for the corresponding scan coordinate.

PESScan%ScanCoord (#)

Type string_fixed_length

Description A human readable description of the scan coordinate.

4.6 Nudged Elastic Band (NEB)

The Nudged Elastic Band (NEB) method¹ can be used to find a reaction path and the transition state between a reactant and a product state.

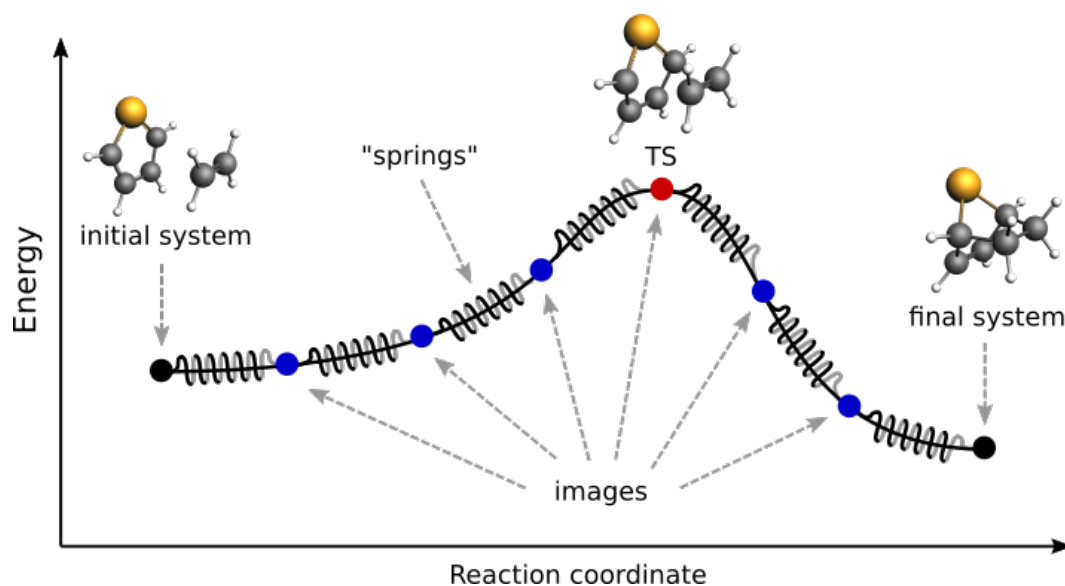


Fig. 4.1: Pictorial representation of a reaction path computed with NEB

¹ G. Henkelman, B.P. Uberuaga and H. Jonsson, *A climbing image nudged elastic band method for finding saddle points and minimum energy paths*, *Journal of Chemical Physics* 113, 9901 (2000) (<https://doi.org/10.1063/1.1329672>)

At the beginning of a NEB calculation, the geometry of the initial and final systems are optimized to minimize their energy (unless the *OptimizeEnds* (page 78) option is set to False).

Then, a rough approximation of the reaction path is build: a set of *images* is created by performing a linear interpolation between the **initial** and **final** systems. If there is more than two systems provided, a spline interpolation is performed between the initial, the intermediate (in the lexicographical order) and the final system (see below).

Finally, a reaction path is found by performing a simultaneous optimization of all the images. In the NEB method the images are not independent from each other. The force on each image depend on its neighboring images: at each step the forces parallel to the reaction path are eliminated and a so-called spring force is added that tries to keep each image in the middle between its neighbors. This does not let images slide to the initial or final reaction state and ensures that they are evenly distributed along the reaction path.

During the NEB path optimization, a climbing image algorithm is used to drive the highest-energy image in the path to the transition state (unless the *Climbing* (page 78) option is set to False).

Be aware that NEB is a computationally expensive method, typically involving hundreds if not thousands of energy and gradients evaluations.

See also:

- [Nudged Elastic Band \(NEB\) Examples](#) (page 399)
- [GUI Nudged Elastic Band tutorial](#)

4.6.1 Input

A NEB calculation in AMS is triggered by setting the `Task` to NEB:

```
Task NEB
```

The NEB method requires two or more input systems. The first, unnamed system is used as the **initial system** and the system called `final` is used as a **final system**. These two systems are mandatory, unless the `LoadPath` feature is used, see below. This is an example of system-definitions for a HCN isomerization reaction:

```
Task NEB

# This is the initial system:
System
  Atoms
    C   0.0000   0.0000   0.0000
    N   1.1800   0.0000   0.0000
    H   2.1960   0.0000   0.0000
  End
End

# This is the final system (note the header 'final' in the next line):
System final
  Atoms
    C   0.0000   0.0000   0.0000
    N   1.1630   0.0000   0.0000
    H  -1.0780   0.0000   0.0000
  End
End
```

Optionally, more systems can be used to provide a better approximation for the reaction path. An intermediate system can have any name, but the name determines its position with respect to others. The intermediate systems are ordered lexicographically using their (case-sensitive) names and then placed evenly in that order between the initial and the final states. After that, the spline interpolation between the geometries (including lattice parameters) will be used to generate

the initial images. For example, if you call the intermediate systems `a`, `b`, and `c` then the initial NEB path will be constructed by interpolating along the `initial-a-b-c-final` chain. When providing more than two input systems it may be a good idea to optimize the end points in advance and set `OptimizeEnds` (page 78) to `False` to prevent creating an unbalanced reaction path. The reason is that the interpolation is performed after the end points are optimized.

Note that not only the atomic coordinates, but also the lattice parameters and the charge (if non-zero) must be set for all input systems.

Important: The order in which atoms are specified in the `System%Atoms` blocks **must be the same for all systems**. The order of the atoms must be consistent because the images-interpolation algorithm maps the `n`-th atom of the initial system to the `n`-th atom of the final system.

If you have run a PESScan calculation for the system and would like to do NEB, or would like to repeat NEB for it with a different number of images then you can use the `LoadPath` feature. You need to provide the file name from which to load the path using the `File` key. The program will load the last geometries for the path points found in the file and use them for interpolation. Note that this will replace both the initial and the final point. Neither the initial nor the final geometry needs to be present in the input in this case because, if present, they will be replaced.

You can choose to use only part of the path, for example if the the PESScan revealed more than one barrier or if its end points do not correspond to minima on the path. In such a case, a list of point to be included in the interpolation should be specified using the `Points` key. Remember that you can specify a list of integers as `i:j`, for example to include points 13 through 25 use `Points 13:25`.

Alternatively, you can choose to use arbitrary geometries from the History section of the `ams.rkf` file. In this case you can specify their indices in the `Geometries` key. When using the `Geometries` key, the `ams.rkf` does not have to come from a PESScan or an NEB calculation. It just needs to have the History section with some geometries. It may come, for example, from molecular dynamics.

NEB

LoadPath

Type Block

Description Provide details about the trajectory to get the initial NEB path from. PESScan and NEB trajectories are supported. Only the last geometry for each point on the trajectory is considered.

File

Type String

GUI name Initial path file

Description Provide an `ams.rkf` file to load the initial path from. All geometries of this calculation, including initial and final, will be taken from the History section of the file.

Note that for a PESScan it should be a 1D path.

Geometries

Type Integer List

GUI name Raw geometry indices

Description Raw indices of the geometries from the History section. By default the last geometry of each path point is used.

Points

Type Integer List

GUI name Path points

Description By default the whole path is used, which may sometimes be not desirable. For example when a PESScan revealed multiple barriers. In this case one can specify indices of the path points to be used. The last geometry of the specified path point will be loaded.

All NEB-specific options are specified in the NEB input block:

```
NEB
  Climbing Yes/No
  ClimbingThreshold float
  Images integer
  InterpolateInternal Yes/No
  InterpolateShortest Yes/No
  Iterations integer
  Jacobian float
  LoadPath
    File string
    Geometries integer_list
    Points integer_list
  End
  MapAtomsToCell Yes/No
  OldTangent Yes/No
  OptimizeEnds Yes/No
  OptimizeLattice Yes/No
  Parallel
    nCoresPerGroup integer
    nGroups integer
    nNodesPerGroup integer
  End
  ReOptimizeEnds Yes/No
  Restart string
  Skewness float
  Spring float
End
```

All keys of the NEB block have reasonable defaults or are optional. Thus, in principle, the NEB block can be omitted altogether. These are the main options:

NEB

Images

Type Integer

Default value 8

GUI name Number of images

Description Number of NEB images (not counting the chain ends). Using more images will result in a smoother reaction path and can help with convergence problems, but it will also increase the computation time.

Iterations

Type Integer

GUI name Maximum number of iterations

Description Maximum number of NEB iterations. The default value depends on the number of degrees of freedom (number of images, atoms, periodic dimensions).

Spring

Type Float
Default value 1.0
Unit Hartree/Bohr²
GUI name Spring value
Description Spring force constant in atomic units.

Skewness

Type Float
Default value 1.0
GUI name Skewness
Description Degree of how much images are shifted towards or away from the TS, which may help tackle problems with a long reaction path (for example involving a loose adsorption complex) without needing too many images. A value greater than 1 will make sure that images are concentrated near the transition state. The optimal value depends on the path length, the number of images (larger [Skewness] may be needed for a longer path and fewer images). Technically [Skewness] is equal to the ratio between the optimized distances to the lower and the higher neighbor image on the path.

Climbing

Type Bool
Default value Yes
GUI name Climb highest image to TS
Description Use the climbing image algorithm to drive the highest image to the transition state.

ClimbingThreshold

Type Float
Default value 0.0
Unit Hartree/Bohr
GUI name CI force threshold
Description Climbing image force threshold. If ClimbingThreshold > 0 and the max perpendicular force component is above the threshold then no climbing is performed at this step. This entry can be used to get a better approximation for the reaction path before starting the search for the transition state. A typical value is 0.01 Hartree/Bohr.

InterpolateInternal

Type Bool
Default value Yes
GUI name Interpolate in Internal coordinates
Description The initial NEB image geometries are calculated by interpolating between the initial and the final state. By default, for non-periodic systems the interpolation is performed in Internal coordinates but the user can choose to do it in the Cartesian ones. For periodic systems the interpolation is always done in Cartesian coordinates.

InterpolateShortest

Type Bool

Default value Yes

GUI name Interpolate across cell boundary

Description Allow interpolation across periodic cell boundaries. Set to false if an atom is intended to move more than half across the simulation box during reaction.

OptimizeEnds

Type Bool

Default value Yes

GUI name Optimize reactants/products

Description Start the NEB with optimization of the reactant and product geometries.

Restart

Type String

GUI name Restart from

Description Provide an ams.rkf file from a previous NEB calculation to restart from. It can be an unfinished NEB calculation or one performed with different engine parameters.

ReOptimizeEnds

Type Bool

Default value No

GUI name Re-optimize reactants/products

Description Re-optimize reactant and product geometries upon restart.

The following keys are related to solid-state NEB (SS-NEB):

NEB

OptimizeLattice

Type Bool

Default value No

GUI name Optimize lattice

Description Turn on the solid-state NEB (SS-NEB).

Jacobian

Type Float

GUI name Jacobian value

Description Scaling factor used to convert the lattice strain to a NEB coordinate value. Default value: $\sqrt{N} \cdot (V/N)^{1/d}$, where V - lattice volume (area for 2D, length for 1D), N - number of atoms, and d - number of periodic dimensions.

MapAtomsToCell

Type Bool

Default value Yes

GUI name Map atoms to cell

Description Translate atoms to the [-0.5,0.5] cell before every step. This option cannot be disabled for SS-NEB.

At each iteration, the images may be computed in parallel. The parallel execution is normally configured completely automatically, but users can override the automatic parallelization using the keys in the `Parallel` block.

NEB**Parallel**

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

The following keys modify other aspects of the NEB and should, in principle, be left to their defaults:

NEB**OldTangent**

Type Bool

Default value No

GUI name Use old tangent

Description Turn on the old central difference tangent.

4.6.2 Frozen atom constraints

It is possible to perform NEB with part of the system frozen, using any of the following keys of the `Constraints` block or a combination thereof:

Constraints**Atom**

Type Integer

Recurring True

Description Fix the position of an atom. Just one integer referring to the index of the atom in the [System%Atoms] block.

AtomList

Type Integer List

Recurring True

Description Fix positions of the specified atoms. A list of integers referring to indices of atoms in the [System%Atoms] block.

FixedRegion

Type String

Recurring True

Description Fix positions of all atoms in a region.

Note: the frozen atom constraints will be enforced both during the geometry optimizations of the initial and final systems and during the NEB optimization.

4.6.3 Optimizations and convergence criteria

The NEB path is optimized using a limited-memory BFGS (l-BFGS) method where the system being optimized is a union of all NEB images with their respective molecular and spring forces.

The NEB convergence thresholds are defined in the *GeometryOptimization%Convergence block* (page 48). NEB is considered converged when the following criteria are satisfied:

- the change in the highest image energy must be less than [GeometryOptimization%Convergence%Energy]
- the max atomic force component for the highest image must be less than [GeometryOptimization%Convergence%Gradients]
- the max atomic force component for all other images must be less than ten times the [GeometryOptimization%Convergence%Gradients] value.

If the optimization of the initial NEB end point fails to converge, you can try using the *FIRE optimization method* (page 55).

4.6.4 Output

Results are printed to the text output and stored in the binary result file 'ams.rkf'. In the 'ams.rkf' file, NEB calculation results are stored in the History section just like in a normal geometry optimization. The NEB section of the RKF file contains additional, NEB-specific, information.

The NEB reaction path can be visualized using the **AMSmovie GUI module**.

4.6.5 Troubleshooting

- In case the geometry optimization of the initial and final systems fails: try using the *FIRE optimization method* (page 55)
- In case the optimization of the NEB path does not converge:
 - make sure that the order in which the atoms are defined is consistent between the initial and final systems (see the *important note* in the *NEB input section* (page 76));
 - try increasing the number of *NEB images* (page 78);
 - try tweaking the *TrustRadius* (page 63) or *TrialStep* (page 63) options (see *Limited-memory BFGS* (page 63)) ;
 - try specifying one or more **intermediate** systems.

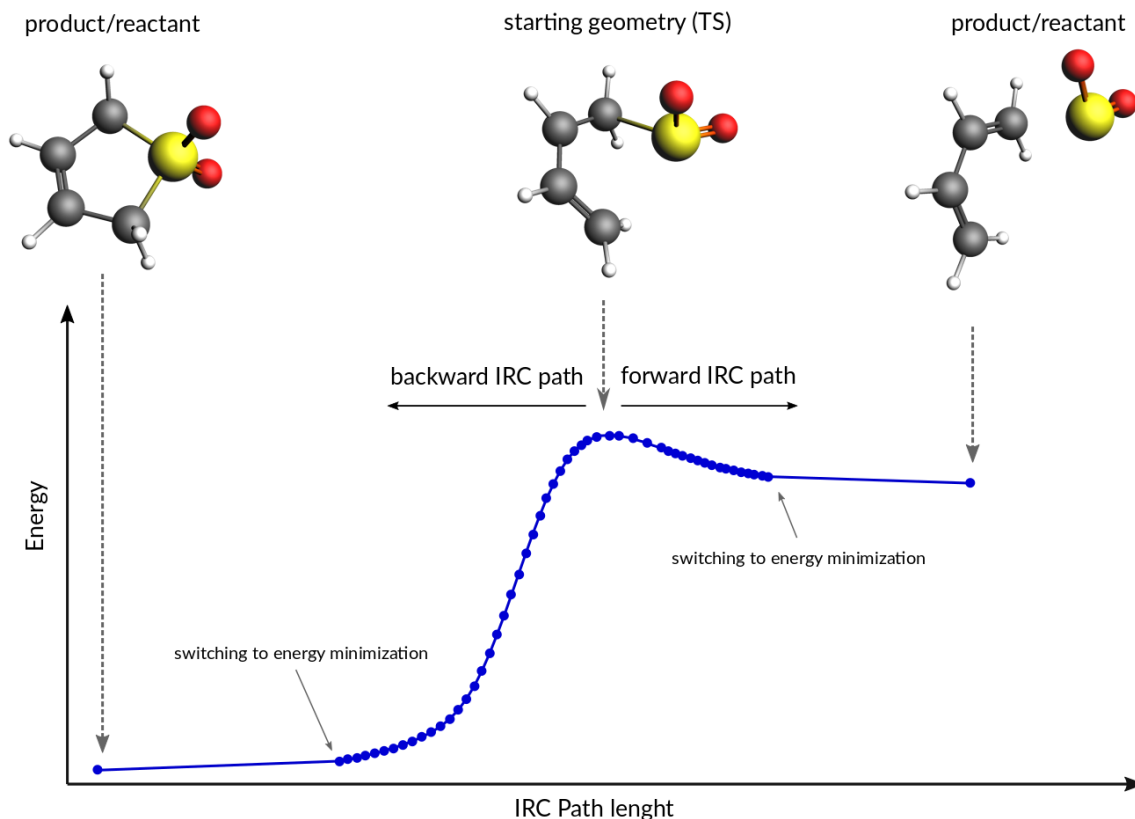
4.7 Intrinsic Reaction Coordinate (IRC)

The path of a chemical reaction can be traced from the transition state (TS) to the products and/or reactants using the Intrinsic Reaction Coordinate (IRC) method^{1,2}. **The method assumes that the starting geometry is a fair approximation of the TS.** A minimum energy profile (MEP) is defined as the steepest-descent path on the potential energy surface from the transition state down towards a local minimum. An IRC path is defined similarly but in the mass-weighted coordinates³, which means that instead of the steepest descent direction it follows that of the maximum instantaneous acceleration. This makes IRC somewhat related to the Molecular Dynamics method. The energy profile is obtained as well as the length and curvature properties of the path, providing the basic quantities for an analysis of the reaction path.

¹ L. Deng, T. Ziegler and L. Fan, *A combined density functional and intrinsic reaction coordinate study on the ground state energy surface of H₂ CO*, *Journal of Chemical Physics* 99, 3823 (1993) (<https://doi.org/10.1063/1.466129>)

² L. Deng and T. Ziegler, *The determination of Intrinsic Reaction Coordinates by density functional theory*, *International Journal of Quantum Chemistry* 52, 731 (1994) (<https://doi.org/10.1002/qua.560520406>)

³ C. Gonzalez and H.B. Schlegel, *Reaction Path Following In Mass-Weighted Internal Coordinates* *J. Phys. Chem.* 94, 5523-5527 (1990) (<https://doi.org/10.1021/j100377a021>)



See also:

[Examples](#) (page 371) and the [PES exploration for hydrohalogenation tutorial](#)

4.7.1 Method details

Calculation of an IRC path consists of two nested loops, the so-called outer and inner loops. The outer loop runs over IRC points and the inner loop is over geometry optimization steps for the given IRC point. The first IRC point starts from the transition state geometry, which is a saddle point, in one of the two possible downhill directions. Each IRC point after that starts from the optimized geometry of the previous point. At the start of every step, the pivot point is determined, which is a point at the $\text{Step}/2$ distance in the direction opposite to the gradient. When working in the mass-weighted coordinates, this direction corresponds to the acceleration of the corresponding atom. The final point of the given IRC step corresponds to the energy minimum point at the same distance ($\text{Step}/2$) from the pivot point further downhill. More precisely, the coordinates of the target point are optimized during the inner loop to minimize projection of the gradient on the hypersphere of radius $\text{Step}/2$ around the pivot point. The angle between the (pivot-start) and (pivot-final) vectors determines the curvature of the reaction path. If this angle becomes smaller than 90 degrees then the IRC scan is considered to have reached vicinity of an endpoint and the program switches to energy minimization (options for this energy minimization can be specified in the [Geometry Optimization](#) (page 48) block.). If the angle is between 90 and 120 degrees then the current IRC step is canceled and a new one is started from the same starting point with half the initial Step parameter. In all other cases the optimized geometry becomes a starting point for the next IRC step. By default, when the forward path is completed the backward one is started from the same TS geometry. When both forward and backward paths are complete, a summary of the whole reaction path is printed to the output.

4.7.2 Input

The IRC scan in AMS is triggered by setting the Task to IRC:

```
Task IRC
```

All IRC-related options are specified in the IRC input block:

```
IRC
  Convergence
    Gradients float
    Step float
  End
  CoordinateType [Cartesian | Delocalized]
  Direction [Both | Forward | Backward]
  InitialHessian
    File string
    Type [Calculate | FromFile]
  End
  KeepConvergedResults Yes/No
  MaxIRCSteps integer
  MaxIterations integer
  MaxPoints integer
  MinEnergyProfile Yes/No
  MinPathLength float
  Restart
    File string
    RedoBackward integer
    RedoForward integer
  End
  Step float
End
```

All keys of the IRC block have reasonable defaults or are optional. Thus, in principle, the IRC block can be omitted altogether. These are some of the main options:

IRC

Direction

Type Multiple Choice

Default value Both

Options [Both, Forward, Backward]

Description Select direction of the IRC path. The difference between the Forward and the Backward directions is determined by the sign of the largest component of the vibrational normal mode corresponding to the reaction coordinate at the transition state geometry. The Forward path correspond to the positive sign of the component. If Both is selected then first the Forward path is computed followed by the Backward one.

Step

Type Float

Default value 0.2

GUI name Step size

Description IRC step size in mass-weighted coordinates, $\sqrt{\text{amu}} \cdot \text{bohr}$. One may have to increase this value when heavy atoms are involved in the reaction, or decrease it if the reactant or products are very close to the transition state.

InitialHessian

Type Block

Description Options for initial Hessian at the transition state. The first eigenvalue of the initial Hessian defines direction of the first forward or backward step. This block is ignored when restarting from a previous IRC calculation because the initial Hessian found in the restart file is used.

File

Type String

GUI name File

Description If 'Type' is set to 'FromFile' then in this key you should specify the RKF file containing the initial Hessian (or the ams results dir. containing it). This can be used to load a Hessian calculated previously with the 'Properties%Hessian' keyword. If you want to also use this file for the initial geometry then also specify it in a 'LoadSystem' block.

Type

Type Multiple Choice

Default value Calculate

Options [Calculate, FromFile]

GUI name Initial Hessian

Description Calculate the exact Hessian for the input geometry or load it from the results of a previous calculation.

The following keys set limits on the number of steps for the inner and outer IRC loops and, related to that, the geometry optimization criteria. Note that tighter criteria may require a greater MaxIterations limit. Please also note that the outer loop limits are valid for each half of the path (forward and backward) separately. That is, if all settings are left at their defaults then up to 200 IRC points may be calculated, each of them may require up to 300 energy evaluations.

IRC

MaxIRCSteps

Type Integer

GUI name Maximum IRC steps

Description Soft limit on the number of IRC points to compute in each direction. After the specified number of IRC steps the program will switch to energy minimization and complete the path. This option should be used when you are interested only in the reaction path area near the transition state. Note that even if the soft limit has been hit and the calculation has completed, the IRC can still be restarted with a 'RedoBackward' or 'RedoForward' option.

MaxPoints

Type Integer

Default value 100

GUI name Maximum points

Description Hard limit on the number of IRC points to compute in each direction. After the specified number of IRC steps the program will stop with the current direction and switch to the next one. If both 'MaxPoints' and 'MaxIRCSteps' are set to the same value then 'MaxPoints' takes precedence, therefore this option should be used to set a limit on the number of IRC steps if you intend to use the results later for a restart.

MaxIterations

Type Integer

Default value 300

GUI name Maximum iterations

Description The maximum number of geometry iterations allowed to converge the inner IRC loop. If optimization does not converge within the specified number of steps, the calculation is aborted.

Convergence

Type Block

Description Convergence at each given point is monitored for two items: the Cartesian gradient and the calculated step size. Convergence criteria can be specified separately for each of these items. The same criteria are used both in the inner IRC loop and when performing energy minimization at the path ends.

Gradients

Type Float

Default value 0.001

Unit Hartree/Angstrom

GUI name Gradient convergence

Description Convergence criterion for the max component of the residual energy gradient.

Step

Type Float

Default value 0.001

Unit Angstrom

GUI name Step convergence

Description Convergence criterion for the max component of the step in the optimization coordinates.

MinPathLength

Type Float

Default value 0.1

Unit Angstrom

Description Minimum length of the path required before switching to energy minimization. Use this to overcome a small kink or a shoulder on the path.

The following keys modify other aspects of the IRC scan:

IRC

CoordinateType

Type Multiple Choice

Default value Cartesian

Options [Cartesian, Delocalized]

GUI name Coordinates used for optimization

Description Select the type of coordinates in which to perform the optimization. Note that the Delocalized option should be considered experimental.

MinEnergyProfile

Type Bool

Default value No

GUI name Minimum energy profile

Description Calculate minimum energy profile (i.e. no mass-weighting) instead of the IRC.

KeepConvergedResults

Type Bool

Default value Yes

Description Keep the binary RKF result file for every converged IRC point. These files may contain more information than the main ams.rkf result file.

It is possible to restart an IRC calculation that crashed, has been killed or exceeded the MaxPoints limit, or to re-compute the path starting from a certain point, using the Restart key:

IRC

Restart

Type Block

Description Restart options. Upon restart, the information about the IRC input parameters and the initial system (atomic coordinates, lattice, charge, etc.) is read from the restart file. The IRC input parameters can be modified from input. Except for 'MaxPoints' and 'Direction' all parameters not specified in the input will use their values from the restart file. The 'MaxPoints' and 'Direction' will be reset to their respective default values if not specified in the input. By default, the IRC calculation will continue from the point where it left off. However, the 'RedoForward' and/or 'RedoBackward' option can be used to enforce recalculation of a part of the reaction path, for example, using a different 'Step' value.

File

Type String

GUI name Restart

Description Name of an RKF restart file generated by a previous IRC calculation. Do not use this key to provide an RKF file generated by a TransitionStateSearch or a SinglePoint calculation, use the 'LoadSystem' block instead.

RedoBackward

Type Integer

Default value 0

Description IRC step number to start recalculating the backward path from. By default, if the backward path has not been completed then start after the last completed step. If the

backward path has been completed and the 'RedoBackward' is omitted then no point on the backward path will be recomputed.

RedoForward

Type Integer

Default value 0

Description IRC step number to start recalculating the forward path from. By default, if the forward path has not been completed then start after the last completed step. If the forward path has been completed and the 'RedoForward' is omitted then no point on the forward path will be recomputed.

4.7.3 Output

A summary of reaction path is printed to the output file at the end of the IRC calculation.

The IRC reaction path can be visualized using the AMSmovie GUI module.

Results of an IRC calculation are also stored in the History section of the 'ams.rkf' file, just like in a normal geometry optimization. In addition to the standard KF variables such as "Coords" and "Energy", the following IRC-specific variables are also created:

- *IRCDirection* - IRC direction to which this point belongs: 1 - forward, 2 - backward.
- *IRCIteration* - the IRC (a.k.a. the outer loop) iteration number.
- *OptIteration* - the geometry optimization (a.k.a. the inner loop) iteration number (0 means the results correspond to the converged geometry at this IRC step).
- *IRCGradMax* - value of the max component of the IRC gradient that determines convergence of the inner loop.
- *IRCGradRms* - the RMS value of the IRC gradient that determines convergence of the inner loop. Both the *ircGradRms* and the *ircGradMax* are given in the mass-weighted atomic units for IRC steps and in the atomic units for the final minimization loop.
- *ArcLength* - length, in Angstrom, of the arc that connects the initial and the final point of this IRC step. The corresponding pivot point is located near the the middle point of the arc.
- *Angle* - value of the angle (in degrees) between lines connecting the pivot point with the initial and final points. A value of 180 degrees means the path is passing straight through the pivot point, while a smaller value means the path makes a bend at this point.
- *PathLength* - sum of the *ArcLength* values from the transition state up to this point, in Angstrom.
- *Converged* - a Fortran logical value containing the convergence status of the given geometry.

The IRC section of the RKF file contains all the data needed for a successful restart procedure.

4.8 Excited state optimizations

It depends on the engine if it is possible to do an electronically excited state optimization, like an electronically excited state *geometry optimization* (page 47), *transition state search* (page 65), *linear transit*, *PES scan* (page 68), or *IRC* (page 83). Required is that the engine should be able to calculate the nuclear gradient for a particular electronically excited state. ADF and DFTB are engines that can do such calculation. If the excited state gradient is available one can also calculate an *IR spectrum* (page 189) of the excited state, and one could calculate a *vibrationally resolved electronic spectrum* (page 224).

One should look in the documentation of the engine how to set up the calculation of the excited state gradient.

4.9 Molecular dynamics

Molecular dynamics (MD) can be used to simulate the evolution of a system in time.

See also:

- [Examples](#) (page 371)
- [AMS GUI Tutorial](#)
- [MD trajectory analysis tool](#) (page 279)

To perform a MD simulation, first select the corresponding Task:

```
Task MolecularDynamics
```

All aspects of the simulation can then be configured using the `MolecularDynamics` block.

```
MolecularDynamics
  AddMolecules
    AtomTemperature float
    ContactDistance float
    Coords float_list
    CoordsBox float_list
    CoordsSigma float_list
    DeviationAngle float
    Energy float
    EnergySigma float
    FractionalCoords float_list
    FractionalCoordsBox float_list
    FractionalCoordsSigma float_list
    Frequency integer
    MinDistance float
    MoleFraction float
    NumAttempts integer
    Rotate Yes/No
    StartStep integer
    StopStep integer
    System string
    Temperature float
    TemperatureSigma float
    Velocity float
    VelocityDirection float_list
    VelocitySigma float
  End
  ApplyForce
    Force float_list
    PerAtom Yes/No
    Region string
  End
  ApplyVelocity
    Components [X | Y | Z | XY | YZ | XZ | XYZ]
    Region string
    Velocity float_list
  End
  Barostat
    BulkModulus float
    ConstantVolume Yes/No
    Duration integer_list
```

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```

Equal [None | XYZ | XY | YZ | XZ]
Pressure float_list
Scale [XYZ | Shape | X | Y | Z | XY | YZ | XZ]
Tau float
Type [None | Berendsen | MTK]
End
BinLog
  BiasEnergy Yes/No
  BoostFactor Yes/No
  ConservedEnergy Yes/No
  Density Yes/No
  Hypertime Yes/No
  KineticEnergy Yes/No
  MaxBiasEnergy Yes/No
  MaxBoostFactor Yes/No
  PotentialEnergy Yes/No
  Pressure Yes/No
  PressureTensor Yes/No
  Step Yes/No
  Temperature Yes/No
  Time Yes/No
  TotalEnergy Yes/No
  Volume Yes/No
End
BondBoost
  Chain
    AtomNames string
    MaxDistances float_list
    MinDistances float_list
  End
  DistanceRestraint string
  Moving Yes/No
  NSteps integer
  NumInstances integer
  Units [Default | MD]
End
CRESTMTD
  AddEnergy Yes/No
  GaussianScaling
    ScaleGaussians Yes/No
    ScalingSlope float
  End
  Height float
  NGaussiansMax integer
  NSteps integer
  Region string
  RestartFile string
  Width float
End
CVHD
  Bias
    DampingTemp float
    Delta float
    Height float
  End
  ColVarBB
    at1

```

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```
        region string
        symbol string
    End
    at2
        region string
        symbol string
    End
    cutoff float
    p integer
    rmax float
    rmin float
    End
    Frequency integer
    StartStep integer
    StopStep integer
    WaitSteps integer
End
CalcPressure Yes/No
Checkpoint
    Frequency integer
    WriteProperties Yes/No
End
CopyRestartTrajectory Yes/No
CosineShear
    Acceleration float
    Enabled Yes/No
    FlowDirection float_list
    ProfileAxis [X | Y | Z]
End
Deformation
    LatticeVelocity # Non-standard block. See details.
    ...
    End
    LengthRate float_list
    LengthVelocity float_list
    Period float
    ScaleAtoms Yes/No
    StartStep integer
    StopStep integer
    StrainRate # Non-standard block. See details.
    ...
    End
    TargetLattice # Non-standard block. See details.
    ...
    End
    TargetLength float_list
    Type [Linear | Exponential | Sine | Cosine]
End
Gravity
    Acceleration float
End
HeatExchange
    HeatingRate float
    Method [Simple | HEX | eHEX]
    Sink
        AtomList integer_list
        Box
```

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```

        Amax float
        Amin float
        Bmax float
        Bmin float
        Cmax float
        Cmin float
    End
    Region string
End
Source
    AtomList integer_list
    Box
        Amax float
        Amin float
        Bmax float
        Bmin float
        Cmax float
        Cmin float
    End
    Region string
End
StartStep integer
StopStep integer
End
InitialVelocities
    File string
    RandomVelocitiesMethod [Exact | Boltzmann | Gromacs]
    Temperature float
    Type [Zero | Random | FromFile | Input]
    Values # Non-standard block. See details.
    ...
End
End
NSteps integer
Plumed
    Input # Non-standard block. See details.
    ...
End
Parallel
    nCoresPerGroup integer
    nGroups integer
    nNodesPerGroup integer
End
End
Preserve
    AngularMomentum Yes/No
    CenterOfMass Yes/No
    Momentum Yes/No
End
Print
    System Yes/No
    Velocities Yes/No
End
Reactor
    ForceConstant float
    MassScaled Yes/No
    NSteps integer

```

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```
    Radius float
End
ReflectiveWall
    Axis float_list
    Region string
    Threshold float
End
Remap
    Type [None | Atoms]
End
RemoveMolecules
    Formula string
    Frequency integer
    SafeBox
        Amax float
        Amin float
        Bmax float
        Bmin float
        Cmax float
        Cmin float
        FractionalCoordsBox float_list
    End
    SinkBox
        Amax float
        Amin float
        Bmax float
        Bmin float
        Cmax float
        Cmin float
        FractionalCoordsBox float_list
    End
    StartStep integer
    StopStep integer
End
ReplicaExchange
    AllowWrongResults Yes/No
    EWMALength integer
    SwapFrequency integer
    TemperatureFactors float_list
    Temperatures float_list
    nReplicas integer
End
Restart string
Shake
    All string
    ConvergeR2 float
    ConvergeRV float
    Iterations integer
    ShakeInitialCoordinates Yes/No
End
Thermostat
    BerendsenApply [Local | Global]
    ChainLength integer
    Duration integer_list
    Region string
    Tau float
    Temperature float_list
```

(continues on next page)

(continued from previous page)

```

    Type [None | Berendsen | NHC]
End
TimeStep float
Trajectory
  PrintFreq integer
  SamplingFreq integer
  TProfileGridPoints integer
  WriteBonds Yes/No
  WriteCharges Yes/No
  WriteCoordinates Yes/No
  WriteEngineGradients Yes/No
  WriteMolecules Yes/No
  WriteVelocities Yes/No
End
fbMC
  Frequency integer
  MassRoot float
  MolecularMoves
    Enabled Yes/No
    RotationStepAngle float
    TranslationStepLength float
  End
  NSteps integer
  PrintFreq integer
  StartStep integer
  StepLength float
  StopStep integer
  Temperature float
  End
End
End

```

4.9.1 General

The time evolution of the system is simulated by numerically integrating the equations of motion. A velocity Verlet integrator is used with a time step set by the `TimeStep` key. The MD driver will perform `NSteps` timesteps in total.

Because the overall computational cost depends on `NSteps` but not on `TimeStep`, it is desirable to set the timestep as large as possible to maximize the sampled timescale with a given computational budget. However, numerical integration errors grow rapidly as the timestep increases. These errors will cause a loss of energy conservation, crashes, and other artifacts. It is thus important to set the `TimeStep` value carefully, as its optimal value strongly depends on the studied system and simulated conditions.

As a rule of thumb, reasonable timesteps for systems not undergoing chemical reactions are 10-20 times lower than the period of the fastest vibration mode. Systems containing hydrogen atoms at room temperature can thus be accurately simulated using a 1 fs timestep. Longer timesteps can be safely used for systems containing only heavy atoms (vibration periods scale with the square root of the atomic mass). Conversely, the timestep needs to be made shorter for high-temperature simulations. The same also applies to simulations of chemical reactions, which are usually accompanied by significant transient local heating. The default timestep of 0.25 fs should work for most of these cases.

MolecularDynamics

NSteps

Type Integer

Default value 1000

GUI name Number of steps

Description The number of steps to be taken in the MD simulation.

TimeStep

Type Float

Default value 0.25

Unit Femtoseconds

Description The time difference per step.

During a long simulation, numerical integration errors will cause some system-wide quantities to drift from their exact values. For example, the system may develop a nonzero net linear velocity, causing an overall translation or flow. Non-periodic (molecular) and 1D-periodic systems may also develop nonzero angular momentum (overall rotation) and a Brownian motion of their center of mass through space. These problems are corrected by periodically removing any accumulated drift. This feature can be controlled using the `Preserve` key.

MolecularDynamics

Preserve

Type Block

Description Periodically remove numerical drift accumulated during the simulation to preserve different whole-system parameters.

AngularMomentum

Type Bool

Default value Yes

GUI name : Angular momentum

Description Remove overall angular momentum of the system. This option is ignored for 2D and 3D-periodic systems.

CenterOfMass

Type Bool

Default value No

GUI name : Center of mass

Description Translate the system to keep its center of mass at the coordinate origin. This option is not very useful for 3D-periodic systems.

Momentum

Type Bool

Default value Yes

GUI name Preserve: Total momentum

Description Remove overall (linear) momentum of the system.

4.9.2 Constrained molecular dynamics

There are two types of constraint available for MD: frozen atoms and Shake/Rattle. Atoms can be kept frozen using the `Atom`, `AtomList` and `FixedRegion` keys of the `Constraints` top-level input block.

Constraints

Atom

Type Integer

Recurring True

Description Fix the position of an atom. Just one integer referring to the index of the atom in the `[System%Atoms]` block.

AtomList

Type Integer List

Recurring True

Description Fix positions of the specified atoms. A list of integers referring to indices of atoms in the `[System%Atoms]` block.

FixedRegion

Type String

Recurring True

Description Fix positions of all atoms in a region.

The Shake/Rattle constraints are implemented following H.C. Andersen, *J Comp. Phys.*, 52 (1983) 24 ([https://doi.org/10.1016/0021-9991\(83\)90014-1](https://doi.org/10.1016/0021-9991(83)90014-1)). The procedure consists of two steps: update of the coordinates to satisfy the constraints (the Shake part) and orthogonalization of atomic velocities to them (the Rattle part). The Shake part is implemented as an additional correcting force that brings each bond length exactly to its constrained value upon the subsequent velocity Verlet integration step. Application of the constraints is an iterative procedure and the convergence greatly depends on how intertwined the constraints are. For diatomic molecules, usually no more than two iterations are necessary, while tens of iterations may be required for rings (a triangle constraint is treated as a 3-membered ring).

Note: During simulations with a changing simulation box (NpT, NpH), the absolute Cartesian coordinates of the frozen atoms cannot be kept fixed. In this case, their fractional cell coordinates are maintained at the original values. Also the Shake constraints cannot be satisfied exactly during such simulations but the difference is usually small enough.

The Shake/Rattle constraints are specified using the Shake input block:

MolecularDynamics

Shake

Type Block

Description Parameters of the Shake/Rattle algorithm.

All

Type String

Recurring True

GUI name Constrain all

Description Constraint description in one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 and the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then all bonds between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk '*' denoting any atom. The distance, if present, must be in Angstrom. If it is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at certain points of the simulation (at the start or right after adding/removing atoms) can be constrained, which means that the bonds may need to be specified in the System block.

Warning: the triangles constraint should be used with care because each constrained bond or angle means removing one degree of freedom from the dynamics. When there are too many constraints (for example, "All triangles H C H" in methane) some of them may be linearly dependent, which will lead to an error in the temperature computation.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

ConvergeR2

Type Float

Default value 1e-08

Description Convergence criterion on the max squared difference, in atomic units.

ConvergeRV

Type Float

Default value 1e-08

Description Convergence criterion on the orthogonality of the constraint and the relative atomic velocity, in atomic units.

Iterations

Type Integer

Default value 100

Description Number of iterations.

ShakeInitialCoordinates

Type Bool

Default value Yes

Description Apply constraints before computing the first energy and gradients.

Note: The list of constrained bonds is built by matching the input against the *bonds as specified* (page 37) in the *System block* (page 31). This means that bonds not specified in the System block will *not* be constrained.

4.9.3 (Re-)Starting a simulation

The state of a system at the beginning of a simulation is defined by the positions and momenta of all atoms. The positions can be set in the input or loaded from a file as described under *Geometry, System definition* (page 31). Initial velocities are then supplied using the `InitialVelocities` block.

Probably the most common way to start up a simulation is to draw the initial velocities from a Maxwell-Boltzmann distribution by setting `Type=Random` and `Temperature` to a suitable value. Alternatively, velocities can be loaded from an `ams.rkf` file produced by an earlier simulation using `Type=FromFile` and `File`. This is the recommended way to start a production simulation from the results of a short preparation/equilibration run.

Velocities of all atoms in units of Å/fs can also be explicitly defined in the `Values` block after setting `Type=Input`. This is mainly useful to repeat or extend simulations done by other programs. For example, velocities can be extracted from the `vels` or `moldyn.vel` files used by the standalone `ReaxFF` program. A simple AWK script is supplied in `scripting/standalone/reaxff-ams/vels2ams.awk` to help with the conversion.

MolecularDynamics

InitialVelocities

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the `.rkf` file.

File

Type String

Description AMS RKF file containing the initial velocities.

RandomVelocitiesMethod

Type Multiple Choice

Default value Exact

Options [Exact, Boltzmann, Gromacs]

GUI name Velocity randomization method

Description Specifies how are random velocities generated. Three methods are available.

Exact: Velocities are scaled to exactly match set random velocities temperature.

Boltzmann: Velocities are not scaled and sample Maxwell-Boltzmann distribution. However, the distribution is not corrected for constraints.

Gromacs: Velocities are scaled to match set random velocities temperature, but removal of net momentum is performed only after the scaling. Resulting kinetic energy is lower based on how much net momentum the system had.

Temperature

Type Float

Unit Kelvin

GUI name Initial temperature

Description Sets the temperature for the Maxwell-Boltzmann distribution when the type of the initial velocities is set to random, in which case specifying this key is mandatory.

AMSinput will use the first temperature of the first thermostat as default.

Type

Type Multiple Choice

Default value Random

Options [Zero, Random, FromFile, Input]

GUI name Initial velocities

Description Specifies the initial velocities to assign to the atoms. Three methods to assign velocities are available.

Zero: All atom are at rest at the beginning of the calculation.

Random: Initial atom velocities follow a Maxwell-Boltzmann distribution for the temperature given by the [MolecularDynamics%InitialVelocities%Temperature] keyword.

FromFile: Load the velocities from a previous ams result file.

Input: Atom's velocities are set to the values specified in the [MolecularDynamics%InitialVelocities%Values] block, which can be accessed via the Expert AMS panel in AMSinput.

Values

Type Non-standard block

Description This block specifies the velocity of each atom, in Angstrom/fs, when [MolecularDynamics%InitialVelocities%Type] is set to Input. Each row must contain three floating point values (corresponding to the x,y,z component of the velocity vector) and a number of rows equal to the number of atoms must be present, given in the same order as the [System%Atoms] block.

The MD module also supports exact restarts of interrupted simulations by pointing the `Restart` key to an `ams.rkf` file. This will restore the entire state of the MD module from the last available checkpoint (if the previous simulation was interrupted) or from the final state (if the previous simulation ended after `NSteps`). An earlier trajectory can thus be seamlessly extended by increasing `NSteps` and using `Restart`.

Note: `Restart` should be combined with `LoadSystem` from the same `ams.rkf` to restore the atomic positions.

Warning: The `Restart` feature is only intended for exact restarts, so the rest of the `MolecularDynamics` settings should be the same as in the original run. Only `NSteps` and engine settings (contents of the `Engine` block) can always be changed safely across restarts.

Although some MD settings (such as the trajectory sampling options) can in practice be changed without problems, changing others (such as thermostat or barostat settings) will cause the restart to fail or produce physically incorrect results. It is thus strongly recommended to only use `Restart` for exact continuation and `InitialVelocities Type=FromFile` together with `LoadSystem` otherwise.

MolecularDynamics

Restart

Type String

GUI name Restart from

Description The path to the `ams.rkf` file from which to restart the simulation.

4.9.4 Thermostats and barostats

By default, the MD simulation samples the microcanonical (NVE) ensemble. Although this is useful to check energy conservation and other basic physical properties, it does not directly map to common experimental conditions. The canonical (NVT) ensemble can be sampled instead by applying a `Thermostat`, which serves as a simulated heat bath around the system, keeping its average temperature at a set value.

AMS offers two thermostats with drastically different properties, mode of operation, and applicability, selected using the `Type` key:

Berendsen The Berendsen friction thermostat drives the system to a particular target temperature by rescaling the velocities of all atoms in each step. This ensures rapid (exponential) convergence of the temperature with a time constant `Tau`. However, this thermostat produces an incorrect velocity distribution and should thus be avoided in all situations where correct energy fluctuations are important. Additionally, using a too short time constant `Tau` tends to cause incorrect equipartition of energy between different degrees of freedom in the system, leading to the “flying ice cube” phenomenon. The time constant `Tau` should thus be set as large as possible to limit these artifacts while still providing sufficient temperature control. Common values of `Tau` for condensed-phase systems lie between 100 fs (strong damping, rapid convergence) and 10 ps (weak coupling with minimal artifacts).

This thermostat is mainly useful for systems far from equilibrium, for example during the initial preparation and equilibration phase of a simulation. The `NHC` thermostat should be preferred where possible.

NHC This enables a chain of coupled Nosé-Hoover thermostats. This method introduces artificial degrees of freedom representing the heat bath and ensures correct sampling of the canonical ensemble. The combined total energy of the system and the heat bath is conserved and shown in the GUI as `Conserved Energy`. Checking this quantity for drift and artifacts thus offers a valuable test of the correctness of the simulation. This thermostat exhibits oscillatory relaxation with a period of `Tau`. It is thus not well suited for systems starting far from equilibrium, because the oscillations may take long to settle. The time constant `Tau` should be at least comparable to the period of some natural oscillation of the system to ensure efficient energy transfer. It is commonly on the order of hundreds of femtoseconds, although higher values may be used if weak coupling is desired.

Multiple independent thermostats can be used to separately control different non-overlapping regions of the system at the same time. This is done by first defining appropriate *Regions* (page 36) in the `System` block and then specifying the `Thermostat` block multiple times with the `Region` key of each thermostat set to an appropriate region expression.

MolecularDynamics

Thermostat

Type Block

Recurring True

Description This block allows to specify the use of a thermostat during the simulation. Depending on the selected thermostat type, different additional options may be needed to characterize the specific thermostat's behavior.

BerendsenApply

Type Multiple Choice

Default value Global

Options [Local, Global]

GUI name Apply Berendsen

Description Select how to apply the scaling correction for the Berendsen thermostat:

- per-atom-velocity (Local) - on the molecular system as a whole (Global).

ChainLength

Type Integer

Default value 10

GUI name NHC chain length

Description Number of individual thermostats forming the NHC thermostat

Duration

Type Integer List

GUI name Duration(s)

Description Specifies how many steps should a transition from a particular temperature to the next one in sequence take.

Region

Type String

Default value *

Description The identifier of the region to thermostat. The default '*' applies the thermostat to the entire system. The value can be a plain region name, or a region expression, e.g. '*-myregion' to thermostat all atoms that are not in myregion, or 'regionA+regionB' to thermostat the union of the 'regionA' and 'regionB'. Note that if multiple thermostats are used, their regions may not overlap.

Tau

Type Float

Unit Femtoseconds

GUI name Damping constant

Description The time constant of the thermostat.

Temperature

Type Float List

Unit Kelvin

GUI name Temperature(s)

Description The target temperature of the thermostat.

You can specify multiple temperatures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one T to the next T (using a linear ramp). For NHC thermostat, the temperature may not be zero.

Type

Type Multiple Choice

Default value None

Options [None, Berendsen, NHC]

GUI name Thermostat

Description Selects the type of the thermostat.

Just like using a `Thermostat` to control the temperature of the system, a `Barostat` can be applied to keep the pressure constant by adjusting the volume. This enables sampling the isenthalpic-isobaric (NpH) ensemble by using only

a barostat or the isothermal-isobaric (NpT) ensemble by combining a barostat and a thermostat. Unlike thermostats, a barostat always applies to the entire system and there can thus be at most one barostat defined.

AMS offers two barostats with similar properties to the related thermostats:

Berendsen The Berendsen friction-like isobaric ensemble method rescales the system in each step to drive the pressure towards a target value. Similarly to the `Berendsen` thermostat, the relaxation is exponential with a time constant `Tau`. Similar considerations for the choice of `Tau` apply as in the case of the thermostat, but the value of `Tau` for the barostat is usually at least several times higher than the corresponding `Tau` used for the thermostat. This barostat does not have any conserved quantity.

MTK This enables the Martyna-Tobias-Klein extended Lagrangian barostat, which generates a true isobaric ensemble by integrating the cell parameters as additional degrees of freedom. This barostat is derived from the Andersen-Hoover isotropic barostat and the Parrinello-Rahman-Hoover anisotropic barostat. Like the `NHC` thermostat, it exhibits oscillatory relaxation unsuitable for systems far from equilibrium. This barostat must always be combined with a `NHC` thermostat. One instance of such thermostat coupled to the atoms as usual, while a second instance is created internally and coupled to the cell degrees of freedom.

MolecularDynamics

Barostat

Type Block

Description This block allows to specify the use of a barostat during the simulation.

BulkModulus

Type Float

Default value 2200000000.0

Unit Pascal

Description An estimate of the bulk modulus (inverse compressibility) of the system for the Berendsen barostat.

This is only used to make `Tau` correspond to the true observed relaxation time constant. Values are commonly on the order of 10-100 GPa (1e10 to 1e11) for solids and 1 GPa (1e9) for liquids (2.2e9 for water). Use 1e9 to match the behavior of standalone ReaxFF.

ConstantVolume

Type Bool

Default value No

Description Keep the volume constant while allowing the box shape to change.

This is currently supported only by the MTK barostat.

Duration

Type Integer List

Description Specifies how many steps should a transition from a particular pressure to the next one in sequence take.

Equal

Type Multiple Choice

Default value None

Options [None, XYZ, XY, YZ, XZ]

Description Enforce equal scaling of the selected set of dimensions. They will be barostatted as one dimension according to the average pressure over the components.

Pressure

Type Float List

Unit Pascal

Description Specifies the target pressure.

You can specify multiple pressures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one p to the next p (using a linear ramp).

Scale

Type Multiple Choice

Default value XYZ

Options [XYZ, Shape, X, Y, Z, XY, YZ, XZ]

Description Dimensions that should be scaled by the barostat to maintain pressure. Selecting Shape means that all three dimensions and also all the cell angles are allowed to change.

Tau

Type Float

Unit Femtoseconds

GUI name Damping constant

Description Specifies the time constant of the barostat.

Type

Type Multiple Choice

Default value None

Options [None, Berendsen, MTK]

GUI name Barostat

Description Selects the type of the barostat.

Temperature and pressure regimes

Arbitrary temperature and pressure regimes can be generated by setting Temperature or Pressure to a list of values, corresponding to the successive set points. This needs to be accompanied by a Duration key specifying the length of each regime segment in steps:

```
Thermostat
  Temperature 0      300    300    500    500    300
  Duration    100    200    100    200    100
End
```

Note that there is always N-1 Duration values for N Temperature values. The target temperature of the thermostat in this example will evolve as follows:

1. Increase linearly from 0 to 300 K over 100 steps.
2. Stay constant at 300 K for 200 steps.

3. Increase linearly from 300 to 500 K over 100 steps.
4. Stay constant at 500 K for 200 steps.
5. Decrease linearly from 500 to 300 K over 100 steps.
6. Stay constant at 300 K for the rest of the simulation.

4.9.5 Trajectory sampling and output

A basic principle of the numerical integration of motion in MD is that the changes in the state of the system between successive time steps are small. This means that storing the results of every step is not useful, because all the data is strongly correlated. Instead, a snapshot of the system is taken every `N` steps, where `N` is set low enough to still capture the fastest motion of interest but high enough to avoid wasting space due to correlations. The resulting sequence of snapshots is then commonly called the trajectory.

AMS writes the trajectory to the `History` and `MDHistory` sections of `ams.rkf`, according to the settings in the `Trajectory` block. A snapshot of the system and various MD variables is stored every `SamplingFreq` timesteps. By default, this frequency is also used to print basic thermodynamic parameters of the simulation to the output and log file. Set `PrintFreq` to override this.

Frequently sampling a long trajectory can generate large volumes of data. If the space usage becomes a concern, one can selectively disable storing some parts of the trajectory to save space using the `Write*` keys. Note however that this will make it impossible to use some analysis methods on the resulting trajectory:

- `WriteBonds` is necessary for reaction network analysis (ChemTraYzer). Disabling `WriteBonds` also makes AMSmovie show only guessed bonds instead of those calculated by the engine.
- `WriteMolecules` is required by the Molecule Fractions panel in AMSmovie.
- `WriteVelocities` is required to calculate the velocity autocorrelation functions needed for diffusivity and IR spectra.

The trajectory itself contains only the data needed for subsequent analysis of the dynamics of the system. However, much more data is usually generated on every integration step. This includes, for example, the internal data used by an engine when evaluating the energies and forces. This information is normally discarded after each step, because it is often very large. However, a `Checkpoint` containing the complete internal state of the MD driver together with a result file generated by the engine is stored every `Frequency` steps. An interrupted simulation can then be restarted from this checkpoint using the `Restart` keyword. Additionally, the engine result files called `MDStep*.rkf` can also be used to extract various engine-specific details about the system, such as the orbitals for QM engines.

MolecularDynamics

Trajectory

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the `.rkf` file.

PrintFreq

Type Integer

GUI name Printing frequency

Description Print current thermodynamic properties to the output every `N` steps. By default this is done every `SamplingFreq` steps.

SamplingFreq

Type Integer

Default value 100

GUI name Sample frequency

Description Write the the molecular geometry (and possibly other properties) to the .rkf file once every N steps.

TProfileGridPoints

Type Integer

Default value 0

Description Number of points in the temperature profile. If TProfileGridPoints > 0, a temperature profile along each of the three lattice axes will be written to the .rkf file. The temperature at a given profile point is calculated as the total temperature of all atoms inside the corresponding slice of the simulation box, time-averaged over all MD steps since the previous snapshot. By default, no profile is generated.

WriteBonds

Type Bool

Default value Yes

Description Write detected bonds to the .rkf file.

WriteCharges

Type Bool

Default value Yes

Description Write current atomic point charges (if available) to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze charges.

WriteCoordinates

Type Bool

Default value Yes

Description Write atomic coordinates to the .rkf file.

WriteEngineGradients

Type Bool

Default value No

Description Write atomic gradients (negative of the atomic forces, as calculated by the engine) to the History section of ams.rkf.

WriteMolecules

Type Bool

Default value Yes

Description Write the results of molecule analysis to the .rkf file.

WriteVelocities

Type Bool

Default value Yes

Description Write velocities to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze the velocities.

Checkpoint**Type** Block**Description** Sets the frequency for storing the entire MD state necessary for restarting the calculation.**Frequency****Type** Integer**Default value** 1000**GUI name** Checkpoint frequency**Description** Write the MD state and engine-specific data to the respective .rkf files once every N steps.**WriteProperties****Type** Bool**Default value** No**Description** Write the properties from the properties section to the ChecoPoint file once every N steps.**CalcPressure****Type** Bool**Default value** No**GUI name** Calculate pressure**Description** Calculate the pressure in periodic systems.

This may be computationally expensive for some engines that require numerical differentiation.

Some other engines can calculate the pressure for negligible additional cost and will always do so, even if this option is disabled.

Print**Type** Block**Description** This block controls the printing of additional information to stdout.**System****Type** Bool**Default value** No**Description** Print the chemical system before and after the simulation.**Velocities****Type** Bool**Default value** No**Description** Print the atomic velocities before and after the simulation.

In rare cases, one may require some properties from every MD step, for example, the pressure tensor for the Green-Kubo viscosity calculation. In this case one can use the `BinLog` (binary log) feature. When enabled, the selected MD variables will be stored in the `BinLog` section of `ams.rkf` in the format similar to that of the `MDHistory` section with a few differences: the blocking factor is larger (1000 instead of 100) and the pressure tensor is stored per component,

for example, P_{xx} is stored in `PressureTensor_xx`, and so on. Note that none of the atomic properties (coordinates, velocities) are included in the binlog.

MolecularDynamics**BinLog**

Type Block

Description This block controls writing the BinLog section in `ams.rkf`, which contains the selected MD state scalars and tensors from every MD step. No per-atom data is written. If you need the per-atom data then you can set the sampling frequency to 1 and get the required data from the MDHistory section. The tensors are written per component, that is, the pressure tensor is written as six variables: `PressureTensor_xx`, `PressureTensor_yy`, etc.. To reduce the file size, all data is written in blocks.

BiasEnergy

Type Bool

Default value No

Description Write the CVDH bias energy.

BoostFactor

Type Bool

Default value No

Description Write the CVDH boost factor.

ConservedEnergy

Type Bool

Default value No

Description Write the conserved energy value.

Density

Type Bool

Default value No

Description Write the density.

Hypertime

Type Bool

Default value No

Description Write the CVDH hypertime.

KineticEnergy

Type Bool

Default value No

Description Write the kinetic energy value.

MaxBiasEnergy

Type Bool

Default value No

Description Write the max CVDH bias energy.

MaxBoostFactor

Type Bool

Default value No

Description Write the max CVDH boost factor.

PotentialEnergy

Type Bool

Default value No

Description Write the potential energy value.

Pressure

Type Bool

Default value No

Description Write the pressure.

PressureTensor

Type Bool

Default value No

Description Write the pressure tensor in Voigt notation. Each component of the tensor is written in its own variable.

Step

Type Bool

Default value No

Description Write the step index during the simulation.

Temperature

Type Bool

Default value No

Description Write the temperature.

Time

Type Bool

Default value No

Description Write the simulation time (fs).

TotalEnergy

Type Bool

Default value No

Description Write the total energy value.

Volume

Type Bool

Default value No

Description Write the simulation cell volume, area or length, depending on the system periodicity.

4.9.6 Lattice deformations (volume regimes)

The `Deformation` block can be used to gradually deform the periodic lattice of the system during a MD simulation. This block can be repeated to define multiple deformations, which will be applied on every MD step in the order in which they are listed in the input.

See also:

Example demonstrating various lattice deformations (page 425)

Warning: While a `Deformation` and a `Barostat` can be used at the same time, remember to set the `Scale` parameter of the barostat so that no dimension is simultaneously being deformed and barostatted.

Each `Deformation` block will be active on MD steps between `StartStep` and `StopStep`.

The time dependence of the lattice parameters is defined by the `Type` key:

Linear This deformation type adds the same constant amount to the selected lattice parameters on every simulation step. When used with `TargetLattice`, `LatticeVelocity`, or `StrainRate`, the lattice matrix H evolves as $H(t) = H_0 + \Delta H \cdot t$, where H_0 is the lattice at `StartStep`.

Exponential When used with `StrainRate`, this type strains the lattice by the given strain matrix ϵ on every step, so that the lattice matrix H evolves as $H(t) = H_0(1 + \epsilon)^t$. When used with `LengthRate`, the length of each lattice vector evolves as $l(t) = l_0(1 + r)^t$.

Sine This is a periodic deformation going from the starting value of the selected lattice parameters to a set target, and then with the same amplitude to the opposite direction from the starting lattice.

Cosine This periodic deformation oscillates between the starting lattice and a defined target.

The period of the oscillation for the `Sine` and `Cosine` types must be set using the `Period` key.

The extent of the deformation is defined by setting one of the six mutually exclusive input keys. These belong to two groups, depending on whether they operate on the lattice matrix as a whole, or just on the lengths of the individual lattice vectors:

TargetLattice, Velocity, and Rate These input keys expect a “lattice-like” matrix of numbers, consisting of up to three rows containing up to three values each. Each row contains the components of a single lattice vector and corresponds to a row of the *Lattice block* (page 32). For systems with 1D or 2D periodicity the matrix may be padded to 3x3 with zeros.

TargetLength, LengthVelocity, and LengthRate These input keys expect a list of up to three values, defining the desired length of each lattice vector or the (absolute or relative) rate of its change.

MolecularDynamics

Deformation

Type Block

Recurring True

Description Deform the periodic lattice of the system during the simulation.

LatticeVelocity

Type Non-standard block

Description Velocity of individual lattice vector components in Angstrom/fs. The format is identical to the System%Lattice block. For Type Sine and Cosine, this defines the maximum velocity (at the inflection point).

LengthRate

Type Float List

Default value [0.0, 0.0, 0.0]

Description Relative rate of change of each lattice vector per step.

LengthVelocity

Type Float List

Default value [0.0, 0.0, 0.0]

Unit Angstrom/fs

Description Change the length of each lattice vector with this velocity. With Type=Exponential, LengthVelocity is divided by the current lattice vector lengths on Start-Step to determine a LengthRate, which is then applied on all subsequent steps. For Type Sine and Cosine, this defines the maximum velocity (at the inflection point).

Period

Type Float

Unit Femtoseconds

Description Period of oscillation for Type Sine and Cosine.

ScaleAtoms

Type Bool

Default value Yes

Description Scale the atomic positions together with the lattice vectors. Disable this to deform only the lattice, keeping the coordinates of atoms unchanged.

StartStep

Type Integer

Default value 1

Description First step at which the deformation will be applied.

StopStep

Type Integer

Default value 0

Description Last step at which the deformation will be applied. If unset or zero, nSteps will be used instead.

StrainRate

Type Non-standard block

Description Strain rate matrix to be applied on every step. The format is identical to the System%Lattice block.

TargetLattice

Type Non-standard block

Description Target lattice vectors to be achieved by StopStep. The format is identical to the System%Lattice block.

TargetLength

Type Float List

Default value [0.0, 0.0, 0.0]

Unit Angstrom

Description Target lengths of each lattice vector to be achieved by StopStep. The number of values should equal the periodicity of the system. If a value is zero, the corresponding lattice vector will not be modified.

Type

Type Multiple Choice

Default value Linear

Options [Linear, Exponential, Sine, Cosine]

Description Function defining the time dependence of the deformed lattice parameters.

Linear increments the lattice parameters by the same absolute amount every timestep. Exponential multiplies the lattice parameters by the same factor every timestep. Only StrainRate, LengthRate, and LengthVelocity are supported for Type=Exponential. Sine deforms the system from the starting lattice to TargetLattice/TargetLength and then by the same amount to the opposite direction, while Cosine deforms the system from the starting lattice to the target and back.

Example: Transition from the initial lattice to a 10 Å cube over 1000 steps:

```
MolecularDynamics
  Deformation
    StopStep 1000
    TargetLattice
      10.0  0.0  0.0
      0.0 10.0  0.0
      0.0  0.0 10.0
    End
  End
End
```

Example: Oscillate the length of the *c* lattice vector between the initial value and 20 Å, leaving the *a* and *b* vectors unchanged:

```
MolecularDynamics
  Deformation
    Type Cosine
    Period 100
    TargetLength 0 0 20
  End
End
```

Example: Stretch the box in the “z” direction by a true exponential strain of 10 ppm per timestep while barostatting the remaining dimensions:

```

MolecularDynamics
  Barostat Type=MTK Pressure=1e5 Tau=1000 Scale=XY
  Deformation
    Type Exponential
    StrainRate
      0.0 0.0 0.0
      0.0 0.0 0.0
      0.0 0.0 1e-5
  End
End
End

```

4.9.7 Molecule Gun: adding molecules during simulation

The molecule gun allows you to “shoot” (add with velocity) a molecule into the simulation box.

See also:

The [GUI tutorial](#) on the molecule gun.

Molecules can be continuously added to the simulation or only once. The initial position can be pre-set or be random within the simulation box or a part thereof. It can be defined either in the Cartesian or fractional coordinates. The initial velocity can be specified either directly (in Angstrom per femtosecond) or as translational temperature or kinetic energy. Possible applications of the molecule gun include e.g. the simulation of enforced collisions or deposition processes on surfaces.

MolecularDynamics

AddMolecules

Type Block

Recurring True

GUI name Add molecules

Description This block controls adding molecules to the system (a.k.a. the Molecule Gun). Multiple occurrences of this block are possible.

By default, molecules are added at random positions in the simulation box with velocity matching the current system temperature. The initial position can be modified using one of the following keywords: Coords, CoordsBox, FractionalCoords, FractionalCoordsBox. The Coords and FractionalCoords keys can optionally be accompanied by CoordsSigma or FractionalCoordsSigma, respectively.

AtomTemperature

Type Float

Default value 0.0

Unit Kelvin

Description Add random velocity corresponding to the specified temperature to individual atoms of the molecule. This only affects rotational and internal degrees of freedom, not the net translational velocity of the inserted molecule as set by the other options.

ContactDistance

Type Float

Default value 0.0

Unit Angstrom

Description Translate the bullet along the velocity vector until it comes within ContactDistance of any other atom.

Coords

Type Float List

Unit Angstrom

Description Place molecules at or around the specified Cartesian coordinates.

This setting takes precedence over other ways to specify initial coordinates of the molecule: [CoordsBox], [FractionalCoords], and [FractionalCoordsBox].

CoordsBox

Type Float List

Unit Angstrom

Description Place molecules at random locations inside the specified box in Cartesian coordinates.

Coordinates of the box corners are specified as: Xmin, Xmax, Ymin, Ymax, Zmin, Zmax. This setting is ignored if Coords is used.

In AMSinput, if this field is not empty it will be used instead of the default Coords.

CoordsSigma

Type Float List

Unit Angstrom

Description Sigma values (one per Cartesian axis) for a Gauss distribution of the initial coordinates. Can only be used together with Coords.

DeviationAngle

Type Float

Default value 0.0

Unit Degree

Description Randomly tilt the shooting direction up to this angle away from the VelocityDirection vector.

Energy

Type Float

Unit Hartree

Description Initial kinetic energy of the molecule in the shooting direction.

EnergySigma

Type Float

Default value 0.0

Unit Hartree

Description Sigma value for the Gauss distribution of the initial kinetic energy around the specified value. Should only be used together with Energy.

FractionalCoords**Type** Float List**Description** Place molecules at or around the specified fractional coordinates in the main system's lattice. For non-periodic dimensions a Cartesian value in Angstrom is expected. This setting is ignored if [Coords] or [CoordsBox] is used.**FractionalCoordsBox****Type** Float List**Description** Place molecules at random locations inside the box specified as fractional coordinates in the main system's lattice.

Coordinates of the box corners are specified as: Xmin, Xmax, Ymin, Ymax, Zmin, Zmax.

For non-periodic dimensions the Cartesian value in Angstrom is expected.

This setting is ignored if [Coords], [CoordsBox], or [FractionalCoords] is used.

FractionalCoordsSigma**Type** Float List**Description** Sigma values (one per axis) for a Gauss distribution of the initial coordinates. For non-periodic dimensions the Cartesian value in Angstrom is expected. Can only be used together with FractionalCoords.**Frequency****Type** Integer**Default value** 0**Description** A molecule is added every [Frequency] steps after the StartStep.

There is never a molecule added at step 0.

MinDistance**Type** Float**Default value** 0.0**Unit** Angstrom**Description** Keep the minimal distance to other atoms of the system when adding the molecule.**MoleFraction****Type** Float**Description** Defines a mixture to be deposited using one AddMolecules block per component.

AMS will randomly alternate between any guns that have MoleFraction set. These need to all have the same settings for StartStep, StopStep and Frequency. Any additional AddMolecules blocks without MoleFraction will remain completely independent.

NumAttempts**Type** Integer**Default value** 10**Description** Try adding the molecule up to the specified number of times or until the MinDistance constraint is satisfied. If all attempts fail a message will be printed and the simulation will continue normally.

Rotate**Type** Bool**Default value** No**Description** Rotate the molecule randomly before adding it to the system.**StartStep****Type** Integer**Default value** 0**Description** Step number when the first molecule should be added. After that, molecules are added every Frequency steps.

For example, if StartStep=99 and Frequency=100 then a molecule will be added at steps 99, 199, 299, etc...

No molecule will be added at step 0, so if StartStep=0 the first molecule is added at the step number equal to [Frequency].

StopStep**Type** Integer**Description** Do not add this molecule after the specified step.**System****Type** String**Description** String ID of the [System] that will be added with this 'gun'.

The lattice specified with this System is ignored and the main system's lattice is used instead.

AMSinput adds the system at the coordinates of the System (thus setting Coords to the center of the System).

Temperature**Type** Float**Unit** Kelvin**Description** Initial energy of the molecule in the shooting direction will correspond to the given temperature.**TemperatureSigma****Type** Float**Default value** 0.0**Unit** Kelvin**Description** Sigma value for the Gauss distribution of the initial temperature the specified value. Should only be used together with Temperature.**Velocity****Type** Float**Unit** Angstrom/fs**Description** Initial velocity of the molecule in the shooting direction.**VelocityDirection**

Type Float List

Description Velocity direction vector for aimed shooting. It will be random if not specified.

In AMSinput add one or two atoms (which may be dummies).

One atom: use vector from center of the system to add to that atom.

Two atoms: use vector from the first to the second atom.

VelocitySigma

Type Float

Default value 0.0

Unit Angstrom/fs

Description Sigma value for the Gauss distribution of the initial velocity around the specified value. Should only be used together with Velocity.

Since the 2022 release of the AMS driver, it is possible to generate molecule mixtures by using multiple guns that each have the `MoleFraction` keyword set: AMS will then randomly alternate between any of these guns. The cooperating guns need to all have the same settings for `StartStep`, `StopStep` and `Frequency`. (Any additional `AddMolecules` blocks without `MoleFraction` will remain completely independent.) The following example shows the generation of a 80:20 mixture of `molA` and `molB`:

```
MolecularDynamics
  AddMolecules
    System molA
    MoleFraction 0.8
    Frequency 2000
    StartStep 1
  End
  AddMolecules
    System molB
    MoleFraction 0.2
    Frequency 2000
    StartStep 1
  End
End

System anthracene
  ...
End

System benzene
  ...
End
```

Note that the exact number of inserted molecules of each type is not deterministic: running the same job twice may give you slightly different ratios. However, when running the job many times, the relative ratios averaged over the different runs should approach the fractions as requested in the input.

4.9.8 Removing molecules during simulation

Molecules *detected* (page 246) by the AMS driver can also be removed from the system. This feature can, for example, be used to remove reaction products.

MolecularDynamics

RemoveMolecules

Type Block

Recurring True

GUI name Remove molecules

Description This block controls removal of molecules from the system. Multiple occurrences of this block are possible.

Formula

Type String

Description Molecular formula of the molecules that should be removed from the system.

The order of elements in the formula is very important and the correct order is: C, H, all other elements in the strictly alphabetic order. Element names are case-sensitive, spaces in the formula are not allowed. Digit '1' must be omitted.

Valid formula examples: C2H6O, H2O, O2S. Invalid formula examples: C2H5OH, H2O1, OH, SO2. Invalid formulas are silently ignored.

Use * to remove any molecule, which must be combined with SinkBox or SafeBox.

Frequency

Type Integer

Default value 0

Description The specified molecules are removed every so many steps after the StartStep. There is never a molecule removed at step 0.

SafeBox

Type Block

Description Part of the simulation box where molecules may not be removed. Only one of the SinkBox or SafeBox blocks may be present. If this block is present the molecule will not be removed if any of its atoms is within the box. For a periodic dimension it is given as a fraction of the simulation box (the full 0 to 1 range by default). For a non-periodic dimension it represents absolute Cartesian coordinates in Angstrom.

Amax

Type Float

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Description Coordinate of the lower bound along the third axis.

FractionalCoordsBox

Type Float List

GUI name Safe box

Description Do not remove molecules that are (partly) inside the safe box.

Borders of the safe box specified as: Amin, Amax, Bmin, Bmax, Cmin, Cmax.

For periodic dimensions fractional coordinates between 0 and 1 and for non-periodic dimensions Cartesian values in Angstrom are expected.

SinkBox

Type Block

Description Part of the simulation box where matching molecules will be removed. By default, molecules matching the formula will be removed regardless of their location. If this block is present then such a molecule will only be removed if any of its atoms is within the box. For a periodic dimension it is given as a fraction of the simulation box (the full 0 to 1 range by default). For a non-periodic dimension it represents absolute Cartesian coordinates in Angstrom.

Amax

Type Float

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Description Coordinate of the lower bound along the third axis.

FractionalCoordsBox

Type Float List

GUI name Sink box

Description Remove molecules that are (partly) inside the sink box.

Borders of the sink box specified as: Amin, Amax, Bmin, Bmax, Cmin, Cmax.

For periodic dimensions fractional coordinates between 0 and 1 and for non-periodic dimensions Cartesian values in Angstrom are expected.

StartStep

Type Integer

Default value 0

Description Step number when molecules are removed for the first time. After that, molecules are removed every [Frequency] steps.

For example, if StartStep=99 and Frequency=100 then molecules will be removed at steps 99, 199, 299, etc...

No molecule will be removed at step 0, so if StartStep=0 the first molecules are removed at the step number equal to [Frequency].

StopStep

Type Integer

Description Do not remove the specified molecules after this step.

Warning: When there is a Molecules%AdsorptionSupportRegion defined, the molecule formulas depend on whether the molecule is adsorbed or not.

4.9.9 Accelerated dynamics

The PLUMED library support in AMS

PLUMED (<http://www.plumed.org/>) is a plugin that works with various MD programs and is also available in AMS. It can be used for on-the-fly analysis of the dynamics, or to perform a wide variety of free energy methods. The interface with the plugin is really simple: you just need to specify the PLUMED input in the MolecularDynamics%Plumed%Input block and it will be passed to the library “as is”. At each MD step, the current state of the system will be passed to the plugin to be updated according to the PLUMED input.

MolecularDynamics

Plumed

Type Block

Description Input for PLUMED. The parallel option is still experimental.

Input

Type Non-standard block

Description Input for PLUMED. Contents of this block is passed to PLUMED as is.

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

Metadynamics for Conformer-Rotamer Ensemble Sampling (CREST-MTD)

This is a very specific implementation of metadynamics that is only meant for exploration of conformer space, as used in the Conformer-Rotamer Ensemble Sampling (CREST) approach. It is an RMSD-based metadynamics that places a new 1-dimensional Gaussian on the potential energy surface every `NSteps` steps. The Gaussian is a function of the RMSD from the current geometry, which will always be zero at the moment of placement. All Gaussians have the same maximum height (`Height`) and the same width (`Width`). There is an upper limit of `NGaussiansMax` to the number of Gaussians present in the system, and when this is exceeded the oldest Gaussian is removed. By default the Gaussians are gradually introduced, using a scaling function that increases exponentially from 0 to 1 with the simulation time. The keyword `ScalingSlope` in the input block `GaussianScaling` determines the slope of the scaling function with respect to time. The default value of 0.03 steps^{-1} yields a scaling factor of nearly 1 after 100 steps. The keyword `ScaleGaussians` in the inputblock `GaussianScaling` determines whether the Gaussians are scaled at all.

By default, all atoms are included in the RMSD calculation. However, the selection can be restricted to specific regions using the `Region` keyword. This can be a single region or a combination thereof using region expressions (for example, `reg1+reg2` for a union).

MolecularDynamics

CRESTMTD

Type Block

GUI name CREST_MTD

Description Input for CREST metadynamics simulation.

AddEnergy

Type Bool

Default value No

Description Add the bias energy to the potential energy (to match the gradients)

GaussianScaling

Type Block

Description Options for gradual introduction of the Gaussians

ScaleGaussians

Type Bool

Default value Yes

Description Introduce the Gaussians gradually, using a scaling function

ScalingSlope

Type Float

Default value 0.03

Description Slope of the scaling function for the Gaussians with respect to time

Height

Type Float

Unit Hartree

Description The height of the Gaussians added

NGaussiansMax

Type Integer

Description Maximum number of Gaussians stored

NSteps

Type Integer

Description Interval of Gaussian placement

Region

Type String

Default value *

Description Restrict the range of atoms for RMSD calculation to the specified region.

RestartFile

Type String

Description Filename for file from which to read data on Gaussians placed previously.

Width

Type Float**Unit** Bohr**Description** The width of the Gaussians added in terms of the RMSD

By default, the gradients of the Gaussians with respect to the atom coordinates are added to the state gradients, but the value of the Gaussians is not added to the energy, which is common in metadynamics. For testing purposes it can be useful to add the Gaussian value to the energy, and this can be done with the keyword `AddEnergy`. Irrespective of this choice, the energy value of the Gaussian at each geometry is printed in the `ams.rkf` file in the section `CrestMTDHistory`. It is also possible to use Gaussians from an earlier CREST-MTD simulation, using the keyword `RestartFile`.

Collective Variable-driven HyperDynamics (CVHD)

The Collective Variable-driven HyperDynamics is a molecular dynamics acceleration method that allows observation of rare events by filling energy minima with a bias potential. In this sense it is similar to metadynamics. The difference of the hyperdynamics is that it ensures that the bias disappears in the transition state region. This difference allows hyperdynamics to calculate the rate of slow processes, for example the ignition phase of combustion.

See also:

The [GUI tutorial](#) on CVHD.

The CVHD implementation in AMS follows the algorithm described in K.M. Bal, E.C. Neyts, *JCTC*, 11 (2015) (<https://doi.org/10.1021/acs.jctc.5b00597>)

The `StartStep`, `Frequency`, `StopStep`, and `WaitSteps` keys define when and how often the bias potential is added, and when it is removed. The `Bias` block defines parameters of the bias potential peaks and the `ColVarBB` block describes parameters of the bond-breaking collective variable.

MolecularDynamics

CVHD

Type Block**Recurring** True**GUI name** CVHD**Description** Input for the Collective Variable-driven HyperDynamics (CVHD).

Bias

Type Block

Description The bias is built from a series of Gaussian peaks deposited on the collective variable axis every [Frequency] steps during MD. Each peak is characterized by its (possibly damped) height and the RMS width (standard deviation).

DampingTemp

Type Float**Default value** 0.0**Unit** Kelvin**GUI name** Bias damping T

Description During well-tempered hyperdynamics the height of the added bias is scaled down with an $\exp(-E/kT)$ factor [PhysRevLett 100, 020603 (2008)], where E is the current value of the bias at the given CV value and T is the damping temperature `DampingTemp`. If `DampingTemp` is zero then no damping is applied.

Delta**Type** Float**Description** Standard deviation parameter of the Gaussian bias peak.**Height****Type** Float**Unit** Hartree**Description** Height of the Gaussian bias peak.**ColVarBB****Type** Block**Recurring** True**GUI name** Collective Variable**Description** Description of a bond-breaking collective variable (CV) as described in [Bal & Neyts, JCTC, 11 (2015)]. A collective variable may consist of multiple ColVar blocks.**at1****Type** Block**Description** Specifies the first bonded atom in the collective variable.**region****Type** String**Default value** ***Description** Restrict the selection of bonded atoms to a specific region. If this is not set, atoms anywhere in the system will be selected.**symbol****Type** String**Description** Atom type name of the first atom of the bond. The name must be as it appears in the System block. That is, if the atom name contains an extension (e.g C.1) then the full name including the extension must be used here.**at2****Type** Block**Description** Specifies the second bonded atom in the collective variable.**region****Type** String**Default value** ***Description** Restrict the selection of bonded atoms to a specific region. If this is not set, atoms anywhere in the system will be selected.**symbol****Type** String**Description** Atom type name of the second atom of the bond. The value is allowed to be the same as [at1], in which case bonds between atoms of the same type will be included.

cutoff**Type** Float**Default value** 0.3**GUI name** Bond order cutoff**Description** Bond order cutoff. Bonds with BO below this value are ignored when creating the initial bond list for the CV. The bond list does not change during lifetime of the variable even if some bond orders drop below the cutoff.**p****Type** Integer**Default value** 6**GUI name** Exponent p**Description** Exponent value p used to calculate the p-norm for this CV.**rmax****Type** Float**Unit** Angstrom**GUI name** R max**Description** Max bond distance parameter Rmax used for calculating the CV. It should be close to the transition-state distance for the corresponding bond.**rmin****Type** Float**Unit** Angstrom**GUI name** R min**Description** Min bond distance parameter Rmin used for calculating the CV. It should be close to equilibrium distance for the corresponding bond.**Frequency****Type** Integer**Description** Frequency of adding a new bias peak, in steps. New bias is deposited every [Frequency] steps after [StartStep] if the following conditions are satisfied: the current CV value is less than 0.9 (to avoid creating barriers at the transition state), the step number is greater than or equal to [StartStep], and the step number is less than or equal to [StopStep].**StartStep****Type** Integer**Description** If this key is specified, the first bias will be deposited at this step. Otherwise, the first bias peak is added at the step number equal to the Frequency parameter. The bias is never deposited at step 0.**StopStep****Type** Integer**Description** No bias will be deposited after the specified step. The already deposited bias will continue to be applied until the reaction event occurs. After that no new CVHD will be started. By default, the CVHD runs for the whole duration of the MD calculation.

WaitSteps**Type** Integer**Description** If the CV value becomes equal to 1 and remains at this value for this many steps then the reaction event is considered having taken place. After this, the collective variable will be reset and the bias will be removed.

During a CVHD calculation, the following variables are saved to the MDHistory section of the RKF file, in addition to other MD properties:

- *BiasEnergy* - value the bias energy at the current MD step, in Hartree.
- *MaxBiasEnergy* - max BiasEnergy since the last sampling step.
- *BoostFactor* - the boost factor at the given MD step. The boost factor is calculated at each MD step as $boost = e^{E_{bias}/kT}$, where T is the MD ensemble temperature.
- *MaxBoostFactor* - max BoostFactor value since the last sampling step.
- *HyperTime* - boosted MD time, in femtoseconds, which is a sum of the hyper-time steps calculated from the current boost factor and the MD time step as $\Delta t_{boost} = boost * \Delta t$. In hyperdynamics, the hyper-time value is directly related to the rate of the process boosted by the corresponding collective variable.

Temperature Replica Exchange

Sampling of rare events can be accelerated using the Replica Exchange Molecular Dynamics (REMD) method, also known as Parallel Tempering. This method runs multiple replicas (copies) of the simulated system in parallel, each in a different ensemble. In the case of Temperature REMD, these ensembles are all NVT or NpT, each at a different temperature. Periodically, Monte Carlo swaps are attempted between neighboring ensembles. If the current configuration of replica A has a sufficient Boltzmann probability in the ensemble of replica B (and vice versa), the two configurations will be swapped. This causes high-energy configuration to migrate into the high-temperature replicas while low-energy configurations eventually end up in the coldest ensemble. This facilitates the crossing of energy barriers in the high-temperature ensembles while keeping the coldest replica at a given temperature of interest. Because each replica always samples an unbiased ensemble, any property can be calculated using standard MD analysis methods without special preparation.

The method is controlled using the ReplicaExchange block:

MolecularDynamics**ReplicaExchange****Type** Block**Description** This block is used for (temperature) Replica Exchange MD (Parallel Tempering) simulations.**AllowWrongResults****Type** Bool**Default value** No**Description** Allow combining Replica Exchange with other features when the combination is known to produce physically incorrect results.**EWMALength****Type** Integer**Default value** 10

Description Length of the exponentially weighted moving average used to smooth swap probabilities for monitoring.

This value is equal to the inverse of the EWMA mixing factor.

SwapFrequency

Type Integer

Default value 100

Description Attempt an exchange every N steps.

TemperatureFactors

Type Float List

Description This is the ratio of the temperatures of two successive replicas.

The first value sets the temperature of the second replica with respect to the first replica, the second value sets the temperature of the third replica with respect to the second one, and so on. If there are fewer values than nReplicas, the last value of TemperatureFactor is used for all the remaining replicas.

Temperatures

Type Float List

Description List of temperatures for all replicas except for the first one.

This is mutually exclusive with TemperatureFactors. Exactly nReplicas-1 temperature values need to be specified, in increasing order. The temperature of the first replica is given by [Thermostat%Temperature].

nReplicas

Type Integer

Default value 1

GUI name Number of replicas

Description Number of replicas to run in parallel.

The number of replicas set by nReplicas must never exceed the total number of processors used for the simulation. If possible, the total number of processors should be an integer multiple of nReplicas to ensure good load balancing.

The temperature of the base (coldest) replica is determined by the Thermostat input block, just like in an ordinary MD simulation. There are two ways to set the temperatures of the remaining replicas, either using Temperatures or TemperatureFactors. The latter is typically more convenient, as it makes it easy to set up the optimal geometric progression of temperatures. In the simplest case, it is enough to supply just a single value in TemperatureFactors, setting the common ratio of temperatures of any two adjacent replicas.

SwapFrequency should be set as low as practical for maximum efficiency. The value of this parameter isn't critical because it doesn't affect the validity of the results. However, setting it too high will decrease overall acceleration by missing some opportunities to exchange. Conversely, using a value that is too low will increase the communication overhead and lead to useless back-and-forth swaps between adjacent replicas. Ideally, SwapFrequency should be comparable to the correlation time of the system to ensure that individual exchange attempts are uncorrelated.

The trajectory of each replica is written to a separate RKF file: *ams.rkf* for the base replica and *replicaX.rkf* for the other replicas. One can easily switch between these files in the GUI using *File* → *Related Files*. In addition to data present in any MD trajectory, these files also contain an extra section *ReplicaExchangeHistory* with the following data items written every SwapFrequency steps:

- *AvgSwapProbability* – Average swap acceptance for each pair of replicas, smoothed using an exponentially weighted moving average with a mixing factor equal to the inverse of *EWMALength*.
- *{Min,Max,Mean,StdDev}PotentialEnergy* – Statistics of the potential energy for each ensemble over the last *SwapFrequency* steps.
- *SystemInEnsemble i* – Identifies the system (continuous trajectory) currently running in ensemble (replica) *i*.
- *EnsembleOfSystem i* – Inverse mapping of *SystemInEnsemble*, giving the current replica number in which the system number *i* runs.
- *TemperatureOfSystem i* – Equivalent to *EnsembleOfSystem* using temperatures instead of integer numbers to identify ensembles.

These data items can be plotted using the MD Replica Exchange menu in AMSmovie. For example, plotting *TemperatureOfSystem* or *EnsembleOfSystem* is useful to visualize the migration of each system through the space of ensembles, where each curve represents one continuous trajectory. Plotting potential energy statistics or average acceptances facilitates tuning the number of replicas and their temperatures to achieve efficient acceleration. The replica exchange method can only work when the potential energy distributions of adjacent ensembles have a sufficient overlap. This can be easily seen by comparing *MaxPotentialEnergy* of ensemble *i* with *MinPotentialEnergy* of ensemble *i+1*. The optimal degree of overlap is such that leads to approximately 20 % of swap attempts getting accepted. The acceptance of swaps can be monitored by plotting *AvgSwapProbability* and the corresponding *TemperatureFactors* can then be adjusted to keep it near the optimal value.

Bond Boost Method

The bond boost method implemented here is described in³. In this method, the distances between atoms that are relevant to the reaction of interest are calculated to determine the orientation of the reactant molecules. If a suitable initial configuration is recognized, an additional restraint energy (possibly consisting of more than one term) is added to the system that is intended to stretch or compress bonds at a pre-defined rate such that this additional energy can help achieve the energy to cross the reaction barrier. A single term of the restraint energy depends on the restraints type and its parameters, see *restraint definitions* (page 264) for details. If more than one suitable configuration is found then the one with the smallest sum of distances is used to create the restraints.

See also:

The [GUI tutorial](#) on the Bond Boost Method.

MolecularDynamics

BondBoost

Type Block

Recurring True

Description Forced reaction (bond boost) definitions. Multiple BondBoost blocks may be specified, which will be treated independently.

Chain

Type Block

Description Specifications of a chain of atoms. When a chain is detected the distance restraints will be activated. No other chain of this type will be detected while any restraints for this chain is active.

AtomNames

³ A. Vashisth, C. Ashraf, W. Zhang, C.E. Bakis, and A.C.T. van Duin, *Accelerated ReaxFF simulations for describing the reactive cross-linking of polymers*, *J. Phys. Chem. A*, 122, 6633-6642 (2018) (<https://doi.org/10.1021/acs.jpca.8b03826>)

Type String

Description Atom names specifying the chain. An atom name can optionally be followed by '@' and a region name, in this case only atoms of this type from the given region will be matched. A leading '@' followed by a number indicates that this position in the chain must be occupied by the atom found earlier at the specified position in the chain. For example "O H N C @1" indicates that the last atom in the chain of the five atoms must be the first oxygen, thus defining a 4-membered ring. This is the only way to define a ring because implicit rings will not be detected. For example, "O H N C O" does not include rings.

MaxDistances

Type Float List

Unit Angstrom

Description Maximum distances for each pair of atoms in the chain. The number of distances must be one less than the number of AtomNames.

MinDistances

Type Float List

Unit Angstrom

Description Minimum distances for each pair of atoms in the chain. The number of distances must be one less than the number of AtomNames.

DistanceRestraint

Type String

Recurring True

Description Specify two atom indices followed by the optimum distance in Angstrom, the first parameter and, optionally, the profile type and the second parameter.

This restraint will try to keep the distance between the two specified atoms at the given value. For periodic systems this restraint follows the minimum image convention.

Each atom index indicates a position of the corresponding atom in the AtomNames key. Currently recognized restraint profile types: Harmonic (default), Hyperbolic, Erf, GaussianWell. The first parameter is the force constant for the Harmonic, Hyperbolic, and Erf profiles, or well depth for GaussianWell. The second parameter is the asymptotic force value F(Inf) for Hyperbolic and Erf profiles, or the factor before x^2 in the exponent for GaussianWell.

Note: the GaussianWell restraint should be used with the Moving flag.

Moving

Type Bool

Default value No

GUI name Move restraint

Description Move the restraints created with this BondBoost. The restraint value will start at the current coordinate's value and will move towards the optimum during the restraint's lifetime. The increment is calculated from the initial deviation and the [NSteps] parameter.

This feature should be used with the GaussianWell restraint types.

NSteps

Type Integer

GUI name Boost lifetime

Description Number of steps the restraints will remain active until removed. Atoms participating in one reaction are not available for the given number of steps.

NumInstances

Type Integer

Default value 1

GUI name Number of instances

Description Number of reactions of this type taking place simultaneously.

Units

Type Multiple Choice

Default value Default

Options [Default, MD]

GUI name Restr. parameter units

Description Change energy, force and force constant units in the DistanceRestraint key from the default (atomic units) to those often used in the MD community (based on kcal/mol and Angstrom). Units for the optimum distances are not affected.

For example:

```
MolecularDynamics
  BondBoost
    NSteps 10000
    Chain
      AtomNames      N.1  C.t  O    H    @1
      MinDistances   3.0  1.2  1.5  0.8
      MaxDistances   3.8  3.0  2.5  1.5
    End
  # Restrains      i j R_0  FC
  DistanceRestraint 1 2  1.5  0.05  Hyperbolic  0.7
  DistanceRestraint 2 3  3.5  0.03  Hyperbolic  0.5
  DistanceRestraint 3 4  1.0  0.03  Hyperbolic  0.5
End
End
```

The AtomNames, MinDistances, and MaxDistances keys constitute the atom chain definitions for the initial configuration. Thus, the example above defines a chain of atoms N.1-C.t-O-H-N.1 with R(N.1-C) in the (3.0,3.8) range, R(C.t-O) in the (1.2,3.0) range, etc.. In this example, the last atoms in the chain is required to be the same as the first one, thus defining a ring. The specified restraints will push pairs of atoms C-N and O-H close together, which will hopefully let them form a bond, and pull atoms C.t and O away from each other, thus breaking the C-O bond. The restraint type is set to Hyperbolic to avoid very large forces that would otherwise result from a harmonic potential at a large deviation.

Note: When detecting coordinates, the program uses the full atom name and not just the element name. An atom name consists of the element name optionally followed by a period and a suffix, just like N.1 and C.t in the example above. Using extended names for some atoms one may allow only a subset of bonds to be boosted.

Force bias Monte Carlo (fbMC)

Configurational sampling and structural relaxation can be accelerated by the Force bias Monte Carlo method. Unlike molecular dynamics, this approach does not use the equations of motion or atomic velocities. Instead, all atoms are randomly displaced in each fbMC steps. AMS uses an uniform-acceptance force bias Monte Carlo flavour of fbMC called tfMC, as published by Mees et al.⁴ Unlike other well-known Monte Carlo methods such as the Metropolis algorithm, fbMC does not generate completely random moves and then test whether these should be accepted or rejected. Instead, the atomic displacements are generated so that atoms preferably move in the direction of the forces acting on them. This special biasing enables fbMC to accept every move, sampling the correct canonical ensemble with high efficiency.

In AMS the fbMC method is implemented as an add-on to molecular dynamics, enabling mixed MC-MD simulations. After every `Frequency` MD steps, the MD procedure is stopped and fbMC takes over, executing `NSteps` Monte Carlo steps. Once the fbMC procedure completes, the MD simulation continues from the new geometry generated by fbMC while reusing atomic velocities from before the start of fbMC.

The fbMC module requires three main input settings. Apart from the `NSteps` and `Frequency` defining the mix of molecular dynamics and Monte Carlo, `Temperature` needs to be set as desired to sample a particular canonical (NVT) ensemble. Although the fbMC procedure always runs in constant temperature mode, the rest of the MD simulation can in principle use any ensemble (with or without a thermostat or barostat).

Note: To run a pure fbMC simulation with no molecular dynamics component, leave `Frequency` set to 1 (the default), set the `MD TimeStep` and `InitialVelocities` to zero, and do not use other MD features such as a thermostat or a barostat.

Note: AMS currently cannot write sampled geometries to the trajectory during the fbMC procedure. To see the evolution of the system during a long fbMC run, split it into multiple shorter fbMC passes to let the MD driver sample the current state between them. To do this, set the `NSteps` for fbMC to the desired trajectory sampling interval, keep `Frequency` set to 1 and set `Trajectory SamplingFreq` to 1.

The amount of acceleration provided by fbMC depends on the `StepLength` parameter, which defines the maximum displacement of the lightest atom in the system. The default value of 0.1 Å is relatively conservative. Increasing `StepLength` leads to faster evolution of the system, but setting it too high can lead to inaccurate sampling or cause crashes by generating geometries that are too distorted.

An estimate of the timescale associated with fbMC (tfMC) steps will be printed to the output.

MolecularDynamics

fbMC

Type Block

Recurring True

GUI name fbMC

Description This block sets up force bias Monte Carlo interleaved with the molecular dynamics simulation.

Frequency

Type Integer

Default value 1

Description Run the fbMC procedure every `Frequency` MD steps.

⁴ M.J. Mees, G. Pourtois, E. C. Neyts, B. J. Thijsse, and André Stesmans, *Uniform-acceptance force-bias Monte Carlo method with time scale to study solid-state diffusion*, Phys. Rev. B 85, 134301 (2012) (<https://doi.org/10.1103/PhysRevB.85.134301>)

MassRoot

Type Float

Default value 2.0

Description Inverse of the exponent used to mass-weight fbMC steps.

MolecularMoves

Type Block

Description Move molecules as rigid bodies in addition to normal atomic moves.

Enabled

Type Bool

Default value No

GUI name Enable molecular moves

Description Enable moving molecules as rigid bodies based on net forces and torques. Ordinary per-atom displacements will then be based on residual atomic forces.

RotationStepAngle

Type Float

Default value 0.1

Unit Radian

Description Maximum allowed angle of rotation of each molecule in one fbMC step.

TranslationStepLength

Type Float

Default value 0.1

Unit Angstrom

Description Maximum allowed displacement of each molecule in each Cartesian coordinate in one fbMC step.

NSteps

Type Integer

GUI name Number of steps

Description Number of fbMC steps to perform on every invocation of the procedure.

PrintFreq

Type Integer

GUI name Printing frequency

Description Print current thermodynamic properties to the output every N fbMC steps. This defaults to the PrintFreq set in the Trajectory block. Setting this to zero disables printing fbMC steps.

StartStep

Type Integer

Default value 1

Description First step at which the fbMC procedure may run.

StepLength

Type Float

Default value 0.1

Unit Angstrom

Description Maximum allowed displacement of the lightest atom in the system in each Cartesian coordinate in one fbMC step.

StopStep

Type Integer

Default value 0

Description Last step at which the fbMC procedure may run. If unset or zero, there is no limit.

Temperature

Type Float

Unit Kelvin

Description Temperature used for fbMC.

Nanoreactor

Nanoreactor is implemented following the article by L.-P. Wang et al.⁵. The nanoreactor is a spherical region of space centered at the origin and surrounded by an elastic wall (represented by a harmonic potential), its size changing over time. The idea of the nanoreactor is to have two phases: reaction and relaxation. In the following, each nanoreactor phase is referred to as a *reactor*. During the relaxation phase, the reactor is large and if the temperature is high enough the reactants are distributed more or less evenly throughout its volume. In the reaction phase, the reactor shrinks and the atoms that now fall outside the reactor's sphere accelerate towards its center. During this phase, high-energy collisions may lead to reactions. After the reaction phase is over, the relaxation phase begins again and the reactor is expanded. This cycle is repeated indefinitely.

Each phase is specified by its own `Reactor` input block. There should be at least two of them but there can be more. The `NSteps` key specifies the duration of the phase in MD steps. The radius of the reactor and the force constant of its wall are set by the `Radius` and `ForceConstant` keys, respectively. To minimize additional strain on internal degrees of freedom of the affected molecules, the force applied by the wall on an atom is proportional to the atom's mass by default. This means that atoms situated at the same distance from the center of the reactor will receive the same acceleration irrespective of their mass. This should be taken into account when choosing a value for the `ForceConstant`. Alternatively, this feature can be disabled using the `MassScaled` key.

MolecularDynamics

Reactor

Type Block

Recurring True

Description Define one phase of the nanoreactor. A reactor is a region of space surrounded by an elastic wall. Atoms inside the region are not affected. Atoms outside it will be pushed back with force depending on the `[ForceConstant]` and the `[MassScaled]` flag.

ForceConstant

⁵ L.-P. Wang, A. Titov, R. McGibbon, F. Liu, V.S. Pande and T.J. Martínez, *Discovering chemistry with an ab initio nanoreactor*, *Nature Chemistry* 6, 1044 (2014) (<https://doi.org/10.1038/NCHEM.2099>)

Type Float

GUI name Reactor force constant

Description Force constant of the reactor wall in Hartree/Bohr² (or Hartree/Bohr²/Dalton if [MassScaled] is true).

MassScaled

Type Bool

Default value Yes

GUI name Scale force by mass

Description If this flag is disabled the force on an atom outside of the reactor depends only on the atomic coordinates and the force constant. Otherwise, the force is also multiplied by the mass of the atom. This means that atoms at the same distance from the wall will receive the same accelerate due to the wall potential.

NSteps

Type Integer

GUI name Reactor lifetime

Description Number of steps for which the reactor will remain active until disabled. The next reactor will be activated immediately after this. After the last reactor is disabled the cycle will repeat.

Radius

Type Float

Unit Angstrom

GUI name Reactor radius

Description Radius of the reactor sphere.

4.9.10 Non-equilibrium MD (NEMD)

T-NEMD for thermoconductivity: heat exchange

There are different methods to study thermal conductivity using non-equilibrium molecular dynamics (NEMD). A common feature of these methods is that they require the system to be divided into three or more zones, each with its own thermostat and other properties. One method maintains the temperature of the heat source and the heat sink zones at the given temperature using two different thermostats and measures the amount of heat transferred. These method does not require any special features besides a standard thermostat and a possibility to calculate the amount of heat accumulated by the thermostat per unit of time. The accumulated thermostat energies are available in the MDHistory section of ams.rkf file, in variables called 'XXXXstat#Energy', where XXXX is a 4-letter abbreviation of the thermo-/barostat ('BerT' for a Berendsen thermostat, 'NHCT' for an NHC thermostat, 'NHTB' for an MTK barostat, etc.) and '#' is a 1-digit index of the thermo-/barostat.

In the other method, the heat flow is constant and the induced temperature gradient is measured. This method is implemented in AMS in three variants: a simple heat exchange, HEX¹ and eHEX². In the simple heat exchange method the atom velocities are scaled up (or down) by a factor corresponding to the amount of heat deposited to the heat source (or

¹ T. Ikeshoji and B. Hafskjold, *Non-equilibrium molecular dynamics calculation of heat conduction in liquid and through liquid-gas interface* Molecular Physics 81, 251-261 (1994) (<https://doi.org/10.1080/00268979400100171>)

² P. Wirtsberger, D. Frenkel, and C. Dellago, *An enhanced version of the heat exchange algorithm with excellent energy conservation properties* Journal of Chemical Physics 143, 124104 (2015) (<http://dx.doi.org/10.1063/1.4931597>)

withdrawn from the heat sink) without paying attention to the conservation of the total momentum of the heat source (or sink). In the HEX method the velocities are scaled in such a way that the total momentum is conserved. This, however, introduces a small but measurable drift in the total energy. The eHEX algorithm improves upon the HEX by adding a third-order time-integration correction to remove the drift.

This method is controlled by the HeatExchange sub-block of the MolecularDynamics block:

MolecularDynamics

HeatExchange

Type Block

Recurring True

GUI name Heat exchange

Description Input for the heat-exchange non-equilibrium MD (T-NEMD).

HeatingRate

Type Float

Unit Hartree/fs

Description Rate at which the energy is added to the Source and removed from the Sink. A heating rate of 1 Hartree/fs equals to about 0.00436 Watt of power being transferred through the system.

Method

Type Multiple Choice

Default value Simple

Options [Simple, HEX, eHEX]

Description Heat exchange method used.

Simple: kinetic energy of the atoms of the source and sink regions is modified irrespective of that of the center of mass (CoM) of the region (recommended for solids).

HEX: kinetic energy of the atoms of these regions is modified keeping that of the corresponding CoM constant.

eHEX: an enhanced version of HEX that conserves the total energy better (recommended for gases and liquids).

Sink

Type Block

Description Defines the heat sink region (where the heat will be removed).

AtomList

Type Integer List

GUI name Sink region

Description The atoms that are part of the sink.

This key is ignored if the [Box] block or [Region] key is present.

Box

Type Block

Description Part of the simulation box (in fractional cell coordinates) defining the heat sink. If this block is specified, then by default, the whole box in each of the three dimensions is used, which usually does not make much sense. Normally, you will want to set the bounds along one of the axes.

Amax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the third axis.

Region

Type String

GUI name Sink region

Description The region that is the sink.

This key is ignored if the [Box] block is present.

Source

Type Block

Description Defines the heat source region (where the heat will be added).

AtomList

Type Integer List

GUI name Source region

Description The atoms that are part of the source.

This key is ignored if the [Box] block or [Region] key is present.

Box

Type Block

Description Part of the simulation box (in fractional cell coordinates) defining the heat source.

If this block is specified, then by default, the whole box in each of the three dimensions is used, which usually does not make much sense. Normally, you will want to set the bounds along one of the axes. This block is mutually exclusive with the FirstAtom/LastAtom setting.

Amax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the third axis.

Region

Type String

GUI name Source region

Description The region that is the source.

This key is ignored if the [Box] block is present.

StartStep

Type Integer

Default value 0

Description Index of the MD step at which the heat exchange will start.

StopStep

Type Integer

Description Index of the MD step at which the heat exchange will stop.

One should be careful when choosing a value for the HeatingRate because a too large value may lead to pyrolysis of the heat source or to an abnormal termination when all the kinetic energy of the heat sink has been drained. The optimal value depends on the size of the system, its heat conductivity and the desired temperature gradient value. The thermal conductivity k can be calculated by dividing the heat flow rate W by the temperature gradient $grad(T)$ and by the flow cross-section area S : $k = W / (S \cdot grad(T))$. See the *trajectory sampling* (page 105) section above on how to obtain the temperature profile from which the $grad(T)$ can be computed.

NEMD for tribology: Applying velocities / forces

Non-equilibrium Molecular Dynamics (NEMD) is a commonly used tool to study phenomena like friction & wear in tribochemical systems. In these MD simulations, an constant external force or velocity is applied to a specific subgroup of atoms. For example, when studying sliding solid surfaces, the ApplyForce feature can be used to exert a compressive normal force in the -Z direction on one of the solid slabs while the ApplyVelocity block simultaneously slides the same group of atoms along the X or Y axis.

In the case of ApplyVelocity, the specified group of atoms (defined as a Region) will move with the specified constant net Velocity. The imposed velocity is automatically excluded from thermostatting and system-wide momentum removal. The Components input key can be used to select just a subset of Cartesian components of the net velocity of the group to be controlled, so that other components can be left to evolve freely. In the sliding example in the previous paragraph, one would use Components=XY to let the Z motion of the sliding slab to freely follow the applied normal force.

In the case of ApplyForce, the selected Region (group of atoms) will experience an additional specified constant Force on each timestep of the simulation. By default, the Force parameter defines the total (net) force acting on the whole Region. This can be changed by setting the PerAtom option to apply the Force to each atom in the Region separately.

See also:

Example demonstrating a NEMD friction simulation (page 444)

MolecularDynamics

ApplyVelocity

Type Block

Recurring True

Description The ApplyVelocity keyword can be used to move an arbitrary group of atoms in the system with a constant net velocity

Components

Type Multiple Choice

Default value XY

Options [X, Y, Z, XY, YZ, XZ, XYZ]

Description Select which components of the Velocity vector are used to set the corresponding components of the net velocity of the specified set of atoms. Any other components of Velocity are ignored and the motion of the selected atoms in those directions is unaffected by ApplyVelocity.

Region

Type String

Recurring True

Description Applies the defined velocity to all atoms in this region.

Velocity

Type Float List

Unit Angstrom/fs

Recurring False

Description The constant velocity that will be applied to the specified atoms.

MolecularDynamics

ApplyForce

Type Block

Recurring True

Description The ApplyForce keyword can be used to apply an arbitrary constant force to a certain (subgroups of) atoms in the system

Force

Type Float List

Unit Hartree/Bohr

Description Defines the constant force vector

PerAtom

Type Bool

Default value No

Description If enabled, the Force vector is applied separately to every atom in the selected Region, so that the total net force on the Region equals the value of Force times the number of atoms in Region. This was the behaviour of ApplyForce in AMS2022. By default, with PerAtom disabled, the Force vector defines the total net force on the Region, so the force applied to each atom equals the value of Force divided by the number of atoms in Region.

Region

Type String

Recurring True

Description Apply the constant force to all atoms in this region.

When the `ApplyVelocity` block is used to slide a region, the measured net force experienced by that region is written to the `MDHistory` section on the trajectory. This force is calculated directly from the gradients returned by an `Engine` and thus excludes the effect of any `ApplyForce` blocks. The ratio of the tangential (sliding) and normal (compression) component of the mean force is thus equal to the friction coefficient. Three variables will be written by any `ApplyVelocity` block:

- `EngineXForceRegionA`: instantaneous force on region *A*, Cartesian component *X*
- `MeanEngineXForceRegionA`: average of `EngineXForceRegionA` over all timesteps since the previous trajectory frame
- `StdevEngineXForceRegionA`: standard deviation of `EngineXForceRegionA` over all timesteps since the previous trajectory frame

NEMD viscosity via cosine shear perturbation

In order to calculate the viscosity using NEMD, apply a periodic perturbation to the system using the `CosineShear` input block. This will add an amount of acceleration to the atoms in the system according to a cosine function running along the specified Cartesian `ProfileAxis`. The acceleration applied to each atom will have the direction of `FlowDirection` and magnitude equal to $a_x(z) = A \cos(\frac{2\pi z}{L_z})$, where *A* is the amplitude defined by the `Acceleration` input key and *L_z* is the length of the periodic box in the *Z* axis (assuming `ProfileAxis=Z` and `FlowDirection="1 0 0"`). It is typically the most efficient to use a box roughly three times taller in the `ProfileAxis` direction than in the other two axes. AMS currently requires the `ProfileAxis` to be aligned with one of the lattice vectors and perpendicular to the remaining lattice vectors.

See also:

Example demonstrating a NEMD viscosity simulation (page 449)

Warning: `CosineShear` simulations are typically performed in the NVT ensemble. While using a `Barostat` is theoretically possible, such a combination has not been physically validated by SCM.

MolecularDynamics

CosineShear

Type Block

Description Apply an external acceleration to all atoms of a fluid using a periodic (cosine) function along a selected coordinate axis. This induces a periodic shear flow profile which can be used to determine the viscosity.

Acceleration

Type Float

Default value 5e-06

Unit Angstrom/fs²

Description Amplitude of the applied cosine shear acceleration profile. The default value should be a rough first guess for water and it needs to be adjusted by experimentation for other systems.

Enabled

Type Bool

Default value No

GUI name Enable cosine shear

Description Apply a cosine shear acceleration profile for a NEMD calculation of viscosity.

FlowDirection

Type Float List

Default value [1.0, 0.0, 0.0]

Description The direction in which to apply the shear acceleration, in Cartesian coordinates. The magnitude of this vector is ignored (AMS will normalize it internally). FlowDirection has to be perpendicular to ProfileAxis.

ProfileAxis

Type Multiple Choice

Default value Z

Options [X, Y, Z]

Description The Cartesian coordinate axis along which the cosine wave runs

This generates a velocity profile in the steady state that looks like: $v_x(z) = V \cos(\frac{2\pi z}{L_z})$. After the system reaches a steady state, the velocity amplitude V will be approximately constant, although typically relatively noisy. Averaging V over a long enough trajectory yields a reasonable estimate of the steady-state flow velocity, which can then be used to calculate the viscosity as $\eta = \frac{A\rho L_z^2}{4\pi^2}$. The measured value of V averaged over every `Trajectory SamplingFreq` timesteps is written to the trajectory as *MeanCosineShearVelocity* in the units of Bohr/fs.

The calculated viscosity value will be different from the equilibrium viscosity of the studied liquid due to shear thinning and heating caused by the applied acceleration A . It is thus necessary to measure the viscosity at several different values of A and extrapolate the obtained values to the zero-shear limit $A = 0$. To do this, it is useful to calculate the “shear parameter” $S = \frac{A^2 m \rho L_z^2}{8\pi^2 N_f k_B}$, where m is the total mass of the system and N_f is the number of degrees of freedom. The measured viscosity η is then approximately a linear function of S , enabling a straightforward extrapolation to zero S . Typical values of the shear parameter S in SI units are on the order of $10^9 - 10^{10} \text{ kg m s}^{-2} \text{ K}$.

Applying reflective walls

Note: This feature is still experimental. It may contain bugs and some input keys are still subject to change in future releases of AMS. If you are interested in trying it out, monitor the [bug fix changelog](https://www.scm.com/support/downloads/changelog/) (<https://www.scm.com/support/downloads/changelog/>) for updates and feel free to get in touch with us at support@scm.com if you run into any issues.

The `ReflectiveWall` keyword can be used to define impenetrable planes in space, causing molecules to bounce off by an elastic collision. Therefore, the main usage of reflective walls is to make sure that molecules will stay within a certain area in space.

The reflective wall is defined by a normal vector (`Axis`) and a `Threshold`. The plane of the wall is perpendicular to `Axis` and passes through a point given by multiplying `Axis` by `Threshold`. Any atom moving in the direction of `Axis` will be reflected back, but the opposite does not apply. Particles moving in the direction opposite to `Axis` will not be affected (the wall works like a one-way mirror). The `Axis` vector does not need to be normalized to unity, AMS will normalize it internally and adjust `Threshold` accordingly.

MolecularDynamics

ReflectiveWall

Type Block

Recurring True

Description Apply a reflective wall in space

Axis

Type Float List

Unit Angstrom

Description Defines the normal vector perpendicular to the plane of the reflective wall. Any particle moving in this direction will be reflected back.

Region

Type String

Recurring True

Description Apply the reflective wall to all atoms in this region.

Threshold

Type Float

Unit Angstrom

Description Defines the threshold value determining the position of the reflective wall. If the dot product of a position of a particle with Axis exceeds Threshold, the particle will be reflected. This means that the plane of the wall passes through a point given by Axis times Threshold.

4.10 Trajectory replay

For some applications it is necessary to run calculations on all (or a subset of) frames from a trajectory obtained in another job. Often this is done with a different engine in order to learn something about the differences in the potential energy surface between the engines. This could easily be scripted with *PLAMS* (page 25), but since the 2022.1 release the AMS driver itself also implements a convenient “Replay” task to do this.

The input for the replay task is quite minimal. The following input file would replay every tenth of the first 1000 frames on the trajectory of `oldjob` with the DFTB engine to calculate nuclear gradients:

```
Task Replay

Replay
  File oldjob.results
  Frames 1:1000:10
End

Properties
  Gradients True
End

Engine DFTB
EndEngine
```

See also:

Example input files (page 453) for replaying PES scans, NEB and MD calculations.

Note that it is not necessary to specify a *System block* (page 31) in the input of a replay job, as the system will just be loaded from the job to be replayed. What properties are evaluated for each frame in the trajectory can be configured in

the `Properties` block of the input file. For a list of available properties, see for example the the manual pages on *Gradients*, *Hessian*, *Stress tensor*, *Elasticity* (page 178) and *Dipole moment*, *Polarizability*, *Bond orders* (page 244).

Depending on the kind of job that is being replayed, you will get a slightly different default behavior for the selection of frames to be replayed:

- For *PES scans* (page 68) only the frames corresponding to the converged PES points will be replayed. The resulting `ams.rkf` output file will contain the `PESScan` section, as if it had been produced by running a PES scan job.
- For *Nudged Elastic Band (NEB)* (page 75) jobs only the frames corresponding to the converged images are replayed. The resulting `ams.rkf` file will have an `NEB` section that looks like it is from a NEB job that converged immediately.
- All other job types (such as *Molecular Dynamics* (page 90)) will just replay whatever is on the `History` section on the `ams.rkf` file. By default all frames are replayed, but a subset can be chosen with the `Replay%Frames` keyword.

Note that the replay task does not use *driver level parallelism* (page 21). The engine is called on each frame in turn, always restarting from the previously calculated frame. (The restarting should not cause problems, but it can be disabled with the `EngineDebugging%IgnorePreviousResults` option, see *developer options* (page 477)).

Details of the Replay task can be configure in the `Replay` block in the input.

```
Replay
  File string
  Frames integer_list
  StoreAllResultFiles Yes/No
End
```

Replay

Type Block

Description Configures the details of the Replay task.

File

Type String

GUI name Restart from

Description Provide an `ams.rkf` file (or a `.results` folder) from a previously run job to replay. The file needs to contain a `History` section.

Frames

Type Integer List

Description List of frames from the `History` section to recompute.

If not specified the recomputed frames are determined automatically based on the task of the job that is being replayed: PES scans and NEB calculations will only have the converged points replayed, while all other tasks will have all frames recomputed.

Specifying the frames to recompute in the input is probably only useful when replaying trajectories from `MolecularDynamics` calculations.

StoreAllResultFiles

Type Bool

Default value No

Description If this option is enabled AMS will produce a separate engine output file for every replayed frame.

While basic properties like energy, gradients, stress tensor, etc. are stored anyway on the History section in the AMS driver output file (if they were requested in the Properties block), engine specific properties (e.g. excitations energies from ADF) will only be available if the full result files are stored.

4.11 Grand Canonical Monte Carlo (GCMC)

Tip: Take a look at the [GCMC tutorial](#) and learn how to setup a GCMC calculation.

4.11.1 General info

About Monte Carlo / the Grand Canonical Ensemble

It is best to read a bit about Monte Carlo and ensembles before working with the GCMC code. Almost every book or review text on molecular simulations will do, for example: Frenkel D, Smit B. Understanding molecular simulation: from algorithms to applications. Academic Press; 2002. 672 p.

Wikipedia also has some pages of interest:

- http://en.wikipedia.org/wiki/Monte_Carlo_method
- http://en.wikipedia.org/wiki/Grand_canonical_ensemble

It is important to note that this method heavily relies on random numbers, and simulations are thus non-repeatable in detail, but should converge to the same answer.

About the AMS GCMC code

The GCMC code was originally developed for standalone Reaxff by Thomas Senftle, working as a Graduate Student at Penn State University under the supervision of Dr. Adri van Duin^{1,2}. The original version was a wrapper code that called an external executable to perform the reaxff minimization step and energy calculation, and relied on file modification and parsing to steer the reaxff code and get the results back.

The code was later rewritten by Hans van Schoot (SCM), in close collaboration with Thomas Senftle, to integrate it directly into the ADF-ReaxFF code. The current version is an AMS re-implementation so the method can be used with almost any engine supported by AMS (support for 3D periodic boundary conditions by the engine is currently a requirement).

4.11.2 Method Details

Overview

The GCMC method will perform a number of Grand Canonical Monte Carlo trial moves (set by the `Iterations` option of the `GCMC` input block), and accept or reject them based on the energy produced by the geometry optimization of the trial geometry for the given engine. The Monte Carlo algorithm will always accept a step if it results in a decrease of the energy, and accept steps that go up in energy with a probability. This section will give some details about how the method works.

MC Moves (Insert/Delete/Displace/ChangeVolume)

¹ T.P. Senftle, R.J. Meyer, M.J. Janik, A.C.T. van Duin, *Development of a ReaxFF potential for Pd/O and application to palladium oxide formation*, J. Chem. Phys. 139, 044109 (2013) (<https://doi.org/10.1063/1.4815820>)

² T.P. Senftle, A.C.T. van Duin, M.J. Janik, *Determining in situ phases of a nanoparticle catalyst via grand canonical Monte Carlo simulations with the ReaxFF potential*, Catalysis Communications 52, 72–77 (<https://doi.org/10.1016/j.catcom.2013.12.001>)

The GCMC method currently supports 4 types of MC Moves: Insert, Delete, Displace (sometimes also called Move), and ChangeVolume. The first three MC moves are always available and the ChangeVolume becomes available only ChangeVolume option is set to True. The first three move types change coordinates of atoms in the system, while the ChangeVolume move changes the lattice only.

On every MC iteration, the method first selects one of the molecules defined by the Molecule input blocks at random and then selects an applicable MC move type. If there are no molecules of this type in the system then no Delete or Displace is attempted. If the selected molecule has the NoAddRemove option set then the Insert and Delete moves will not be attempted. If no MC move is possible with the selected molecule type then another one is selected or a VolumeChange is attempted, if allowed. If no moves with any of the provided molecules is possible (i.e. if all molecules have NoAddRemove set to True, there is nothing to displace and the volume is fixed) then the program will stop.

The Insert and Displace MC move will rotate the molecule randomly and put it at a random position, and then check if the minimum interatomic distance between the molecule and the rest of the system is within the MinDistance and MaxDistance boundaries. If the condition is not satisfied, a new set of coordinates is generated and the check is performed again. This is repeated up to NumAttempts times before stopping with an error.

The volume change is controlled by the VolumeChangeMax keyword. This sets the volume change limit, and it should be a value between 0 and 1. The new volume will be calculated as: $V_{new} = \exp(\text{random}(-1:1) * \text{VolumeChangeMax}) * V_{old}$.

Calculating the chemical potential

The chemical potential of the molecule (or atom) reservoir is used when calculating the Boltzmann accept/reject criteria after a MC move is executed. This value can be derived from first principles using statistical mechanics, or equivalently, it can be determined from thermochemical tables available in literature sources.

For example, the proper chemical potential for a GCMC simulation in which single oxygen atoms are exchanged with a reservoir of O2 gas, should be equal to 1/2 the chemical potential of O2 at the temperature and pressure of the reservoir^{Page 325, 1}:

$$\mu_O^{MC}(T, P) = \frac{1}{2}\mu_{O_2}^{MC}(T, P) = \frac{1}{2} \left[\mu_{O_2}^{ref}(T, P_{ref}) + kT \ln \left(\frac{P}{P_{ref}} \right) - E_{O_2}^{diss} \right]$$

where the reference chemical potential $\mu_{O_2}^{ref}(T, P_{ref})$ is the experimentally determined chemical potential of O2 at T and P_{ref} , $kT \ln \left(\frac{P}{P_{ref}} \right)$ is the pressure correction to the free energy, and $E_{O_2}^{diss}$ is the dissociation energy of the O2 molecule.

Calculating energies

Because the GCMC simulation adds and deletes atoms or molecules during the runtime, it cannot directly compare the AMS energies for the MC acceptance criteria: inserting a molecule will usually lower the total energy of the system, causing the MC to always accept it, and always reject a deletion. To compensate this, the GCMC method calculates a “corrected” MC energy to compare the trial energy with, consisting of the previously accepted AMS energy and a correction depending on the move:

$$E_{old}^{MC} = E_{old}^{AMS} + \mu^{MC} \text{ for an Insert move;}$$

$$E_{old}^{MC} = E_{old}^{AMS} - \mu^{MC} \text{ for a Delete move;}$$

$$E_{old}^{MC} = E_{old}^{AMS} \text{ for a Displace move;}$$

$$E_{old}^{MC} = E_{old}^{AMS} - P(V_{new} - V_{old}) + N_{inserted} \ln \left(\frac{V_{new}^{avail}}{V_{old}^{avail}} \right) kT \text{ for a ChangeVolume move.}$$

Here, μ^{MC} is the chemical potential of the inserted/deleted molecule, P is the pressure, V is the volume, and $N_{inserted}$ is the total number of MC molecules. The “new” and “old” subscripts refer to the current and the last accepted values. The V^{avail} values are calculated from the MC-available volume as described below.

Calculating volumes

The available volume can be calculated in a few different ways, depending on the VolumeOption setting:

- *Free*: volume = total volume - occupied volume - specified vacuum volume (NonAccessibleVolume)

- *Total*: volume = total cell volume
- *Accessible*: volume = specified accessible volume (AccessibleVolume)
- *FreeAccessible*: volume = specified accessible volume (AccessibleVolume) - occupied volume

Here, the occupied volume is calculated as a sum of volumes of atoms that do not belong to the MC part of the system (i.e. that were not inserted during calculation and are not Removables). The volume of an atom is calculated using the average of the covalent and the Van der Waals radii of the atom defined in the atominfo module used throughout AMS.

The AccessibleVolume and NonAccessibleVolume keywords can be used to get a more accurate available volume.

Acceptance criteria

An MC move is always accepted if the AMS energy is lower than the corrected MC energy of the last accepted MC move, or if the energy increase is small enough. If the new energy is higher, the code generates a random number between 0 and 1, and accepts the move if the random number is greater than:

```
prob = preFactor * exp(-Beta*deltaE)
```

The prefactor is calculated (for insert and delete moves) using the deBroglie wavelength of the inserted molecules, the number of inserted molecules and the available MC volume of the system.

4.11.3 Input

The GCMC functionality in AMS is triggered using the following Task key:

```
Task GCMC
```

```
GCMC
  AccessibleVolume float
  Box
    Amax float
    Amin float
    Bmax float
    Bmin float
    Cmax float
    Cmin float
  End
  Ensemble [Mu-VT | Mu-PT]
  Iterations integer
  MapAtomsToOriginalCell Yes/No
  MaxDistance float
  MinDistance float
  Molecule
    ChemicalPotential float
    NoAddRemove Yes/No
    SystemName string
  End
  NonAccessibleVolume float
  NumAttempts integer
  Pressure float
  Removables # Non-standard block. See details.
  ...
End
Restart string
SwapAtoms
```

(continues on next page)

(continued from previous page)

```

    Probability float
    Regions string
End
    Temperature float
    UseGCPreFactor Yes/No
    VolumeChangeMax float
    VolumeOption [Free | Total | Accessible | FreeAccessible]
End

```

The following keys are common for all GCMC calculations and should always be specified. The ChemicalPotential value should correspond to the μ^{MC} expression above, and not to the experimental chemical potential μ^{ref} , which means it should include the (engine-dependent) free molecule's energy.

GCMC**Molecule****Type** Block**Recurring** True**GUI name** Molecules

Description This block defines the molecule (or atom) that can be inserted/moved/deleted with the MC method. The coordinates should form a reasonable structure. The MC code uses these coordinates during the insertion step by giving them a random rotation, followed by a random translation to generate a random position of the molecule inside the box. Currently, there is no check to make sure all atoms of the molecule stay inside the simulation box. The program does check that the MaxDistance/MinDistance conditions are satisfied.

ChemicalPotential**Type** Float**Unit** Hartree**Description** Chemical potential of the molecule (or atom) reservoir.

It is used when calculating the Boltzmann accept/reject criteria after a MC move is executed. This value can be derived from first principles using statistical mechanics, or equivalently, it can be determined from thermochemical tables available in literature sources. For example, the proper chemical potential for a GCMC simulation in which single oxygen atoms are exchanged with a reservoir of O2 gas, should equal 1/2 the chemical potential of O2 at the temperature and pressure of the reservoir:

$$\text{cmpot} = \text{Mu_O}(T,P) = 1/2 * \text{Mu_O2}(T,P) = 1/2 * [\text{Mu_ref}(T,P_ref) + kT * \text{Log}(P/Pref) - E_diss]$$

where the reference chemical potential [Mu_ref(T,P_ref)] is the experimentally determined chemical potential of O2 at T and Pref; kT*Log(P/Pref) is the pressure correction to the free energy, and E_diss is the dissociation energy of the O2 molecule.

NoAddRemove**Type** Bool**Default value** No**GUI name** Fix molecule

Description Set to True to tell the GCMC code to keep the number of molecules/atoms of this type fixed.

It will thus disable Insert/Delete moves on this type, meaning it can only do a displacement move, or volume change move (for an NPT ensemble).

SystemName

Type String

GUI name Molecule

Description String ID of a named [System] to be inserted. The lattice specified with this System, if any, is ignored and the main system's lattice is used instead.

Iterations

Type Integer

GUI name Number of GCMC iterations

Description Number of GCMC moves.

Temperature

Type Float

Default value 300.0

Unit Kelvin

Description Temperature of the simulation. Increase the temperature to improve the chance of accepting steps that result in a higher energy.

The following keys are related to Insert and Displace moves.

GCMC

NumAttempts

Type Integer

Default value 1000

GUI name Max tries

Description Try inserting/moving the selected molecule up to the specified number of times or until all constraints are satisfied. If all attempts fail a message will be printed and the simulation will stop. If the MaxDistance-MinDistance interval is small this number may have to be large.

MinDistance

Type Float

Default value 0.3

Unit Angstrom

GUI name Add molecules not closer than

Description Keep the minimal distance to other atoms of the system when adding the molecule.

MaxDistance

Type Float

Default value 3.0

Unit Angstrom

GUI name Add molecules within

Description The max distance to other atoms of the system when adding the molecule.

The following keys influence computation of the acceptance probability and of the MC energy correction.

GCMC

UseGCPreFactor

Type Bool

Default value Yes

GUI name Use GC prefactor

Description Use the GC pre-exponential factor for probability.

VolumeOption

Type Multiple Choice

Default value Free

Options [Free, Total, Accessible, FreeAccessible]

GUI name Volume method

Description Specifies the method to calculate the volume used to calculate the GC pre-exponential factor and the energy correction in the Mu-PT ensemble: Free: $V = \text{totalVolume} - \text{occupiedVolume} - \text{NonAccessibleVolume}$; Total: $V = \text{totalVolume}$; Accessible: $V = \text{AccessibleVolume}$; FreeAccessible: $V = \text{AccessibleVolume} - \text{occupiedVolume}$. The AccessibleVolume and NonAccessibleVolume are specified in the input, the occupiedVolume is calculated as a sum of atomic volumes.

AccessibleVolume

Type Float

Default value 0.0

Description Volume available to GCMC, in cubic Angstroms. AccessibleVolume should be specified for “Accessible” and “FreeAccessible” [VolumeOption].

NonAccessibleVolume

Type Float

Default value 0.0

GUI name Non-accessible volume

Description Volume not available to GCMC, in cubic Angstroms. NonAccessibleVolume may be specified for the “Free” [VolumeOption] to reduce the accessible volume.

The following keys apply to the ensemble choice and options for the Mu-PT ensemble.

GCMC

Ensemble

Type Multiple Choice

Default value Mu-VT

Options [Mu-VT, Mu-PT]

Description Select the MC ensemble: Mu-VT for fixed volume or Mu-PT for variable volume. When the Mu-PT ensemble is selected the [Pressure] and [VolumeChangeMax] should also be specified.

VolumeChangeMax

Type Float

Default value 0.05

Description Fractional value by which logarithm of the volume is allowed to change at each step. The new volume is then calculated as $V_{\text{new}} = \exp(\text{random}(-1:1) * \text{VolumeChangeMax}) * V_{\text{old}}$

Pressure

Type Float

Default value 0.0

Unit Pascal

Description Pressure used to calculate the energy correction in the Mu-PT ensemble. Set it to zero for incompressible solid systems unless at very high pressures.

The GCMC code can insert multiple atom/molecule types in a single simulation, so it needs to keep track of what atom belongs to which insert. This information is automatically stored and updated when insertion/deletion/moving of atoms or molecules during the simulation, but is by default unknown for the atoms of the starting geometry. The GCMC code will therefore by default not modify the atoms in the original input in the MC trial moves. The `Restart` key and the `Removables` block are two ways to provide information about Deletable/Movable atoms/molecules in the input structure. If the `Restart` key is present the `Removables` block will be ignored.

GCMC

Restart

Type String

Description Name of an RKF restart file. Upon restart, the information about the GCMC input parameters, the initial system (atomic coordinates, lattice, charge, etc.) and the MC molecules (both already inserted and to be inserted) are read from the restart file. The global GCMC input parameters and the MC Molecules can be modified from input. Any parameter not specified in the input will use its value from the restart file (i.e. not the default value). Molecules found in the restart file do not have to be present as named Systems in the input, however if there is a System present that matches the name of a molecule from restart then the System's geometry will replace that found in the restart file. It is also possible to specify new Molecules in the input, which will be added to the pool of the MC molecules from restart.

Removables

Type Non-standard block

Description The Removables can be used to specify a list of molecules that can be removed or moved during this GCMC calculation. Molecules are specified one per line in the format following format: `MoleculeName atom1 atom2 ...`. The `MoleculeName` must match a name specified in one of the `[Molecule]` blocks. The atom indices refer to the whole input System and the number of atoms must match that in the specified Molecule. A suitable Removables block is written to the standard output after each accepted MC move. If you do so then you should also replace the initial atomic coordinates with the ones found in the same file. If a `[Restart]` key is present then the Removables block is ignored.

An example of the Removables block:

```
Removables
  Oatom 41
  O2 44 45
  Oatom 42
  Oatom 43
End
```


This example specifies that 5 atoms belong to 4 different GCMC molecules of two different types, `Oatom` and `O2`. Thus in addition to the main input `System` there should be at least two additional `Systems` defined, one called “Oatom” (containing one atom) and the other “O2” (containing two atoms). The first one was inserted three times (atoms 41, 42, and 43) and the second one was inserted once.

Finally there are more technical keywords:

GCMC

MapAtomsToOriginalCell

Type Bool

Default value Yes

Description Keeps the atom (mostly) in the original cell by mapping them back before the geometry optimizations.

Note that the `GeometryOptimization` block is also read by the GCMC task, and the settings used for the individual optimizations. The documentation for these keywords can be found in the *Geometry Optimization* (page 47) section of this manual.

4.11.4 Output

In addition to the standard KF variables in the “History” section on `ams.rkf` such as “Coords” and “Energy”, the following GCMC-specific variables are also created for each accepted MC step:

- *MCMove* - integer index of the MC move.
- *MCMoveType* - string containing the type of the MC move.
- *MCMolecule* - string containing the name of the inserted/displaced/removed molecule.
- *Converged* - a Fortran logical value containing the convergence status of the given geometry.

Results of a GCMC calculation are stored in the GCMC section of the RKF file, in a number of variables. The following variables contain a summary of the MC statistics up to and including the latest step:

- *NIterMCtried* - the latest iteration number.
- *NIterMCaccept* - the number of accepted MC moves.
- *NIterMCreject* - the number of rejected MC moves.
- *NMCacceptAdd* - the number of accepted MC molecule insertions.
- *NMCacceptRemove* - the number of accepted MC molecule removals.
- *NMCacceptMove* - the number of accepted MC molecule moves.
- *NMCacceptVolume* - the number of accepted volume changes.
- *NMCrejectAdd* - the number of rejected MC molecule insertions.
- *NMCrejectRemove* - the number of rejected MC molecule removals.
- *NMCrejectMove* - the number of rejected MC molecule moves.
- *NMCrejectVolume* - the number of rejected volume changes.

The following variables (actually arrays of the size `Iterations`) in the GCMC section contain the detailed information about all MC moves in the current simulation. Only the first *NIterMCtried* elements of each array contain valid data.

- *HistoryAccepted* - MC move status value (1 - accepted, 0 - rejected, -1 - not done yet).
- *HistoryAMSEnergy* - the AMS energy (the E^{AMS} above).

- *HistoryMCEnergy* - the corrected MC energy ($E^{MC} = E^{AMS} - \Sigma\mu_i^{MC}$, where $\Sigma\mu_i^{MC}$ is the total chemical potential of all inserted molecules).
- *HistoryVolume* - the simulation box volume.
- *HistoryMoveType* - the MC move type index (0 - insert, 1 - delete, 2 - displace, 3 - change volume). The name of the move type with index i can be found in the *MoveType(i)* variable.
- *HistoryMoleculeType* - the inserted/deleted/displaced molecule type index. The name of the molecule type with index i can be found in the *MoleculeName(i)* variable.
- *HistoryMoleculeIndex* - the inserted/deleted/displaced molecule index within its type.

4.12 Automated PES Exploration

In chemistry and materials science, two types of Potential Energy Surface (PES) critical points are of particular interest: local minima and (first-order) saddle points.

The `PESExploration` task consists of a set of algorithms (which we will refer to as *jobs*) that will automatically explore the PES of a given system, looking for local minima and saddle points.

The available PES exploration jobs are:

Process Search (page 160) A composite method for finding escape mechanisms from a state. This will find both local minima and saddle points.

Basin Hopping (page 164) A Monte Carlo method for finding local minima.

Saddle Search (page 161) A single-ended method for finding nearby saddle points.

Landscape Refinement (page 168) Given a pre-calculated Energy Landscape, re-optimize local minima and saddle points using a different computational engine/settings.

Binding Sites (page 173) Given a pre-calculated Energy Landscape, compute the binding sites.

The AMS driver links to the client program of the [EON software package](http://theory.cm.utexas.edu/eon/index.html) (<http://theory.cm.utexas.edu/eon/index.html>)¹ and uses its implementation of the dimer method. EON is developed by the University of Texas at Austin and the University of Iceland. See also the *Required citations* (page 483) section.

See also:

- PES Exploration GUI tutorials:
 - Automated reaction pathway discovery for hydrohalogenation
 - Cluster Growth: Cobalt Clusters
 - Water dissociation on an oxide surface
- Examples:
 - *Example: Basin Hopping for Ar 13 cluster* (page 417)
 - *Example: PES Exploration, Process Search for alanine with PLAMS* (page 418)
 - *Example: PES Exploration, Binding Sites for O on Pt 111* (page 419)

Tip: There is a separate tool specifically for the generation of conformers, see this *manual page* (page 326). While the PES exploration can in principle also be used to find conformers, using the dedicated *Conformers tool* (page 326) is usually

¹ Samuel T Chill, Matthew Welborn, Rye Terrell, Liang Zhang, Jean-Claude Berthet, Andreas Pedersen, Hannes Jónsson and Graeme Henkelman *EON: software for long time simulations of atomic scale systems*, *Modelling Simul. Mater. Sci. Eng.* 22 055002 (2014) (<https://doi.org/10.1088/0965-0393/22/5/055002>)

easier and faster. Note that the set of minima found by the Conformers tool can be used as input for a PES exploration, see *this example* (page 422).

4.12.1 Overview

While many details of a PES exploration calculation depend on the specific *job* (page 154) selected, some aspects are common to all PES explorations jobs. Here we give a brief overview of a typical PES exploration, using a Process Search job as example.

A PES exploration calculation generally consists of multiple *expeditions*, each with several *explorers*.

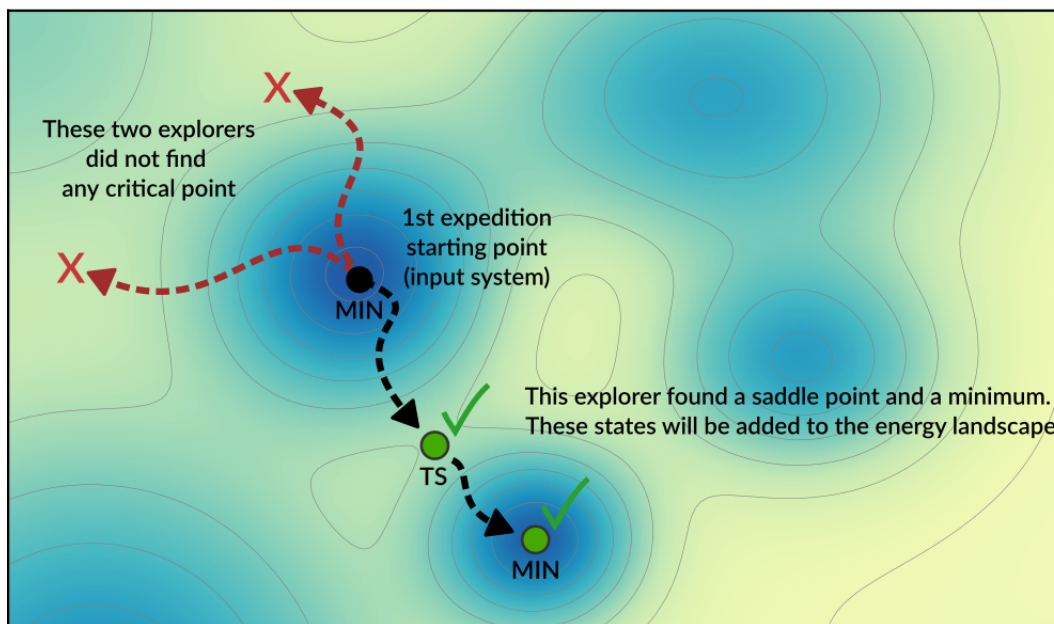
Explorers are given an initial structure, and their goal is to find a nearby critical point (a local minimum, a saddle point or both). The explorer moves around the PES by modifying the atomic positions of the system and by using the specified *Engine* (page 250) to compute energy and gradients.

An *expedition* is a collection of *explorers* all starting from the same point on the PES.

Before setting off for the first expedition, the input structure is optimized and added to the *Energy Landscape*, which is the database of all interesting points found during the exploration (see the section *Results: the “Energy Landscape”* (page 156) for more details).

Starting from this initial structure, a number of PES explorers (3 in the diagram below) will set off in random directions exploring the potential energy surface and looking for nearby critical points.

1st expedition with 3 explorers

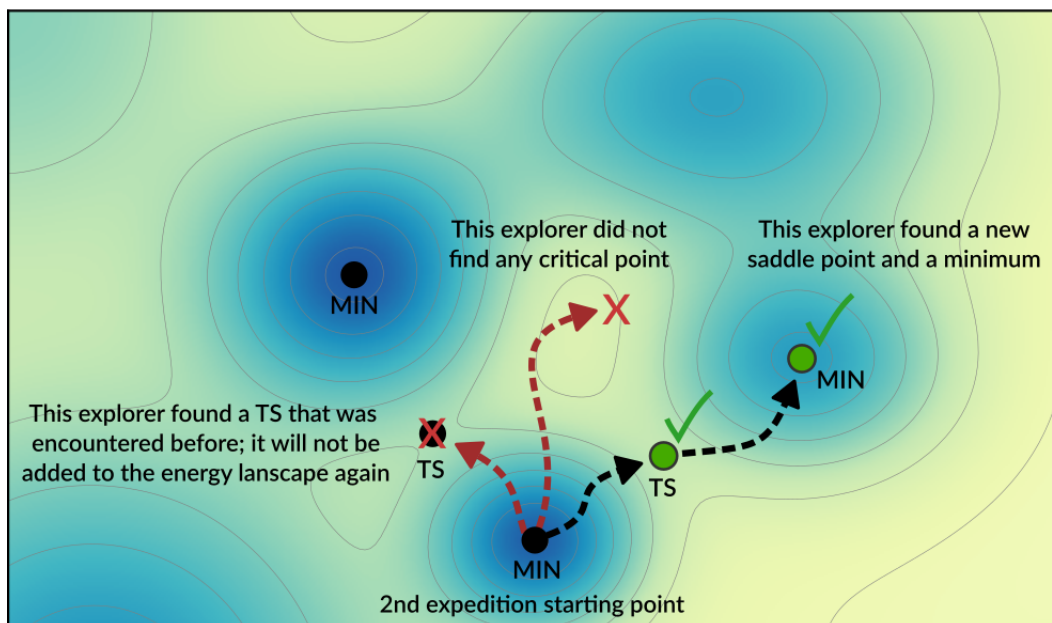


Explorers have “stop conditions” (e.g. a maximum number of steps or a maximum energy above the starting point) so in general not all explorers will successfully find a critical point. In this case, only one of the explorers found relevant critical points: a saddle point and a local minimum. These newly found critical points are added to the Energy Landscape.

After the first expedition is over, the program will start with the second expedition. The starting point for the next expedition will be a randomly chosen local minimum from the list of minima present in the Energy Landscape (the possible starting points for an exploration are called *seed states*. See also the *DynamicSeedStates* (page 154) option).

In this example, the starting point of the second expedition is the new local minimum found during the first expedition. A new set of explorers will set off in random directions from this point.

2nd expedition with 3 explorers



In the diagram above, one of the explorer found a saddle point that was already found in a previous exploration. This structure will not be added to Energy Landscape since it was already *seen* before (see the [Structure comparison](#) (page 159) section for more details). The newly found critical points are added to the Energy Landscape.

Usually, many expeditions and/or many explorers are needed to map the PES, but you should keep in mind that the computation time of the calculation will roughly be proportional to the product `NumExpeditions` \times `NumExplorers`.

By having many explorers you will have a higher chance of comprehensively mapping the PES near the starting point of each expedition. By having many expeditions, you will have a higher chance of traveling further away from the initial structure.

It should be emphasized that the PES exploration task is stochastic in nature, as it uses random numbers to perform initial-displacements. This means that if you run the same calculation twice you might find different critical points.

4.12.2 Job selection and main options

To use one of the PES Exploration procedures you should set the *Task* (page 10) to `PESExploration` and specify one of the jobs in the `PESExploration%Job` key:

```
Task PESExploration

PESExploration
  Job [ProcessSearch | BasinHopping | SaddleSearch | LandscapeRefinement | ↵
↵BindingSites]
End
```

The input options for the various jobs are described in the corresponding sections: [Process Search](#) (page 160), [Basin Hopping](#) (page 164), [Saddle Search](#) (page 161), [Landscape Refinement](#) (page 168), [Binding Sites](#) (page 173).

It is then important pick an appropriate number of expeditions and explorers. Having many expeditions and explorers will result in a more comprehensive PES exploration, but since the computation time will roughly be proportional to the product `NumExpeditions` \times `NumExplorers` you'll need to find an appropriate balance.

```

PESExploration
  NumExpeditions integer
  NumExplorers integer
  DynamicSeedStates Yes/No
End

```

PESExploration**Type** Block**Description** Configures details of the automated PES exploration methods.**NumExpeditions****Type** Integer**Default value** 1**Description** Sets the number of subsequent expeditions our job will consist of. Larger values result in a more comprehensive exploration of the potential energy surface, but will take more computational time.**NumExplorers****Type** Integer**Default value** 1**Description** Sets the number of independent PES explorers dispatched as part of each expedition. Larger values will result in a more comprehensive exploration of the potential energy surface, but will take more computational time. By default an appropriate number of explorers are executed in parallel.**DynamicSeedStates****Type** Bool**Default value** Yes**Description** Whether subsequent expeditions may start from states discovered by previous expeditions. This should lead to a more comprehensive exploration of the potential energy surface. Disabling this will focus the PES exploration around the initial seed states.

The following miscellaneous input option generally apply to most PES exploration calculations:

```

PESExploration
  WriteHistory [None | Converged | All]
  Temperature float
  FiniteDifference float
End

```

PESExploration**Type** Block**Description** Configures details of the automated PES exploration methods.**WriteHistory****Type** Multiple Choice**Default value** Converged**Options** [None, Converged, All]

Description When to write the molecular geometry (and possibly other properties) to the history on the `ams.rkf` file. The default is to only write the converged geometries to the history. Can be changed to write no frames at all to the history, or write all frames (should only be used when testing because of the performance impact). Note that for parallel calculations, only the first group of processes writes to `ams.rkf`.

Temperature

Type Float

Default value 300.0

Unit Kelvin

Description The temperature that the job will run at. This may be used in different ways depending on the job, e.g. acceptance probabilities for Monte-Carlo based jobs, thermostating for dynamics based jobs, kinetic prefactors for jobs that find transition states. Some jobs may not use this temperature at all.

FiniteDifference

Type Float

Default value 0.0026458861

Unit Angstrom

Description The finite difference distance to use for Dimer, Hessian, Lanczos, and optimization methods.

4.12.3 Results: the “Energy Landscape”

The results of a PES Exploration are the structures and energies of the critical points found. There are multiple ways for you to inspect the results:

- The energy landscape can be visualized using the `AMSMovie` GUI module (In `AMSMovie`: File → Open and select the `ams.rkf` file of your calculation). See the GUI tutorials (e.g. [Automated reaction pathway discovery for hydrohalogenation](#)) for more details.
- The results are printed to the text output under the header `Final Energy Landscape`, see [below](#) (page 156).
- The results are stored on the `ams.rkf` binary results file in the section `EnergyLandscape`
- In `PLAMS`, you can use the `get_energy_landscape` method of the `AMSResults` object to conveniently extract the results.

Results on the text output

These are printed at the end of the text output under the header `Final Energy Landscape`. Here is an output example for a `ProcessSearch` job for the simple HCN molecule (computed with the `DFTB` engine):

```

-----
Final Energy Landscape
-----

```

Id	Energy (a.u.)	RE (eV)	RE (kcal/mol)	Counts	Crit. point
1	-5.782789	0.00000	0.0000	4	Min
2	-5.748792	0.92510	21.3334	4	Min

(continues on next page)

(continued from previous page)

```

      3          -5.689025      2.55143      58.8375      4          TS
↔1 <--> 2

Number of configurations          3
Number of local minima           2
Number of transition states       1
Energy range (a.u.)              0.093763
Energy range (eV)                2.55143
Energy range (kcal/mol)          58.8375

Configurations
-----
3
Id 1 Energy(hartree)   -5.78278852 isTS=False
H      -5.05604362312999      1.04394551246415      0.36836337958238
C      -4.06812264817497      0.95005534859126      -0.01533183100739
N      -3.00601476684712      0.84907755770632      -0.42810754191928
3
Id 2 Energy(hartree)   -5.74879169 isTS=False
H      -4.01886309319822      1.09046314142766      1.01610923624838
C      -4.06910389782095      0.79751242545583      -1.12016730790896
N      -4.04221404713293      0.95510285187825      0.02898207831626
3
Id 3 Energy(hartree)   -5.68902502 isTS=True
H      -4.51488871821561      1.04261603660424      0.52096081259126
C      -4.32990923520194      0.88203060069718      -0.58636688911847
N      -3.28538308473452      0.91843178146029      -0.00966991681712

```

From this you can see that 3 critical points were found: 2 minima (Id 1 and Id 2) and 1 transition state (Id 3) connecting the first two states (indicated by 1 <--> 2).

Under `Counts` you can see how many times each state was encountered during the exploration (often the same state is found multiple times) See the [Structure comparison](#) (page 159) section for more details on how states are compared.

RE is the “relative energy” with respect to the lowest-energy state found.

Under the header `Configurations` you will find the XYZ geometries (in Angstrom) corresponding to the various critical points.

4.12.4 Continue a PES exploration from a previous calculation

You can load an Energy Landscape obtained from a PES exploration calculation (or by the [Conformers utility](#) (page 326)) and use it as starting point for a new PES exploration. In this way you can extend your Energy Landscape, and potentially use different PES exploration algorithms.

To load a previously computed energy landscape, use the `PESExploration%LoadEnergyLandscape%Path` option (note: you should still provide an input system in the [System](#) (page 31) block even if you are loading a previous Energy Landscape. The input system will be optimized and added to the energy landscape as a minimum).

It is often convenient to load only some of the states from a previous calculation; this can be done via the `Remove` or `KeepOnly` input options. Specify the seed states with the `SeedStates` option.

These are all the input options related to the loading an Energy Landscape:

```

PESExploration
  LoadEnergyLandscape
  KeepOnly integer_list

```

(continues on next page)

(continued from previous page)

```
Path string
Remove integer_list
SeedStates integer_list
End
End
```

PESExploration

LoadEnergyLandscape

Type Block

Description Options related to the loading of an Energy Landscape from a previous calculation.

KeepOnly

Type Integer List

GUI name List of states to keep

Description Upon loading the Energy Landscape, only keep the states specified here. The states should be specified via a list of integers referring to the indices of the states you want to keep.

Path

Type String

GUI name Load energy landscape from

Description The path to load an energy landscape from. Accepts either AMS result folders, or .con files in the native EON format (only available through the text input file).

Remove

Type Integer List

GUI name List of states to remove

Description Upon loading the Energy Landscape, remove (i.e. do not load) the states specified here. The states should be specified via a list of integers referring to the indices of the states you want to remove (i.e. the states you don't want to load).

SeedStates

Type Integer List

GUI name List of seed states

Description By default when you start a new PES Exploration from a loaded Energy Landscape, expeditions can start from any of the loaded minima. By using this input option, you can instruct the program to only use some of the states as 'expedition starting point'. The states that serve as 'expedition starting points' should be specified via a list of integers referring to the indices of the states.

4.12.5 Troubleshooting

The PES exploration in AMS is quite sensitive to noise on the potential energy surface. A too noisy PES may result in bad convergence of the individual explorers, or states being rejected because their *PES point character* (page 180) is not the expected one.

In case of problems we therefore advise to set engine options that result in a smoother PES. Often this can be accomplished by setting the `NumericalQuality` keyword in the engine input.

Especially the `ReaxFF` engine has a rather noisy PES by default, which may cause problems in a PES exploration job. Please refer to the `ReaxFF` manual for advice on how to smoothen the `ReaxFF` potential energy surface:

- [ReaxFF manual: Smoothened potential energy surface](#)
- [ReaxFF manual: Geometry optimization issues](#)

4.12.6 Structure comparison

During a PES exploration some critical points will most likely be encountered more than once.

Whenever a critical point is found, the program will ask itself: is this a new structure, or have I already encountered this before? If the structure was not seen before (i.e. it's a novel configuration), it will be added to the list of structures found during the exploration. If the structure was already found before, the program will simply increase a counter keeping track of how many times a specific structure was found during the PES exploration.

When deciding if two structures are the same or not, the program will compare both the geometry and the energy of the two configurations. Several parameters and thresholds can be tweaked in the `PESExploration%StructureComparison` block to tell AMS under which conditions two systems should be considered equal.

```
PESExploration
  StructureComparison
    CheckRotation Yes/No
    CheckSymmetry Yes/No
    DistanceDifference float
    EnergyDifference float
    IndistinguishableAtoms Yes/No
    NeighborCutoff float
    RemoveTranslation Yes/No
  End
End
```

PESExploration

StructureComparison

Type Block

Description Settings for structure comparison.

CheckRotation

Type Bool

Description Rotates the system optimally before comparing structures. The default is to do this only for molecular systems when there are no fixed atom constraints.

CheckSymmetry

Type Bool

Default value No

Description Considers that two systems are equal if they are equivalent by symmetry.

DistanceDifference

Type Float

Default value 0.1

Unit Angstrom

Description If the distance between two mapped atoms is larger than this threshold, the two configurations are considered different structures.

EnergyDifference

Type Float

Default value 0.01

Unit eV

Description If the energy difference between two configurations is larger than this threshold, the two configurations are considered to be different structures.

IndistinguishableAtoms

Type Bool

Default value Yes

Description If yes, the order of the atoms does not affect the structural comparison. Atoms of the same element are then indistinguishable.

NeighborCutoff

Type Float

Default value 3.3

Unit Angstrom

Description Atoms within this distance of each other are considered neighbors.

RemoveTranslation

Type Bool

Description Translates the system optimally before comparing structures. The default is to do this only when there are no fixed atom constraints.

4.12.7 Process Search job

Overview

Process Search is a composite method for finding escape mechanisms from a state. Each PES explorer will perform the following steps:

- Starting from a minimum, a *SaddleSearch* (page 161) calculation is performed to find a nearby saddle point
- If a saddle point is found, two images are placed on either side of the saddle along the min mode.
- The two images are then minimized; one of the images is expected to fall back into the original minimum, while the other image is expected to end up in the product state on the other side of the saddle. If this is case, the product, TS and reactant states are added to the energy landscape.

The Process Search procedure will therefore not only find minima and saddle points, but it will also keep track of which minima each saddle point is connecting.

See also:

- GUI tutorials [Automated reaction pathway discovery for hydrohalogenation and Water dissociation on an oxide surface.](#)

Input options

To perform a Process Search calculation you should specify:

```
Task PESExploration

PESExploration
  Job ProcessSearch

  ProcessSearch
    # Options for the Process Search procedure. See description below.
  End

  SaddleSearch
    # Options for the Saddle Search part of the Process Search procedure.
  End
End
```

The options for the saddle search part of a Process Search job are described in the [SaddleSearch](#) (page 161) section.

Options specific to the Process Search procedure can be specified in the PESExploration%ProcessSearch block:

```
PESExploration
  ProcessSearch
    MinimizationOffset float
  End
End
```

PESExploration

ProcessSearch

Type Block

Description Input options specific to the process search procedure.

MinimizationOffset

Type Float

Default value 0.2

Description After a saddle is found, images are placed on either side of the saddle along the mode and minimized to ensure that the saddle is connected to the original minimum and to locate the product state. MinimizationOffset is the distance those images are displaced from the saddle.

4.12.8 Saddle Search job

Overview

Saddle Search is a single-ended method for finding nearby saddle points.

In a Saddle Search calculation, each PES explorer starts by performing a random displacement from the initial geometry (or seed state). Then, starting from this point, the explorer searches for a nearby saddle point using a minimum-mode following method (the available min-mode following methods are dimer³⁴⁵ and Lanczos⁶).

If you already know which atoms are likely to be involved in the reactions, you can use the `DisplaceAtomsInRegion` option to nudge the Saddle Search procedure towards the right part of the PES (*regions* (page 36) can be specified in the *system input block* (page 31), or via the “Model → Regions” panel in AMSinput).

Input options

To perform a Saddle Search calculation you should specify:

```
Task PESExploration

PESExploration
  Job SaddleSearch

  SaddleSearch
    # Options for the Saddle Search procedure. See description below.
  End
End
```

Options for the Saddle Search procedure can be specified in the `PESExploration%SaddleSearch` block.

Note: these options also affect the Saddle Search part of *Process Search Jobs* (page 160).

```
PESExploration
  SaddleSearch
    ConvergedForce float
    DisplaceAtomsInRegion string
    DisplaceMagnitude float
    MaxEnergy float
    MaxIterations integer
    MinEnergyBarrier float
    MinModeMethod [dimer | lanczos]
  End
End
```

PESExploration

SaddleSearch

Type Block

³ G. Henkelman and H. Jónsson, *A dimer method for finding saddle points on high dimensional potential surfaces using only first derivatives*, J. Chem. Phys. 111, 7010-7022 (1999) (<http://dx.doi.org/10.1063/1.480097>)

⁴ A. Heyden, A.T. Bell, and F.J. Keil *Efficient methods for finding transition states in chemical reactions: Comparison of improved dimer method and partitioned rational function optimization method*, J. Chem. Phys. 123, 224101 (2005) (<http://dx.doi.org/10.1063/1.2104507>)

⁵ J. Kästner and P. Sherwood *Superlinearly converging dimer method for transition state search*, J. Chem. Phys. 128, 014106 (2008) (<http://dx.doi.org/10.1063/1.2815812>)

⁶ R. Malek and N. Mousseau, *Dynamics of Lennard-Jones clusters: A characterization of the activation-relaxation technique*, Phys. Rev. E 62, 7723 (2000) (<http://dx.doi.org/10.1103/PhysRevE.62.7723>)

Description Configuration for the Saddle Search procedure (used in SaddleSearch and ProcessSearch Jobs).

ConvergedForce

Type Float

Default value -1.0

Unit eV/Angstrom

Description Convergence threshold for nuclear gradients. Note: Special value of -1.0 means using the same convergence criterion as the PES explorer's geometry optimizer.

DisplaceAtomsInRegion

Type String

Default value

Description A string corresponding to the name of a region. When performing the initial random displacement, only displace atoms in the specified region. This can help the Saddle Search procedure to start off in a desired region of the PES.

DisplaceMagnitude

Type Float

Default value 0.1

Unit Angstrom

Description The standard deviation of the Gaussian displacement in each degree of freedom for the selected atoms.

MaxEnergy

Type Float

Default value 20.0

Unit eV

Description The energy (relative to the starting point of the saddle search) at which a saddle search explorer considers the search bad and terminates it.

MaxIterations

Type Integer

Default value 400

Description Maximum number of iterations for each saddle search run.

MinEnergyBarrier

Type Float

Default value 0.001

Unit eV

Description Minimum energy barrier to accept a new transition state.

MinModeMethod

Type Multiple Choice

Default value dimer

Options [dimer, lanczos]

Description The minimum-mode following method to use.

4.12.9 Basin Hopping job

Overview

Basin hopping² is an iterative Monte Carlo method for PES exploration and global minimization.

An “iteration” in basin hopping consists of the following steps:

1. The atomic coordinates of the system are randomly perturbed (the details of this random perturbation can be configured via the keywords `Displacement`, `DisplacementDistribution`, `SingleAtomDisplace`, `SwapProbability`. See *below* (page 165) for more details).
2. A local optimization of the randomly perturbed structure is performed (see also the *Optimizer* (page 172) section)
3. The new optimized structure is accepted or rejected based of its energy (if the energy of the newly optimized structure lower than the lowest energy so far, the new structure is readily accepted. Otherwise it is accepted with probability $e^{(-\Delta E/kT)}$ where ΔE is the difference between the energy at the previous iteration and the current energy, T is temperature specified in the `PESExploration%Temperature` keyword, see *Job selection and main options* (page 154)).

By iteratively performing these steps, the basin hopping procedure explores the highly-dimensional configuration space of the system, looking for the global minimum and finding local minima along the way. The number of iteration can be specified via the `Steps` keywords (see *below* (page 165) for more details).

For a more comprehensive PES exploration, AMS can perform several expeditions (potentially with several explorers for each expedition) in a single calculation. See the `NumExpeditions` and `NumExplorers` keywords in the *Job selection and main options* (page 154) section for more details.

See also:

- *Example: Basin Hopping for Ar 13 cluster* (page 417)
- GUI tutorials *Cluster Growth: Cobalt Clusters and Water dissociation on an oxide surface*.

Input options

To perform a Basin Hopping calculation you should specify:

```
Task PESExploration
PESExploration
  Job BasinHopping
  Temperature float
  BasinHopping
    # Options for the Basin Hopping procedure. See description below.
  End
End
```

² David J. Wales and Jonathan P. K. Doye *Global Optimization by Basin-Hopping and the Lowest Energy Structures of Lennard-Jones Clusters Containing up to 110 Atoms*, J. Phys. Chem. A 1997, 101, 28, 5111–5116 (<https://doi.org/10.1021/jp970984n>)

The PESExploration%Temperature keyword is described in the *Job selection and main options* (page 154) section.

The following input keywords are specific to Basin Hopping procedure:

```
PESExploration
  BasinHopping
    DisplaceAtomsInRegion string
    Displacement float
    PushApartDistance float
    Steps integer
  End
End
```

PESExploration

BasinHopping

Type Block

Description Configures the details of the Basin Hopping subtask.

DisplaceAtomsInRegion

Type String

Default value

Description If you specify a region name here, only the atoms belonging to this region will be displaced during the basin hopping procedure. For more details on regions, see the documentation on the System definition.

Displacement

Type Float

Default value 0.5

Unit Angstrom

Description Displacement in each degree of freedom.

PushApartDistance

Type Float

Default value 0.4

Unit Angstrom

Description Push atoms apart until no atoms are closer than this distance. This criterion is enforced for the initial structure and all those generated by random displacements.

Steps

Type Integer

Default value 20

Description Number of displace & optimize Monte-Carlo steps to take.

4.12.10 Fragmented states

When studying adsorption processes, it is required to review those situations where a transition state (TS) does not mediate the adsorption process. They are formally known as **non-activated exothermic adsorption** processes. These processes are not discovered naturally in the PES exploration. Since the AMS2022 release, there is a systematic way of including those processes. To this aim, we defined the **fragmented states**, where the adsorbate and adsorbent are infinitely far away from each other.

The fragmented states can be included in the *Energy Landscape* (page 156) through the use of the `CalculateFragments` keyword:

```
PESExploration
  CalculateFragments Yes/No
End
```

PESExploration

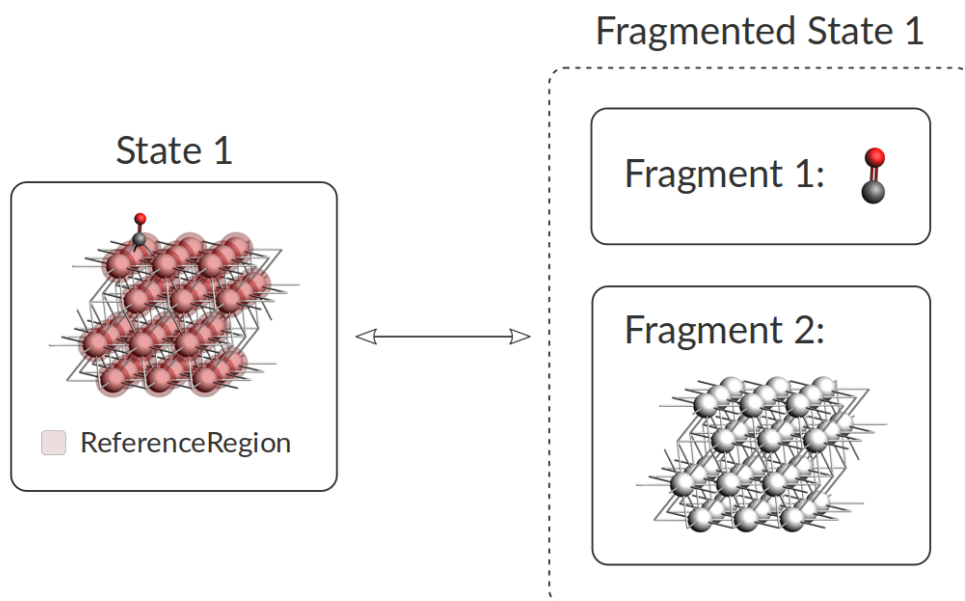
CalculateFragments

Type Bool

Default value No

Description Must be used together with an adsorbent set as the `StatesAlignment%ReferenceRegion`. Runs a final calculation of the adsorbate and adsorbent (marked by the `ReferenceRegion`) individually. The fragmented state is included in the energy landscape.

The keyword has to be used together with a *reference region* (page 177) set via the `StatesAlignment%ReferenceRegion` keyword. The calculation of the fragmented states will happen at the very end of a PES exploration. For every minimum in the energy landscape, two geometry optimizations will be performed: one with only the atoms belonging to the reference region (the adsorbent), the other with only the atoms outside of the reference region (the adsorbate). This relaxes the structure of the adsorbent in the *absence* of the adsorbate, and vice versa.



The total energy of the fragmented state is then simply taken as the sum of the energies of both fragments, and the

adsorption energy is the difference between the adsorbed and fragmented state.

$$E(\text{fragmented state 1}) = E(\text{fragment 1}) + E(\text{fragment 2})$$

$$E_{ad} = E(\text{state 1}) - E(\text{fragmented state 1})$$

You will find fragmented states and the fragments in the *text output* (page 156) following the Final Energy Landscape section. The example shown above would look like this:

```

-----
Final Energy Landscape
-----

```

Id	Energy (a.u.)	RE (eV)	RE (kcal/mol)	Counts	Crit. point
1	-7.651642	0.00000	0.0000	1	Min
2	-7.651572	0.00191	0.0441	1	Min
3	-7.623820	0.75709	17.4589	1	Min
4	-7.622548	0.79170	18.2571	7	TS _↔
↔2<-->3					
5	-7.622430	0.79491	18.3310	5	TS _↔
↔3<-->1					

```

Number of configurations          5
Number of local minima           3
Number of transition states       2
Energy range (a.u.)              0.029212
Energy range (eV)                0.79491
Energy range (kcal/mol)          18.3310

Fragments
-----
Number of fragments                2

```

Id	Formula	Energy (a.u.)	Region
1	CO	-0.424454	active
2	Pt36	-7.154286	surface

```

Fragmented States
-----
Number of fragmented states       1

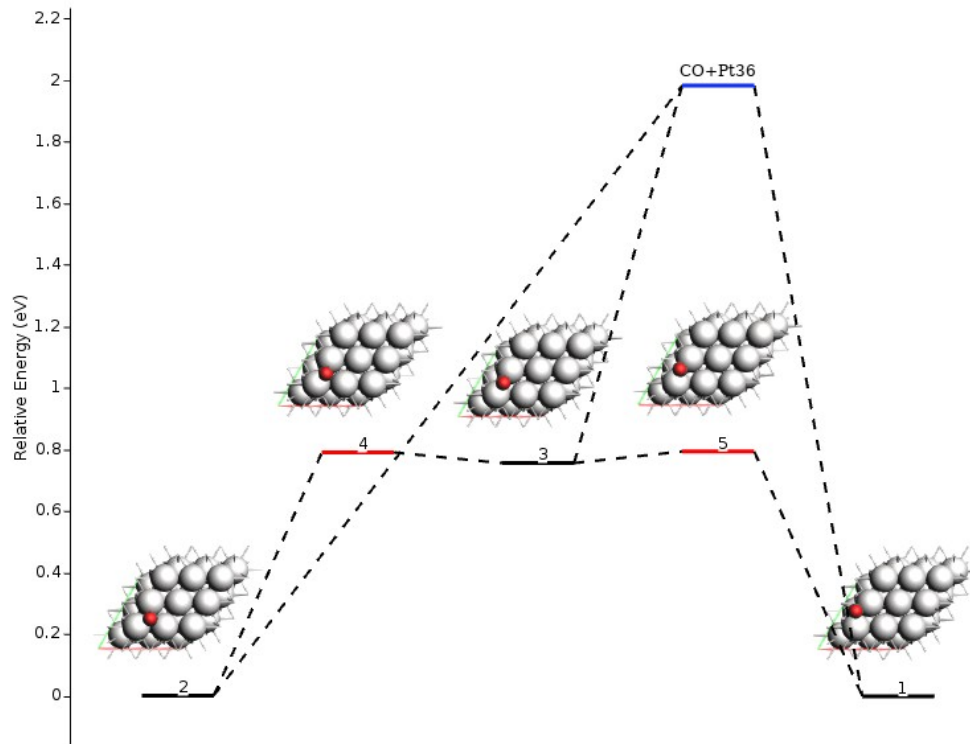
```

Id	Fragments	Energy (a.u.)	RE (eV)	RE (kcal/mol)	
1	1,2	-7.578740	1.98377	45.7467	-->1 -->2 -->3

Notice the following: 1) one fragment may be included in multiple fragmented states, and 2) multiple states may be connected to the same fragmented state. The latter happens when the individual optimizations of adsorbate and adsorbent yield the same results for multiple states. By definition, these states are considered connected if the difference in energy is lower than `PESExploration%SaddleSearch%MaxEnergy`, which by default is 20.0 eV. Interestingly, you may find, for example, that an adsorbed fragment is in multiple fragmented states together with different surface defects. In other words: the adsorbed fragment is always the same when you remove it from the surface, but the surface may look different, depending on the geometry from which the adsorbent is removed.

The following figure shows a graphical representation of the energy landscape of the example above (made with

amsmovie). The blue line represents the fragmented state.



4.12.11 Landscape Refinement

The `LandscapeRefinement` Job can be used to re-optimize the critical points (local minima and saddle points) found in a previous PES exploration calculation using a different engine or different engine settings.

Since PES exploration calculations can be computationally demanding, a possible strategy is to first perform a PES exploration using either a fast engine or computationally cheap settings for the engine of choice, and then to *refine* the energy landscape obtained using a more accurate (and computationally more expensive) method.

See also:

Check the [tutorial](#) on automated reaction pathway discovery for hydrohalogenation. There the landscape refinement is used to go from the DFTB level of theory to DFT.

The `LandscapeRefinement` job needs a previously computed Energy Landscape. See the section [Continue a PES exploration from a previous calculation](#) (page 157) for more details.

To perform a Landscape Refinement calculation you should specify:

```
Task LandscapeRefinement
PESExploration
  Job LandscapeRefinement
  LoadEnergyLandscape
    Path path/to/previous/calculation/ams.results
  End
End
```

Warning: If you perform a LandscapeRefinement of an Energy Landscapes obtained with *ProcessSearch* (page 160) job, the connections between TS and minima are **NOT** recomputed by default unless the parameter `LandscapeRefinement%RelaxFromSaddlePoint` is activated. By turning on `LandscapeRefinement%RelaxFromSaddlePoint`, both reactants and products can be reconstructed for each transition state using a geometry optimization that follows the imaginary vibrational mode.

Lets say, for example, that after a *ProcessSearch* calculation using DFTB we found a TS connecting minima with Id 3 and 4. After a *LandscapeRefinement* using a different engine (for example ADF) it is no longer assured that the refined TS will still connect the same two minima.

When you visualize a refined energy landscape using *AMSmovie*, be aware that some of the connections might be incorrect.

4.12.12 Creating and/or Extending an Energy Landscape from the Input File

It is pretty common to have a set of structures or geometries from the literature or previous calculations that you want to use to continue an energy exploration or an energy landscape refinement. In this case, you can use *System* blocks in your input file to create and/or extend an energy landscape.

The header of the *System* (page 31) block is extended using the following syntax:

```
System label ts=Yes/No reactant=string/int product=string/int
  Atoms header
  ...
  End
  ...
End
```

The label `label` is a string. It is required and unequivocally identifies each *System* block defined by the user. The parameters `ts`, `reactant`, and `product` are optional. The latter two, however, can be specified only if `ts` is set to `Yes`. They are otherwise ignored. Notice that it is possible to have transition states with no reactants, or products, or none of them.

The example below illustrates how to use this feature:

```
PESExploration
  Job LandscapeRefinement
End

Task PESExploration

System state1
  Atoms
  H      -1.08012803      1.17268451      0.09177647
  O      1.82672244      -0.54837752      0.33538717
  N      0.81411565      0.05127399      0.25048411
  C     -0.17673006      0.63776902      0.16748225
  End
End

System state2
  Atoms
  H      -0.71003072      1.06490526      0.04975824
  O      1.41363000      0.55626133      0.07710644
  N      0.55490964      -0.71415530      0.51752525
```

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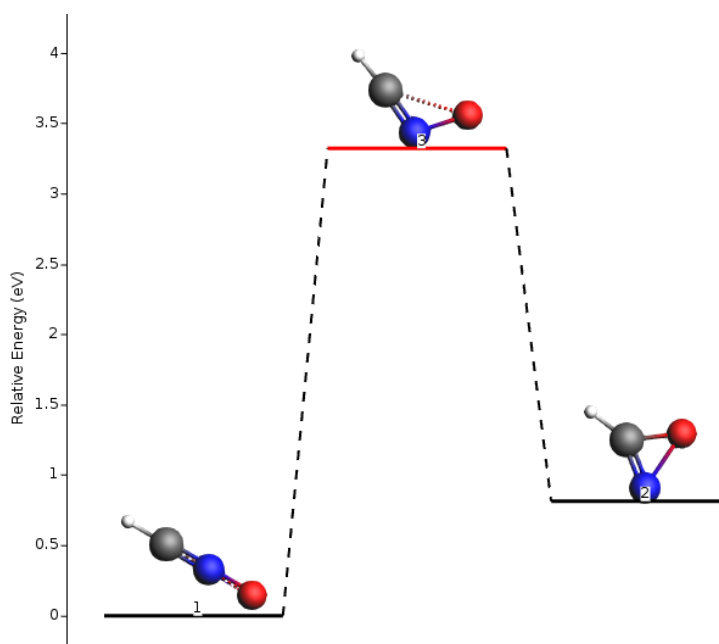
```

      C      0.12547108      0.40633871      0.20074007
    End
  End
System state3 ts=Yes reactant=state1 product=state2
  Atoms
    H      -0.78063395      1.32905463     -0.01879702
    O      1.78011528      -0.06505936     0.19126583
    N      0.53076199      -0.47128241     0.41047761
    C     -0.14626334      0.52063714     0.26218359
  End
End
Engine DFTB
EndEngine

```

This example executes an Energy Landscape Refinement calculation at the DFTB level of theory for the energy landscape loaded from the `System` blocks. It loads the coordinates of two local minima (`state1`, and `state2`) and one transition state (`state3`). The transition state is connected with both minima, being `state1`, the reactant, and `state2`, the product. Below you can see the output text lines and a graphical representation of the obtained energy landscape:

Id	Energy (a.u.)	RE (eV)	RE (kcal/mol)	Counts	Crit. point
1	-10.424825	0.00000	0.0000	1	Min
2	-10.394956	0.81277	18.7428	1	Min
3	-10.302822	3.31986	76.5577	1	TS 1<-->2



To add states to an existing Energy Landscape, use the keyword `PESExploration%LoadEnergyLandscape%Path` to specify the KF file to load. Then, define new links to its states using their ids. The following example shows how to use this feature:

```

PESExploration
  Job LandscapeRefinement

```

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(continued from previous page)

```

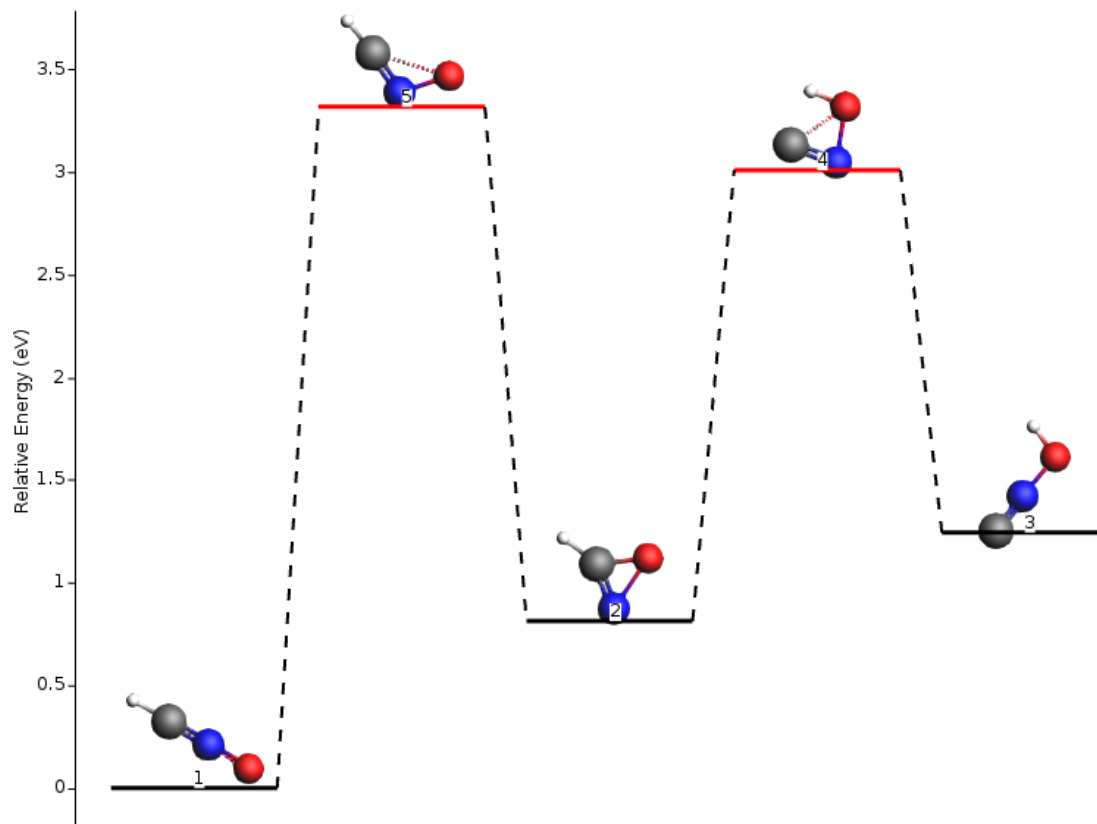
LoadEnergyLandscape
  Path previous.results
End
End
Task PESExploration
System state3
  Atoms
    H      0.51485007      1.62340128      -0.20665749
    O      1.05880703      0.84482125      -0.00604063
    N      0.23989165      -0.13660458      0.36835485
    C      -0.42956874      -1.01826795      0.68947328
  End
End
System state4 ts=Yes reactant=2 product=state3
  Atoms
    H      -0.10604142      1.11162691      0.00025950
    O      1.08875440      0.73993713      0.03512861
    N      0.74116588      -0.56372211      0.45954036
    C      -0.33989886      0.02550806      0.35020153
  End
End
Engine DFTB
EndEngine

```

This example performs an Energy Landscape Refinement calculation at the DFTB level of theory on the energy landscape loaded from the previous calculation's directory results (`previous.results`). It also loads the coordinates of an additional local minimum (`state3`) and one transition state (`state4`) from the input file using the `System` blocks. The latter transition state is linked to the product `state3` (defined in the same input file) and the reactant state with `id=2` from the loaded energy landscape (see image above). The output text lines and the graphical representation of the obtained energy landscape are shown below. Notice that the states have been rearranged according to energy.

Id	Energy (a.u.)	RE (eV)	RE (kcal/mol)	Counts	Crit. point
1	-10.424825	0.00000	0.0000	1	Min
2	-10.394956	0.81277	18.7428	1	Min
3	-10.379113	1.24388	28.6845	1	Min
4	-10.314160	3.01134	69.4432	1	TS 2<-->3
5	-10.302822	3.31986	76.5577	1	TS 1<-->2

Note: If you want to combine this feature of creating and/or extending an energy landscape with any other job (`PESExploration%Job`) other than `LandscapeRefinement`. Don't forget to include a `System` block with no header (or label) to define the main chemical system.



4.12.13 Optimizer

Geometry optimizations are performed for most PES Explorations job types. In the `PESExploration%Optimizer` block you may configure some of the parameters for these geometry optimizations:

```
PESExploration
  Optimizer
    ConvergedForce float
    MaxIterations integer
    Method [CG | QM | LBFGS | FIRE | SD]
  End
End
```

PESExploration

Optimizer

Type Block

Description Configures the details of the geometry optimizers used by the PES explorers.

ConvergedForce

Type Float

Default value 0.005

Unit eV/Angstrom

Description Convergence threshold for nuclear gradients.

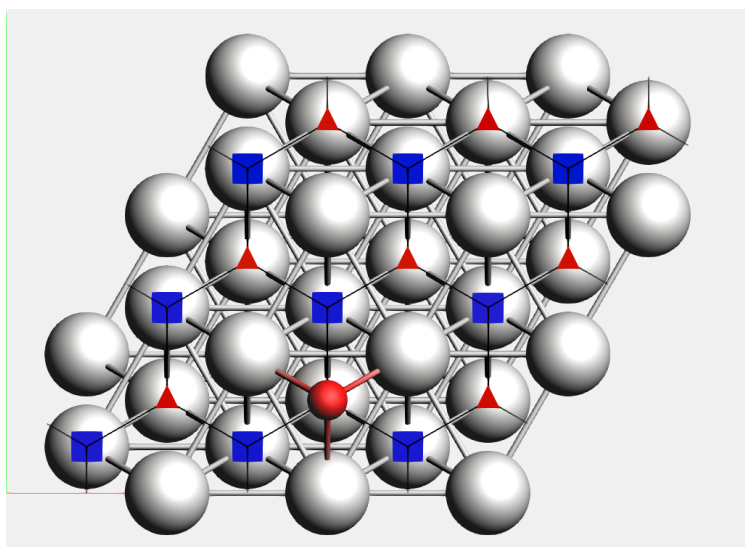
MaxIterations**Type** Integer**Default value** 400**Description** Maximum number of iterations allowed for optimizations.**Method****Type** Multiple Choice**Default value** CG**Options** [CG, QM, LBFGS, FIRE, SD]**Description** Select the method for geometry optimizations.

4.12.14 Binding Sites

Binding sites can be determined from an Energy Landscape.

When computing binding sites you will first need to define a **reference region**, which typically will be a surface or a cluster (*regions* (page 36) can be specified in the *system input block* (page 31), or via the “Model → Regions” panel in AMSinput). AMS will then go through all the local minima of Energy Landscape and mark as ‘binding sites’ the positions where an atom of an adsorbed molecule is neighboring atoms in the reference region.

For instance, in *Example: PES Exploration, Binding Sites for O on Pt 111* (page 419), the platinum surface is the reference region, while the oxygen atom is the adsorbate. In the picture below, you can see the oxygen binding sites on the platinum 111 surface (the two different types of binding sites are marked by a blue square and a red triangle respectively).



Lines connecting the the binding sites will be drawn if 1) there is a transition state connecting two local minima associated to these binding-sites (notice that may there are multiple local minima associated with the same binding site), and 2) there is at least an atom (from the adsorbate region) that changes its position from the first binding site to the second one mediated by the same transition state described above. In this process, AMS will align as much as possible all local minima and transition states to the input's file structure but ignoring the atoms in the region adsorbate trying to establish a common reference frame (see also the `StatesAlignment` input block below).

See also:

- *Example: PES Exploration, Binding Sites for O on Pt 111* (page 419)

- Cluster Growth: Cobalt Clusters

Binding sites are labeled according to the number of neighbors they have on each of their coordination shells. It has the format $N\langle\text{int}\rangle\langle\text{int}\rangle\dots$. For example, the label $N334$ denotes three neighbors in the first shell, three in the second, and four in the third. The parameter `PESExploration%BindingSites%MaxCoordinationShellsForLabels` or the largest shell contained in the unit cell, determines the maximum number of coordination shells to consider. For labeling purposes, the center of the binding site is taken to be 1.5 \AA from the center of the atoms in the first shell in the direction of the adsorbed atom position. `PESExploration%BindingSites%DistanceDifference` is an important parameter to remember. It is critical because it specifies the tolerance for determining whether or not two atoms are in the same coordination shell based on their distances from the binding site.

The figure below depicts the four types of binding sites observed on a Pt(111) surface. There, you can see the AMS label (e.g., $N33$, $N34$, ...) as well as the traditional one (e.g., *fcc*, *hcp*, ...). The distances between the binding site and the highlighted atoms on that coordination shell (or neighborhood) are listed below each geometry. If two numbers are listed, it is because two different distances are involved, but they are considered in the same coordination shell because their difference is less than `PESExploration%BindingSites%DistanceDifference`.

The following is an example of the section in the output file describing the obtained binding sites. In particular, you can find the above details regarding distances involved in calculating their labels.

```

-----
Binding Sites
-----

Number of binding sites:          4
Number of connections:           3

Binding sites:

  id  Label  Aver.E(a.u.)  Stdev.E(a.u.)      x          y          z      Parents
  ---  ---  -
  1   N34   -3.773094     0.000000     3.59065   2.09219   3.88471   1(1)
  2   N33   -3.772967     0.000000     4.93783   2.86841   3.88471   2(1)
  3  N223   -3.746180     0.000000     4.25120   2.47351   3.88462   3(1)
  4   N16   -3.683784     0.000000     3.60490   3.59820   3.88382   6(1)

Labels details:

  Label          Center example (A)      Radius (A)
  ---          -
  N33           4.94   2.87   3.88      2.16 - 2.66
                                   3.45 - 3.95
  N34           3.59   2.09   3.88      2.16 - 2.66
                                   3.45 - 3.95
  N223          4.25   2.47   3.88      2.02 - 2.52
                                   2.76 - 3.26
                                   3.86 - 4.36
  N16           3.60   3.60   3.88      1.50 - 2.00
                                   3.04 - 3.54

```

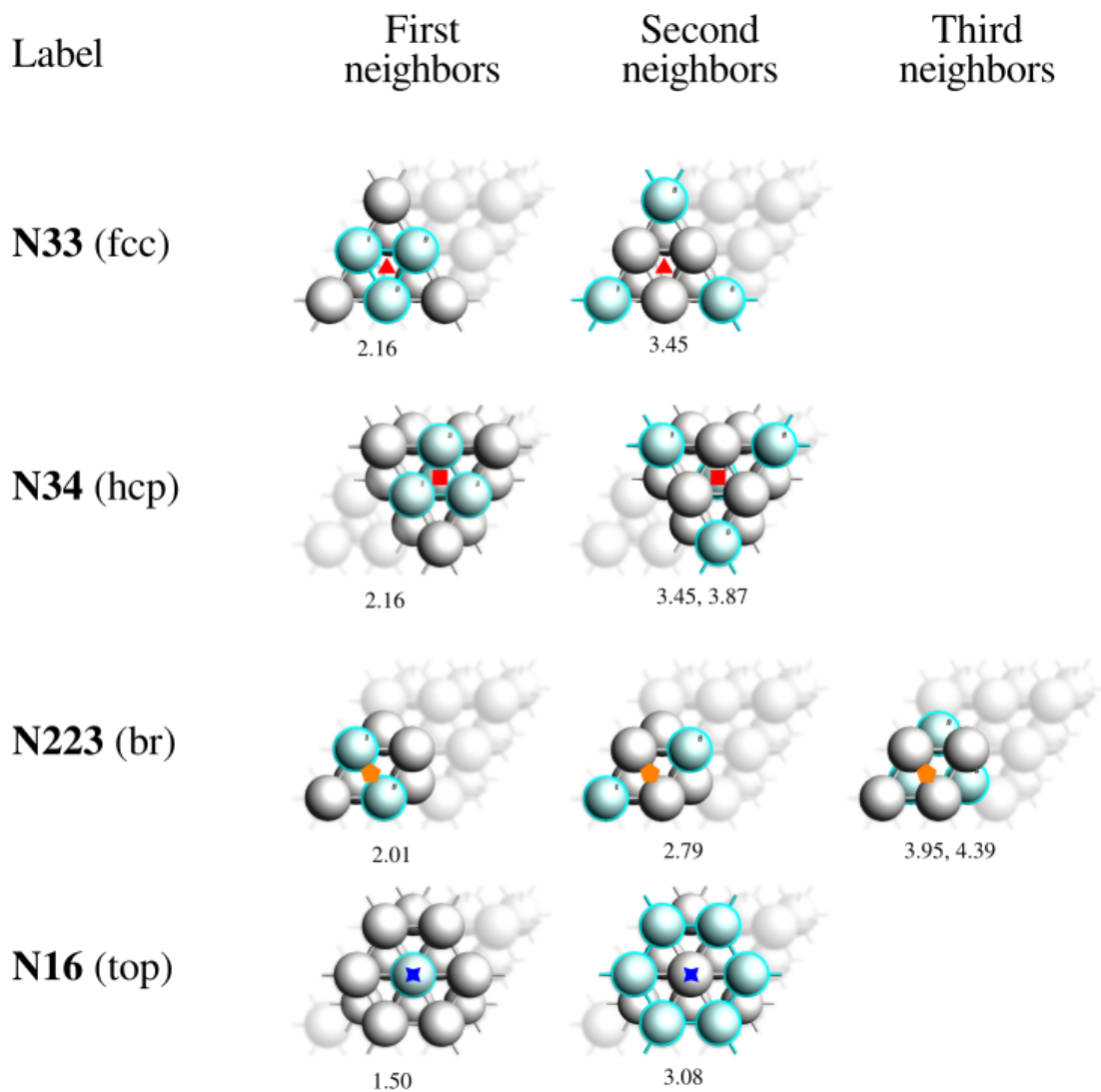



Fig. 4.2: Binding sites obtained for a CO molecule adsorbed on a Pt(111) surface using PESExploration%BindingSites%DistanceDifference = 0.5 Å.

Input options

There are two distinct ways of triggering the computation of binding sites. You can either:

compute the binding sites at the end of a *Process Search* (page 160), *Basin Hopping* (page 164) or *Landscape Refinement* (page 168) calculation by setting the PESExploration%BindingSites%Calculate option to yes:

```
PESExploration
  Job [ProcessSearch | BasinHopping | LandscapeRefinement]

  BindingSites
    Calculate Yes
  End

  StatesAlignment
    ReferenceRegion reference_region_name
  End
End
```

or

compute the binding sites by setting the PESExploration%Job to BindingSites and load a previously computed Energy Landscape (see *Example: PES Exploration, Binding Sites for O on Pt 111* (page 419)):

```
PESExploration
  Job BindingSites

  LoadEnergyLandscape
    Path path/to/previous/calculation/ams.results
  End

  StatesAlignment
    ReferenceRegion reference_region_name
  End
End
```

The following input options are related to the calculation of binding sites:

```
PESExploration
  BindingSites
    Calculate Yes/No
    DistanceDifference float
    MaxCoordinationShellsForLabels integer
    NeighborCutoff float
    ReferenceRegion string
  End
End
```

PESExploration

BindingSites

Type Block

Description Options related to the calculation of binding sites.

Calculate

Type Bool

Default value No

Description Calculate binding sites at the end of a job. Not needed for Binding Sites job.

DistanceDifference

Type Float

Default value -1.0

Unit Angstrom

Description If the distance between two mapped binding-sites is larger than this threshold, the binding-sites are considered different. If not specified, its value will set equal to [PESExploration%StructureComparison%DistanceDifference]

MaxCoordinationShellsForLabels

Type Integer

Default value 3

Description The binding site labels are given based on the coordination numbers of shells in the reference region, using the following format: N<int><int>..., e.g., the label 'N334' means 3 atoms in the first coordination shell, 3 in the second one, and 4 in the third one. This parameter controls the maximum number of shells to include.

NeighborCutoff

Type Float

Default value -1.0

Unit Angstrom

Description Atoms within this distance of each other are considered neighbors for the calculation of the binding sites. If not specified, its value will set equal to [PESExploration%StructureComparison%NeighborCutoff]

ReferenceRegion

Type String

Default value

Description Defines the region that is considered as the reference for binding sites detection. Binding sites are projected on this region using the geometry from the reference system. If not specified, its value will set equal to [PESExploration%StatesAlignment%ReferenceRegion]

The following input options are related to the definition of the reference region and alignment thereof:

```
PESExploration
  StatesAlignment
    DistanceDifference float
    ReferenceRegion string
  End
End
```

PESExploration

StatesAlignment

Type Block

Description Configures details of how the energy landscape configurations are aligned respect to the main chemical system [System].

DistanceDifference

Type Float

Default value -1.0

Unit Angstrom

Description If the distance between two mapped atoms is larger than this threshold, the configuration is considered not aligned. If not specified, its value will set equal to [PESExploration%StructureComparison%DistanceDifference]

ReferenceRegion

Type String

Default value

Description Defines the region that is considered as the reference for alignments. Atoms outside this region are ignored in the alignments.

4.12.15 References

GRADIENTS, HESSIAN, STRESS TENSOR, ELASTICITY

No matter what application the AMS driver is used for, in one way or another it always explores the potential energy surface (PES) of the system. One can furthermore ask AMS to calculate additional properties of the PES in the points that are visited. These are mostly (but not exclusively) derivatives of the energy, e.g. we can ask AMS to calculate the gradients or the Hessian in the visited points. In general all these PES point properties are requested through the `Properties` block in the AMS input:

```
Properties
  Gradients Yes/No
  StressTensor Yes/No
  Hessian Yes/No
  SelectedRegionForHessian string
  PESPointCharacter Yes/No
  ElasticTensor Yes/No
End
```

This properties described on this page in the AMS manual are all related to derivatives of the energy.

Note that because these properties are tied to a particular point on the potential energy surface, they are found on the *engine output files* (page 19). Note also that the properties are not always calculated in every PES point that the AMS driver visits during a calculation. By default they are only calculated in *special* PES points, where the definition of special depends on the *task* (page 45) AMS is performing: For a *geometry optimization* (page 47) properties would for example only be calculated at the final, converged geometry. This behavior can often be modified by keywords special to the particular running task.

5.1 Nuclear gradients

The first derivative with respect to the nuclear coordinates can be requested as follows:

```
Properties
  Gradients Yes/No
End
```

Properties

Gradients

Type Bool

Default value No

GUI name Nuclear gradients

Description Calculate the nuclear gradients.

Note that these are gradients, not forces, the difference being the sign. The gradients are printed in the output and written to the *engine result file* (page 19) belonging to the particular point on the PES in the `AMSResults%Gradients` variable as a $3 \times n_{\text{atoms}}$ array in atomic units (Hartree/Bohr).

5.2 Hessian

The calculation of the second derivative of the total energy with respect to the nuclear coordinates is enabled by:

```
Properties
  Hessian Yes/No
  SelectedRegionForHessian string
End
```

Properties

Hessian

Type Bool

Default value No

Description Whether or not to calculate the Hessian.

SelectedRegionForHessian

Type String

GUI name Hessian only for

Description Compute the Hessian matrix elements only for the atoms in a particular region. If not specified, the Hessian will be computed for all atoms.

The Hessian is not printed to the text output, but is saved in the engine result file as variable `AMSResults%Hessian`. Note that this is just the plain partial second derivatives (no mass-weighting) of the total energy. The $3 \times N_{\text{atoms}}$ columns/rows of the matrix are grouped by atom: the first three rows/columns correspond to the first atom, etc..

Note that the AMS driver also supports the *Mobile Block Hessian* (page 193) (MBH) method, which allows treating parts of the system as rigid blocks.

Often one is not interested in the Hessian matrix itself, but just in using it for the calculation of IR frequencies or to characterize a PES point (as e.g. a local minimum or a saddle point). For these application, see the following pages in the manual:

- *IR frequencies* (page 189)
- *PES point character* (page 180)

5.3 PES point character

A PES point can according to the slope and curvature of the PES at that point be classified in the following categories:

- A local minimum on the PES with vanishing nuclear gradients and no negative frequencies.
- A transition state with vanishing nuclear gradients and exactly one negative frequency, i.e. a first order saddle point on the PES.
- A higher order saddle point, i.e. a stationary point on the PES with vanishing nuclear gradients but more than one imaginary frequency.

- A non-stationary point on the PES. Here the gradients are non-zero.

This classification can easily be done if both the gradients and the normal modes have already been calculated. However, calculating the full Hessian needed for the entire set of normal modes is very expensive and undesirable if one only wants to know the character of a PES point. The AMS driver can quickly, and without calculating the full Hessian, characterize a PES point into one of the above categories. This can be used to confirm the success of e.g. a *transition state search* (page 65) or *geometry optimization* (page 47). A PES point can be characterized by requesting `PESPointCharacter` as a property:

```
Properties
  PESPointCharacter Yes/No
End
```

Properties

PESPointCharacter

Type Bool

Default value No

GUI name Characterize PES point

Description Determine whether the sampled PES point is a minimum or saddle point. Note that for large systems this does not entail the calculation of the full Hessian and can therefore be used to quickly confirm the success of a geometry optimization or transition state search.

This will calculate the few lowest normal modes using an iterative diagonalization of the Hessian¹ based on a Davidson algorithm implemented in the PRIMME library². The procedure has been optimized for finding a small number of low-lying eigenvalues in as few matrix-vector multiplications (and thus single point calculations) as possible. This is facilitated by performing the iterative method using a pre-conditioning matrix based on an approximation of the Hessian. The approximate Hessian is obtained from the full Hessian at a lower level of theory. This calculation also provides the initial guesses for the desired normal modes. What the lower level of theory is depends on the main engine used in the calculation: DFTB with the GFN1-xTB model is used as the lower level of theory for relatively slow engines, e.g. DFT based engines. For semi-empirical engines like DFTB or MOPAC, the lower level of theory is currently UFF. It is currently not possible to change the engine used to obtain the preconditioning Hessian and the approximate modes.

- Note that the iterative calculation of the normal modes is skipped when ...
 1. ... the nuclear gradients are so large that the PES point is considered non-stationary. The calculation of the modes is then just not necessary for classifying it.
 2. ... the full normal modes or Hessian have also been requested. The iterative calculation is then not necessary, as all modes are already known.
 3. ... the molecule is very small. (For small systems the iterative calculation of the few lowest normal modes is not faster than the full calculation of all modes, so all modes are calculated instead.)
- The classification as a stationary or non-stationary point uses the gradient convergence criterion from the geometry optimizer as the tolerance, see *geometry optimization* (page 47). This makes sure that the criterion for what is considered converged/stationary is always in sync between the optimizer and the PES point characterization.
- For periodic systems the PES point characterization does not take the lattice degrees of freedom into account. A PES point where the nuclear gradients are small enough would for example be classified as a stationary point, even if the system is under stress.

Details of the iterative procedure can be configured in the `PESPointCharacter` block:

¹ P. Deglmann and F. Furche, *Efficient characterization of stationary points on potential energy surfaces*, J. Chem. Phys. 117, 9535 (2002) (<https://doi.org/10.1063/1.1523393>)

² A. Stathopoulos and J. R. McCombs, *PRIMME: Preconditioned Iterative MultiMethod Eigensolver: Methods and software description*, ACM Transactions on Mathematical Software, Vol. 37, No. 2, (2010), 21:1–21:30. (<https://doi.org/10.1145/1731022.1731031>)

```

PESPointCharacter
  Displacement float
  NegativeEigenvalueTolerance float
  NumberOfModes integer
  Tolerance float
End

```

PESPointCharacter**Type** Block**Description** Options for the characterization of PES points.**Displacement****Type** Float**Default value** 0.04**Description** Controls the size of the displacements used for numerical differentiation: The displaced geometries are calculated by taking the original coordinates and adding the mass-weighted mode times the reduced mass of the mode times the value of this keyword.**NegativeEigenvalueTolerance****Type** Float**Default value** -0.0001**Unit** Hartree/Bohr²**Description** The threshold in Hessian eigenvalue below which a mode is considered imaginary, i.e. indicating a transition state. This is a small negative number, as very small negative eigenvalues may be due to numerical noise on an essentially flat PES and do not indicate true transition states.**NumberOfModes****Type** Integer**Default value** 2**Description** The number of (lowest) eigenvalues that should be checked.**Tolerance****Type** Float**Default value** 0.016**Description** Convergence tolerance for residual in iterative Davidson diagonalization.

- Note that the residual tolerance that can be achieved is limited by the numerical differentiation that is performed. The default values should apply in most cases, but if convergence becomes a problem one may choose to increase the tolerance or to increase the step size (slightly). Note that the default residual tolerance is lower than for the other mode selective methods. This is because PRIMME uses a different convergence criteria than mode tracking/refinement. The higher value used as a default will therefore not result in decreased levels of accuracy. The method will bail if the number of iterations exceeds the number of normal modes as at this point still achieving convergence becomes unlikely, in part due to the next point.
- In order to avoid producing the known and irrelevant rigid modes, the method searches for normal modes orthogonal to six (or five) rigid modes. Imperfections due to the numerical differentiation may mean that the translational and rotational rigid modes are not exact eigenmodes of the Hessian that is constructed. As a result, some part of the lowest vibrational normal mode may lie in the span of the theoretical rigid modes and therefore be inaccessible to

the Davidson method. This places a lower bound on the residual tolerance that can be achieved, which is directly related to the numerical differentiation accuracy. The take-away: do not set the tolerance too low, the default usually suffices.

- Behind the scenes, the method actually computes a few more modes than requested. In the case of multiplicities, eigenvalues may still converge out of order. These additional eigenvalues essentially guarantee that the obtained modes are indeed the lowest ones.

5.4 Thermodynamics, gas phase Gibbs free energy

At the end of a completed IR Frequencies (normal modes) calculation, a survey is given of thermodynamic properties: entropy, internal energy, constant volume heat capacity, enthalpy and Gibbs free energy, see:

- *IR frequencies* (page 189)
 - *Thermodynamics* (page 209)
 - *Gibbs free energy change for a gas phase reaction* (page 212)

5.5 Stress tensor

For periodic systems (chains, slabs, bulk) one can also request the clamped-ion stress tensor (note: the clamped-ion stress is only part of the *true* stress tensor):

```
Properties
  StressTensor Yes/No
End
```

Properties

StressTensor

Type Bool

Default value No

GUI name Stress tensor

Description Calculate the stress tensor.

The clamped-ion stress tensor σ_α (Voigt notation) is computed via numerical differentiation of the energy E WRT a strain deformations ϵ_α keeping the atomic fractional coordinates constant:

$$\sigma_\alpha = \frac{1}{V_0} \left. \frac{\partial E}{\partial \epsilon_\alpha} \right|_{\text{constant atomic fractional coordinates}}$$

where V_0 is the volume of the unit cell (for 2D periodic system V_0 is the area of the unit cell, and for 1D periodic system V_0 is the length of the unit cell).

The clamped-ion stress tensor (in Cartesian notation) is written to the engine result file in `AMSResults%StressTensor`.

5.6 Elastic tensor

The elastic tensor $c_{\alpha,\beta}$ (Voigt notation) is computed via second order numerical differentiation of the energy E WRT strain deformations ϵ_α and ϵ_β :

$$c_{\alpha,\beta} = \frac{1}{V_0} \frac{\partial^2 E}{\partial \epsilon_\alpha \partial \epsilon_\beta}$$

where V_0 is the volume of the unit cell (for 2D periodic system V_0 is the area of the unit cell, and for 1D periodic system V_0 is the length of the unit cell).

For each strain deformation $\epsilon_\alpha, \epsilon_\beta$, the atomic positions will be optimized. The elastic tensor can be computed for any periodicity, i.e. 1D, 2D and 3D. Computing the elastic tensor will also calculate the bulk modulus, Young's modulus, and shear modulus, as well as the Poisson ratio.

See also:

Example: Elastic tensor (page 471)

To compute the elastic tensor, request it in the `Properties` input block of AMS:

```
Properties
  ElasticTensor Yes/No
End
```

Note: The elastic tensor should be computed at the fully optimized geometry. One should therefore perform a geometry optimization of all degrees of freedom, **including the lattice vectors**. It is recommended to use a tight gradient convergence threshold for the geometry optimization (e.g. Quality “Good”). Note that all this can be done in one job by combining the *geometry optimization task* (page 47) with the elastic tensor calculation.

The elastic tensor (in Voigt notation) is printed to the output file and stored in the *engine result file* (page 19) in the `AMSResults` section (for 3D system, the elastic tensor in Voigt notation is a 6x6 matrix; for 2D systems is a 3x3 matrix; for 1D systems is just one number).

Options for the numerical differentiation procedure can be specified in the `ElasticTensor` input block:

```
ElasticTensor
  ConvergenceQuality [Normal | Good | VeryGood]
  StrainStepSize float
End
```

ElasticTensor

Type Block

Description Options for numerical evaluation of the elastic tensor.

ConvergenceQuality

Type Multiple Choice

Default value Good

Options [Normal, Good, VeryGood]

GUI name Convergence

Description The tightness of the convergence of the geometry optimizations for each strain deformation. This should not be set higher than the overall convergence quality of the preceding geometry optimization configured by the `GeometryOptimization%ConvergenceQuality` keyword.

StrainStepSize

Type Float

Default value 0.001

Description Step size (relative) of strain deformations used for computing the elastic tensor numerically.

Pressure (page 261) or *non-isotropic external stress* (page 262) can be included in your simulation via the corresponding *engine addons* (page 258).

The elastic tensor calculation supports AMS' *double parallelization* (page 21), which can perform the calculations for the individual displacements in parallel. This is configured automatically, but can be further tweaked using the keys in the `NumericalDifferentiation%Parallel` block:

```
ElasticTensor
  Parallel
    nCoresPerGroup integer
    nGroups integer
    nNodesPerGroup integer
  End
End
```

ElasticTensor

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

5.7 Numerical differentiation options

The following options apply whenever AMS computes gradients, Hessians or stress tensors via numerical differentiation.

```
NumericalDifferentiation
  NuclearStepSize float
  StrainStepSize float
End
```

NumericalDifferentiation

Type Block

Description Define options for numerical differentiations, that is the numerical calculation of gradients, Hessian and the stress tensor for periodic systems.

NuclearStepSize

Type Float

Default value 0.005

Unit Bohr

Description Step size for numerical nuclear gradient calculation.

StrainStepSize

Type Float

Default value 0.001

Description Step size (relative) for numerical stress tensor calculation.

AMS may use symmetry (key `NumericalDifferentiation%UseSymmetry`) in case of numerical differentiation calculations. If symmetry is used only symmetry unique atoms are displaced. Symmetry is only recognized if the starting geometry has symmetry. Symmetry is only used for molecules if the molecule has a specific orientation in space, like that the z-axis is the main rotation axis. If the GUI is used one can click the Symmetrize button (the star), such that the GUI will (try to) symmetrize and reorient the molecule. There are some cases that even after such symmetrization, the orientation of the molecule is not what is needed for the symmetry to be used in case of numerical differentiation calculations. If that is the case or if key `NumericalDifferentiation%UseSymmetry` is set to 'False', then no symmetry will be used.

The numerical differentiation calculation supports AMS' *double parallelization* (page 21), which can perform the calculations for the individual displacements in parallel. This is configured automatically, but can be further tweaked using the keys in the `NumericalDifferentiation%Parallel` block:

```
NumericalDifferentiation
  Parallel
    nCoresPerGroup integer
    nGroups integer
    nNodesPerGroup integer
  End
End
```

NumericalDifferentiation

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

VIBRATIONAL SPECTROSCOPY

6.1 General

The starting point is the Hessian of the system, being the second derivative of the energy with respect to the atomic coordinates.

The eigenvalues of the Hessian are the frequencies and the eigen vectors are the normal modes.

As the calculation of the full Hessian is very expensive there are several ways to avoid it, so that you only get a part of the full spectrum, or only modes for a region of the system, see *IR frequencies and normal modes* (page 189) section.

A full, partial, or approximate Hessian in itself can be useful for a (Hessian-based) geometry optimization or a transition state search.

Vibrational spectra are obtained by differentiating a property along the normal modes at a (local) minimum of the PES. So for spectra you need to optimize the geometry first, otherwise you get negative frequencies.

The Normal modes and or vibrational spectra can be requested via the `Properties` block

```
Properties
  NormalModes Yes/No
  Raman Yes/No
  VROA Yes/No
  VCD Yes/No
  Phonons Yes/No
End
```

When requesting the normal modes, the IR intensities are calculated, as they are very cheap.

See also:

[Tutorials on Vibrational Spectroscopy](#)

6.1.1 Where are the results?

Because the results of a vibrational spectroscopy calculation are tied to a particular point on the potential energy surface, they are found on the *engine output files* (page 19). Note also that the properties are not always calculated in every PES point that the AMS driver visits during a calculation. By default they are only calculated in *special* PES points, where the definition of special depends on the *task* (page 45) AMS is performing: For a *geometry optimization* (page 47) properties would for example only be calculated at the final, converged geometry. This behavior can often be modified by keywords special to the particular running task.

6.2 IR frequencies and normal modes

6.2.1 All vibrational Modes

The calculation of the normal modes of vibration can be requested with:

```
Properties
  NormalModes Yes/No
End
```

Typically used icw with *Task SinglePoint* (page 45), *Task GeometryOptimization* (page 47), or *Task TransitionStateSearch* (page 65). In case of geometry optimization or transition state search the normal modes will only be calculated at the final, converged geometry.

Properties

NormalModes

Type Bool

Default value No

GUI name Frequencies

Description Calculate the frequencies and normal modes of vibration, and for molecules also the corresponding IR intensities if the engine supports the calculation of dipole moments.

The molecular normal modes are normally calculated within the harmonic oscillation model. If the molecule is in its equilibrium conformation, it sits in the lowest point (at least locally) on the PES. The cross-section of the PES profile close to this point can then be assumed to be approximately parabolic, such that the second derivative of the energy w.r.t a nuclear coordinate can be interpreted as a force constant for the harmonic oscillation of an atom along this coordinate. Since molecular vibrations in polyatomics involve the simultaneous displacement of multiple atoms, this harmonic oscillator model can be generalized to multiple nuclear coordinates. The normal modes and their frequencies then become eigenvectors and eigenvalues of a force constant matrix, the Hessian:

$$H_{ij} = \frac{\partial^2 E}{\partial R_i \partial R_j}$$

The (non-mass-weighted) Hessian is saved in the engine result file as variable `AMSResults%Hessian`. It is not printed to the text output. The column/row indices are ordered as: x-component of atom 1, y-component of atom 1, z-component of atom 1, x-component of atom 2, etc.

Most *engines* (page 250) cannot calculate the Hessian analytically. Only the ADF engine can calculate the Hessian analytically, however, only for a limited number of XC functionals, see the [ADF manual](#). In case the Hessian is not calculated analytically the Hessian is constructed column-wise through numerical differentiation of the energy gradients w.r.t. each nuclear coordinate. AMS will set up 2 single-point calculations (1 for the positive displacement, 1 for the negative displacement), and the requested engine will return the energy gradients at these displacements. These gradients are calculated analytically for most engines.

Note: Numerical calculation of the full Hessian requires 6N single points calculation, which can take a considerable amount of time for large systems. A mode selective method can be a fast alternative, see [mode scanning](#) (page 195), [mode refinement](#) (page 196), and [mode tracking](#) (page 199).

When requesting the normal modes calculation, integrated IR intensities are simultaneously calculated during the finite differentiation steps when constructing the Hessian (as long as dipole moments are supported by the engine). These IR

intensities are calculated from the numerical dipole gradients:

$$I_{IR} = \frac{N\pi}{3c^2} \sum_{\alpha} \left(\sum_j \frac{\partial \mu_{\alpha}}{\partial R_j^m} Q_j^m \right)^2$$

Where α denotes the x-,y- and z-components of the dipole moment μ , and Q^m is the mass-weighted vibrational normal mode.

The resulting IR spectrum can be visualized by opening the engine result file with AMSspectra. The normal modes of vibration and the IR intensities are saved to the *engine result file* (page 19) in the Vibrations section.

Note: The calculation of the normal modes of vibration needs to be done the system's equilibrium geometry. So one should either run the normal modes calculation using an already optimized geometry, or combine both steps into one job by using the *geometry optimization task* (page 47) together with the `Properties%NormalModes` keyword.

Symmetry labels of the normal modes may be calculated if AMS uses symmetry in the calculation (key `UseSymmetry`). If symmetry is used, the normal modes are projected against symmetric displacements for each irrep. If that is not successful the symmetry label is 'MIX'. Symmetry is only recognized if the geometry is (almost) perfectly symmetric and has a specific orientation in space. You can use the `Symmetrize` key in the *System block* (page 31) to symmetrize and reorient the molecule. If the AMSinput GUI module is used, one can click the Symmetrize button (the star) and the GUI will try to symmetrize and reorient the molecule. Unless one is an expert user, best is not to specify an explicit symmetry in any part of the input.

Rescanning Imaginary modes

The `ReScanModes` keyword can be used to calculate more accurately frequencies of specific modes after a normal modes calculation. It is identical to the `ScanFreq` option that was available for older versions of ADF and BAND. Primarily used to identify spurious imaginary modes, and is on by default for this purpose. See also the *Mode Scanning* (page 195) task, which is an extension of this method, but which is not on by default. One should not specify an explicit symmetry in any part of the input, otherwise the rescanning of the normal modes might fail.

```
NormalModes
  ReScanModes Yes/No
  ReScanFreqRange float_list
End
```

NormalModes

ReScanModes

Type Bool

Default value Yes

GUI name Re-scan modes

Description Whether or not to scan imaginary modes after normal modes calculation has concluded.

ReScanFreqRange

Type Float List

Default value [-10000000.0, 10.0]

Unit cm-1

Recurring True

GUI name Re-scan range

Description Specifies a frequency range within which all modes will be scanned. 2 numbers: an upper and a lower bound.

6.2.2 Symmetric Displacements

```
NormalModes
  Displacements Symmetric
End
```

Specify `Displacements Symmetric` to calculate the energy Hessian using finite differences in symmetry-adapted displacements, and the corresponding normal modes.

```
NormalModes
  SymmetricDisplacements
    Type [All | Infrared | Raman | InfraredAndRaman]
  End
End
```

If `Type Infrared` or `Type Raman` is specified then only irreps that result in non-zero intensities for the corresponding spectroscopy will be included in the calculation. Using this feature may save a lot of time for large symmetric molecules by skipping calculation of normal modes that would not contribute to the spectrum anyway. If `Type InfraredAndRaman` is specified then vibrations that have a non-zero IR or Raman intensity will be calculated. If `Type All` is specified then all vibrations will be calculated. For multi-dimensional irreps (such as E and T) only the first component will be computed. For any component beyond the first, the frequencies and intensities will be copied from the first one.

NormalModes

SymmetricDisplacements

Type Block

Description Configures details of the calculation of the frequencies and normal modes of vibration in symmetric displacements.

Type

Type Multiple Choice

Default value All

Options [All, Infrared, Raman, InfraredAndRaman]

GUI name Symm Frequencies

Description For symmetric molecules it is possible to choose only the modes that have non-zero IR or Raman intensity (or either of them) by symmetry.

In order to calculate the Raman intensities the Raman property must be requested.

Warning: Specifying `Type Raman` alone does not trigger calculation of the Raman intensities. In order to calculate the Raman spectrum one should also specify `Raman True`.

Note: `Displacements Symmetric` will also produce a $3N$ -by- $3N$ Hessian matrix but if the `Type` key's argument is not `All` then this matrix will likely have many zero eigenvalues.

6.2.3 Mobile Block Hessian (MBH)

```
NormalModes
  Displacements Block
End
```

Specify `Displacements Block` for the Block Normal Modes option (also known as **Mobile Block Hessian**, or **MBH**¹²). MBH is useful when calculating vibrational frequencies of a small part of a very large system (molecule or cluster). Calculation of the full spectrum of such a system may be inefficient and is unnecessary if one is interested in one particular part. Besides, it may be difficult to extract normal modes related to the interesting sub-system out of the whole spectrum. Using Block Normal Modes it is possible to treat parts of the system as rigid blocks. Each block will usually have only six frequencies related to its rigid motions compared to $3*N$ for when each atom of the block is treated separately.

MBH is suitable to calculate frequencies in partially optimized structures. Assume a geometry optimization is performed with the `Block` key in the `Constraints` input block [see constrained geometry optimizations]. During the geometry optimization, the shape of the block is not changed. The internal geometry of the block is kept fixed, but the block as a whole can still translate or rotate.

At the end of such a partial geometry optimization, the position and orientation of the block is optimized, thus the total force on the block is zero. However, there might be still some residual forces within a block, since those degrees of freedom were not optimized. A traditional frequency calculation performed on this partially optimized structure might result in non-physical imaginary frequencies without a clear interpretation. Therefore one should use an adapted formulation of normal mode analysis: the Mobile Block Hessian method. MBH does not consider the internal degrees of freedom of the block (on which residual forces) apply, but instead uses the position/orientation of the block as coordinates. In the resulting normal mode eigenvectors, all atoms within the same block move collectively.

Of course, MBH can also be applied on a fully optimized structure.

Accuracy

```
NormalModes
  BlockDisplacements
    AngularDisplacement float
    BlockAtoms integer_list
    BlockRegion string
  Parallel
    nCoresPerGroup integer
    nGroups integer
    nNodesPerGroup integer
  End
  RadialDisplacement float
End
End
```

NormalModes

BlockDisplacements

¹ A. Ghysels, D. Van Neck, V. Van Speybroeck, T. Verstraelen and M. Waroquier, *Vibrational Modes in partially optimized molecular systems*, *Journal of Chemical Physics* 126, 224102 (2007) (<https://doi.org/10.1063/1.2737444>)

² A. Ghysels, D. Van Neck and M. Waroquier, *Cartesian formulation of the Mobile Block Hessian Approach to vibrational analysis in partially optimized systems*, *Journal of Chemical Physics* 127, 164108 (2007) (<https://doi.org/10.1063/1.2789429>)

Type Block

Description Configures details of a Block Normal Modes (a.k.a. Mobile Block Hessian, or MBH) calculation.

AngularDisplacement

Type Float

Default value 0.5

Unit Degree

Description Relative step size for rotational degrees of freedom during Block Normal Modes finite difference calculations. It will be scaled with the characteristic block size.

BlockAtoms

Type Integer List

Recurring True

Description List of atoms belonging to a block. You can have multiple BlockAtoms.

BlockRegion

Type String

Recurring True

Description The region to be considered a block. You can have multiple BlockRegions, also in combination with BlockAtoms.

Parallel

Type Block

Description Configuration for how the individual displacements are calculated in parallel.

nCoresPerGroup

Type Integer

Description Number of cores in each working group.

nGroups

Type Integer

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Cores per task

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

RadialDisplacement

Type Float

Default value 0.005

Unit Angstrom

Description Step size for translational degrees of freedom during Block Normal Modes finite difference calculations.

The second derivatives of the energy with respect to Cartesian displacements of the free atoms and those with respect to block motions (3 translation plus 3 rotations) are calculated by numerical differentiation of the gradient. The accuracy of the second derivatives is determined by the accuracy of the gradient evaluation and the step size in the numerical differentiation. The `RadialDisplacement` and `AngularDisplacement` parameters can be specified to set the step size for Cartesian displacements (translations) and block rotations respectively. The step size for angles is automatically scaled with the block size.

Note: Blocks should consist of at least 3 atoms (i.e. block of 1 or 2 atoms are not supported).

6.2.4 Mode Scanning

Mode Scanning can be used to obtain more accurate approximations for properties obtained by numerical differentiation along the vibrational normal modes (frequencies, intensities, Raman, etc.), without changing the modes themselves. Mode Scanning is an extension of the frequency scanning options (`ScanFreq`) that were part of ADF and BAND in earlier versions of the Amsterdam Modeling Suite. These latter options are still available as the `ReScanModes` keyword in the `NormalModes` block, if these are requested during a calculation.

- Primarily used to identify spurious imaginary modes.
- Improve numerical accuracy of normal mode properties.
- Rescanning modes using a different level of theory.

Theory

Vibrational normal modes are usually obtained as eigenvectors of the Hessian matrix. A common problem with this scheme however, is that due to numerical errors in constructing this Hessian, low-frequency vibrations may be reported to have imaginary frequencies instead. The Mode Scanning task allows for re-calculation of the frequency of these modes. The Mode Scanning task does not change the normal modes itself, only its properties. This Mode Scanning task allows you to confirm whether reported imaginary frequencies are attributed to transition states or whether they are simply due to numerical errors.

Given a user-supplied mode Q , the frequency is calculated from the force constant:

$$k = \frac{\partial^2 E}{\partial^2 Q}$$

$$\nu = \frac{1}{2\pi c} \sqrt{\frac{k}{\mu_r}}$$

This is again done by numerical differentiation of the energy gradients, requiring AMS to set up 2 single point calculations per selected normal mode. Integrated IR intensities are also calculated simultaneously (if dipole moments are supported by the *engine* (page 250)):

$$I_{IR} = \frac{N\pi}{3c^2} \sum_{\alpha} \left(\frac{\partial \mu_{\alpha}}{\partial Q^m} \right)^2$$

Where the derivative is with respect to the mass-weighted normal mode.

It is also possible to use this method to selectively re-calculate the normal mode properties for different engine settings. This has two distinct uses:

- If the modes were originally generated using a finite difference method, a different stepsize can be used. For strong vibrations (high frequencies), large stepsizes may cause inaccuracies due to increasing anharmonic contributions. For weak vibrations (low frequencies) on the other hand, stepsizes can often be too small. The displacements associated with these vibrations are small, which can give incorrect sampling of the PES profile. This should be compensated for by choosing a larger stepsize. The stepsize can be set using the `Displacement` key.
- Users can also recalculate modes using higher levels of theory. Modes generated from a full frequency analysis using e.g. DFTB can be recalculated using e.g. LDA DFT to obtain more realistic integrated IR intensities. The method used for the single point calculations can be set in the *Engine block* (page 250).

Input

A numerical frequency calculation is performed by requesting the `VibrationalAnalysis` task with `Type ModeScanning`:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeScanning
  Displacement 0.001
  NormalModes
    ModeFile adf.rkf
    # select all modes with imaginary frequencies
  ModeSelect
    ImFreq true
  End
End
End
```

The Mode Scanning tasks uses only the `NormalModes` block for its input handling. Here, `ModeFile` specifies the AMS output file containing the normal modes for which you want to calculate the frequencies. The `ModeSelect` block is used to specify which of the modes in this file should be recalculated, since we are often only interested in a select few of them. A more detailed overview of this block is given in the section *Selecting Modes* on the [main page](#) (page 207). Finally, `Displacement` can be used to specify the stepsize (in Bohr) for the finite differences. The stepsize is provided for displacements along the Cartesian normal modes.

The Mode Scanning module is the main driving force for the *Mode Tracking* (page 199) and *Vibrational Mode Refinement* (page 196) tasks, which provide more advanced options for refining not only the properties of the modes, but also the modes themselves. Consult the relevant pages for more information. Alternatively, a simplified version of Mode Scanning is available which follows the old implementation in ADF and BAND (as the `ScanFreq` option). This version can be enabled when doing a full frequency analysis by enabling the `Properties%NormalModes` keyword. See the *Full Analysis* (page 190) page for further details.

6.2.5 Mode Refinement

With this option you can improve the normal modes, by importing previously calculated modes and then applying a more accurate engine, or more accurate settings, typically for only part of the spectrum. The vibrational Mode Refinement method not only refines frequencies from a previous calculation, but also tries to correct the vibrational modes themselves.

- Refinement of spectral regions requires a sufficient number of modes in the basis to be accurate.
- 1-step refinement. No iterative improvement possible. (Unless followed by a separate Mode Tracking calculation.)
- Quality of the results depends on accuracy of the selected guess modes.

If we start from e.g. a semi-empirical method such as in MOPAC, we can get approximations for the vibrational modes. Mode Refinement then re-calculates part of the Hessian for a subset of these modes using a more accurate method such

as GGA DFT, and updates the normal modes themselves to fit this more accurate method. It is intended to circumvent the expensive calculation of the Hessian if you are only interested in a (small) part of the full spectrum. This is based on the method in reference³.

Because the Mode Refinement method uses linear combinations of the guess modes, its accuracy depends on the set of modes that is supplied.

- If we want to e.g. obtain a mode which includes a C=O stretch, then the initial set must contain a mode which has this C=O stretch, otherwise this cannot be included in the refined modes.
- If we are refining a region containing many similar modes, e.g. vibrations of aromatic ring backbones, and we only use part of this spectral region for the initial set, the set of refined modes will “drift” towards the centre of the spectral region as a result of mode-mixing. This is again an artefact of missing character in the modes.
- This mode-mixing may result in reduced accuracy for some of the modes, as this procedure minimizes the total error for all of the modes. Instead of having a couple of modes with large errors, mode-mixing tends to spread out the error across multiple normal modes. Adding 1 “bad” mode to the basis can then negatively affect your results.
- The advantage of Mode Refinement over Mode Tracking is the ability to refine entire spectral regions at once. If we have a good basis, Mode Refinement can be less computationally expensive than Mode Tracking. If you want to refine larger sections of the spectrum, Mode Refinement is therefore recommended. If you only want to calculate a select few modes, use Mode Tracking to avoid basis dependence and to assure accuracy of the obtained modes.
- For characteristic peaks, Mode Tracking shows very good convergence, and will thus be cheaper to use than Mode Refinement. For (semi-)degenerate modes however, Mode Refinement works better due to the poor tracking performance for these modes.

See also:

The [GUI tutorial](#) on Mode Refinement.

Theory

We are going to start from a set of normal modes b , obtained from e.g. a semi-empirical or force-field method. First, this task runs the *numerical frequency* (page 195) calculation for all selected normal modes, but this time using an ab initio method such as DFT. During the finite difference steps, we also calculate the projection of the Hessian onto the normal modes:

$$\sigma_i = H^m \cdot b_i^m = \frac{\partial^2 E}{\partial R_i^m \partial b^m}$$

This term is calculated through finite differences on the analytical gradients of the electronic energy along the mass-weighted normal modes b^m . The index i denotes the $3N$ nuclear coordinates. These projections are then used to construct a Rayleigh matrix:

$$\tilde{H}^m = B^{mT} \cdot H^m \cdot B^m = B^{mT} \cdot \Sigma$$

Here, B^m and Σ are matrices containing the b^m and σ vectors. The eigenvectors of \tilde{H}^m give us the coefficient series for linear combinations of the normal modes b^m such that we obtain a new set of modes q :

$$q^m = \sum_k c_k \cdot b_k^m$$

These modes q are the closest approximation to the DFT-modes that we could obtain from a linear combination of the approximate modes b . In other words: the approximate modes b are used as a basis for finding the modes from a more sophisticated theory.

³ T.Q. Teodoro, M.A.J. Koenis, S.E. Galembeck, V.P. Nicu, W.J. Buma, L. Visscher, *A frequency range selection method for vibrational spectra*, J. Phys. Chem. Lett., 9 (23), 6878 (2018) (<https://doi.org/10.1021/acs.jpcclett.8b02963>)

Input

This method inherently features a trade-off:

- The computational benefit comes from only performing the finite difference calculations for the selected modes. By only selecting a small set of modes that we are interested in, we minimize computational expense.
- The more modes we select, the larger the basis for constructing the refined modes. Running for a larger number of modes yields better results. (In the extreme case, running for all $3N$ modes equates to constructing the full Hessian.)

In practice, Mode Refinement requires you to select a reasonable portion of the spectrum to get accurate results. Specifically, you should select all modes in a region of the spectrum which look similar. Ring structures for instance often feature broad frequency regions with many ring distortions. Even if you are only interested in a couple of these, you should still select all modes in this region, to assure sufficient basis size. Vibrational modes involving ring substituents can however be omitted, which is where we save computation time.

If you are interested only in IR-active vibrations, you could further minimize the basis by only selecting the approximate modes which are IR-active (since adding the non-active modes to the linear expansion does not affect the IR-intensity of the refined modes). Do note that if the semi-empirical method used for calculating the approximate modes yields poor approximations for the dipole gradients, it may be safer to include also modes with very low IR intensity. This is because their low IR-activity may have only been due to the low accuracy of the approximate method.

See also:

A [tutorial](#) showing this basis representability.

A Mode Refinement calculation is set up by requesting the `VibrationalAnalysis` task with the `Type ModeRefinement`:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeRefinement
  Displacement 0.001
  NormalModes
    ModeFile adf.rkf
    ModeSelect
    ...
  End
  ScanModes true
End
End
```

The details of the calculation are specified in the `NormalModes` block. Here, `ModeFile` specifies the AMS output file containing the normal modes for which you want to calculate the frequencies. The `ModeSelect` block is used to specify which of the modes in this file will be selected for refinement. A more detailed overview of this block is given in the section *Selecting modes* on the [main page](#) (page 207). Finally, `Displacement` can be used to specify the stepsize (in Bohr) for the finite differences. The stepsize is provided for displacements along the Cartesian normal modes.

The `ScanModes` key in the `NormalModes` block can be used to automatically run a *numerical frequencies* (page 195) calculation on the new modes q . Mode Refinement uses a linear combination of modes and properties, all obtained through finite differences. These results may still contain some minor errors due to the accumulation of numerical errors from the linear expansion, or stepsize issues in the numerical frequency calculations. While commonly not necessary, it is possible to run an additional numerical refinement calculation on the new modes to minimize these errors. Only in exceptional cases will these errors be significant. Running this additional refinement step is therefore only necessary if you need complete certainty that the results are accurate.

6.2.6 Mode Tracking

The Mode Tracking task is an interface for mode- and intensity-tracking methods, adapted from the MoViPac suite⁴⁻⁵. These methods can be used to obtain select normal modes, without having to calculate the entire vibrational spectrum. It does this through an iterative procedure.

- Calculations are conducted for each mode separately. Converges fastest for characteristic (non-highly degenerate) modes.
- Iterative approximation to the true modes. Guaranteed to give the correct normal modes if the procedure converges.
- Will not necessarily reproduce the entire spectrum as multiple guess modes can converge to the same normal mode.

Mode Tracking uses information about the known parts of the Hessian to expand its basis iteratively:

- Missing C-O stretch character can thus be recovered in this procedure, and there is no basis dependency.
- For large regions with similar modes however, it is possible that multiple guess modes converge to the same normal mode. Running mode tracking for all modes in this region might not reproduce all unique normal modes.
- The advantage of Mode Refinement over Mode Tracking is the ability to refine entire spectral regions at once. If we have a good basis, Mode Refinement can be less computationally expensive than Mode Tracking. If you want to refine larger sections of the spectrum, Mode Refinement is therefore recommended. If you only want to calculate a select few modes, use Mode Tracking to avoid basis dependence and to assure accuracy of the obtained modes.
- For characteristic peaks, Mode Tracking shows very good convergence, and will thus be cheaper to use than Mode Refinement. For (semi-)degenerate modes however, Mode Refinement works better due to the poor tracking performance for these modes.

Mode Tracking starts with a *numerical frequency* (page 195) calculation, which refines the initial guess b^m for the selected mode. The error of this mode with respect to the true Hessian eigenvector is calculated. This error is used in a (Jacobi-)Davidson algorithm to generate an additional mode. In subsequent iterations, we use these modes as approximations to the true normal modes. In this way, the error of the mode is minimized iteratively, yielding a closer approximation to true normal modes. This is how Mode Tracking differs from the Mode Refinement methods, in that it guarantees that the obtained modes are correct (assuming the procedure has converged).

See also:

The [GUI tutorial](#) on Mode Tracking.

Theory

During the numerical frequency calculation, we obtain also the projection of the Hessian onto this mode:

$$\sigma_i = H^m \cdot b_i^m = \frac{\partial^2 E}{\partial R_i^m \partial b^m}$$

This term is calculated through finite differences on the analytical gradients of the electronic energy along the mass-weighted normal modes q^m . The index i denotes the $3N$ nuclear coordinates. From this projection a Rayleigh matrix is generated:

$$\tilde{H}^m = B^{mT} \cdot \Sigma$$

Here, B^m and Σ are matrices containing the b^m and σ vectors for all foregoing iterations. During each iteration k , if we have not converged, we generate an updated guess vector b_k^m , and so the number of vectors in the matrices above is equal

⁴ T. Weymuth, M.P. Haag, K. Kiewisch, S. Luber, S. Schenk, C.R. Jacob, C. Herrmann, J. Neugebauer, M. Reiher, *MoViPac: Vibrational Spectroscopy with a Robust Meta-Program for Massively Parallel Standard Inverse Calculations*, *Journal of Computational Chemistry* 33, 2186 (2012) (<https://doi.org/10.1002/jcc.23036>)

⁵ S. Luber, J. Neugebauer, M. Reiher, *Intensity tracking for theoretical infrared spectroscopy of large molecules*, *Journal of Chemical Physics* 130, 064105 (2009) (<https://doi.org/10.1063/1.3069834>)

to the number of iterations k . The eigenvectors of \tilde{H}^m give us the coefficient series for linear combinations of the guess modes b^m such that we obtain approximations for the true normal modes:

$$Q^m = \sum_k c_k \cdot b_k^m$$

Each iteration, we expand the vector basis B^m , which allows this series expansion to come closer to the true normal modes each time. We can also calculate the error of this mode with respect to how close it is to being an eigenvalue of the real Hessian:

$$r = \sum_k c_k \cdot [\sigma_k - \lambda \cdot b_k]$$

Here, λ is the corresponding eigenvalue of \tilde{H}^m . r is the residual vector, giving the error for each vector element. It should be zero if the mode is an exact eigenvector of the true Hessian.

Since \tilde{H}^m may give multiple eigenvectors, several approximate modes will be generated during those iterations. Out of these, 1 mode is identified as the mode of interest according to the specified *tracking method* (page 203). If the residual of this mode has been minimized sufficiently, the procedure has converged. If not, we generate a new guess vector b_k^m . There are 2 algorithms for generating this new guess, set by UpdateMethod in the ModeTracking block:

Davidson method

The Davidson method uses a pre-conditioner D to generate a new guess mode from the residual vector of the mode selected by the tracking method:

$$b_k^m = D^{-1} \cdot r$$

This preconditioner is constructed from an approximation of the Hessian:

$$D = H_A - \lambda \cdot I$$

The Davidson method works reasonably well, but can have trouble converging if the approximate modes or the Hessian are too accurate. This results as the new vectors that are generated do not necessarily extend the span of the basis.⁶

vdVorst-Sleijpen-Jacobi-Davidson

This variant of the Jacobi-Davidson scheme from Sleijpen & vdVorst² automatically makes the new guess vector orthogonal to the normal mode selected by the tracking method:

$$b_k^m = \left(\frac{Q^m D^{-1} r}{Q^m D^{-1} Q^m} \right) D^{-1} Q^m - D^{-1} r$$

The new vector is therefore guaranteed to extend the span of the basis as much as possible, and thus also eliminates the aforementioned issue with the Davidson method. In general, it is therefore recommended to use this Jacobi-Davidson method since it is found to converge faster, and be more reliable, as a result of yielding better guess modes.

⁶ G.L.G. Sleijpen, H.A. van der Vorst, *A Jacobi-Davidson Iteration Method for Linear Eigenvalue Problems*, SIAM Journal on Matrix Analysis and Applications 17, 401 (1996) (<https://doi.org/10.1137/S0895479894270427>)

Input

```

Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeTracking
  ...
  ModeTracking
    HessianGuess [Unit | File | UFF | Inline]
    HessianInline # Non-standard block. See details.
    ...
  End
  HessianPath string
  UpdateMethod [JD | D | I]
  MaxIterations integer
  ...
  GramSchmidt [True | False]
  GramSchmidtIterations integer
  GramSchmidtTolerance float
End
End

```

There are 4 methods to obtain the approximate Hessian H_A , used by both update methods. They are set by `HessianGuess`:

HessianGuess [Unit | File | UFF | Inline]

UFF is the default, which generates the approximate Hessian using UFF. While this Hessian may not yield the correct modes by itself, it produces good results as a preconditioner since it correctly represents the molecular structure.

File will read the Hessian from an AMS output file, which can be specified in `HessianPath`. Using a Hessian from a more advanced method will generally yield better results for the Jacobi-Davidson method. The Davidson method will however experience difficulties with convergence as the Hessian becomes too accurate.[?]

Inline will read a Hessian specified in the input file, in the `HessianInline` block. This allows you to use Hessians generated in external programs:

```

Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeTracking
  ModeTracking
    HessianGuess Inline
    # Approximate Hessian for H2O: 3 x nAtoms = 9 so 9x9 Hessian
    HessianInline
      0.62088786  0.00000000  0.00000000  -0.31044393  0.00000000  -0.
↪21902068  -0.31044393  0.00000000  0.21902068
      0.00000000  0.00000000  0.00000000  0.00000000  0.00000000  0.
↪00000000  0.00000000  0.00000000  0.00000000
      0.00000000  0.00000000  0.32143213  -0.15284008  0.00000000  -0.
↪16071607  0.15284008  0.00000000  -0.16071607
      -0.31044393  0.00000000  -0.15284008  0.33598889  0.00000000  0.
↪18593038  -0.02554496  0.00000000  -0.03309030
      0.00000000  0.00000000  0.00000000  0.00000000  0.00000000  0.
↪00000000  0.00000000  0.00000000  0.00000000
      -0.21902068  0.00000000  -0.16071607  0.18593038  0.00000000  0.
↪15761846  0.03309030  0.00000000  0.00309761
      -0.31044393  0.00000000  0.15284008  -0.02554496  0.00000000  0.
↪03309030  0.33598889  0.00000000  -0.18593038

```

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```

0.00000000  0.00000000  0.00000000  0.00000000  0.00000000  0.
↪00000000  0.00000000  0.00000000  0.00000000
0.21902068  0.00000000  -0.16071607  -0.03309030  0.00000000  0.
↪00309761  -0.18593038  0.00000000  0.15761846
    End
    End
End

```

Unit uses the unit matrix. This is evidently not a good approximation for the Hessian, and is not intended to be used for proper Mode Tracking runs. However: using a poor approximation for the Hessian can result in basis vectors being generated that we would not obtain otherwise. Running Mode Tracking with this option can allow you to “probe” the vector space to obtain guesses for normal modes, which can be used as starting points for proper Mode Tracking calculations. It is however generally recommended to instead do e.g. a DFTB or UFF run if your goal is to obtain guess modes.

UpdateMethod [JD | D | I]

JD vdVorst-Slejpen variant of Jacobi-Davidson (Mode tracking default).

D Davidson

I No preconditioner (VST default). This is not recommended for typical mode tracking applications, but is useful for a variation of mode tracking, *Vibronic-Structure Tracking* (page 236).

In later iterations, the basis B^m will become larger. In order to improve the guess modes even further, an iterative Gram-Schmidt procedure is used to orthogonalize the new guess mode to the existing basis. An iterative procedure is necessary to account for numerical noise.

GramSchmidt [True | False] Expert key. Sets whether to perform this Gram-Schmidt orthogonalization step. It is True by default.

GramSchmidtTolerance float Expert key. Sets the absolute tolerance for orthogonality of the basis. It is evaluated with respect to the norm of the overlap vector between the new guess mode and the basis of the previous iteration $\|b_k^{mT} B^m\|$.

GramSchmidtIterations Expert key. Sets the maximum number of allowed iterations during the Gram-Schmidt procedure.

The default settings for the Gram-Schmidt procedure should work for almost all systems.

MaxIterations integer Finally, the Mode Tracking input block contains the MaxIterations key. It sets the maximum allowed number of iterations that the Mode Tracking calculation may go through. If this number is reached, the calculation will stop even if convergence was not achieved. If no value is supplied, a default of $3N/2$ will be used. This is approximately the maximum number of iterations where the procedure remains computationally competitive with the construction of the full Hessian.

Additional input parameters

```

Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeTracking
  Displacement float
  ...
  NormalModes
    ScanModes [True | False]
    ...

```

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```
End
End
```

Displacement float is the displacement stepsize (in Bohr) that is used for calculating frequencies, IR intensities and the Hessian projections through finite differences. The stepsize is provided for displacements along the Cartesian normal modes.

ScanModes [True | False] key (False by default) in the `NormalModes` vibrational analysis sub-block can be used to automatically run a *numerical frequencies* (page 195) calculation on the new modes Q after the Mode Tracking calculation has finished. Ritz vectors are obtained here as linear combinations of the guess modes, which in turn follow from finite difference calculations. This makes it possible for numerical errors to accumulate in the normal modes. Only in exceptional cases will these errors be significant, and running this additional refinement step is therefore only necessary if you need complete certainty that the results are accurate.

Input: Tracking methods

The `TrackingMethod` parameter allows you to select what property of the normal modes you want to track. At the end of each iteration, we obtain a set of approximate normal modes. The tracking method identifies which of these modes fits best for some criterion, and either returns this mode as the calculation result, or, if convergence was not achieved, uses it to generating a new basis mode for the next iteration. In general these methods are distinguished in 3 categories:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeTracking
  ModeTracking
    TrackingMethod [OverlapInitial, DifferenceInitial, FreqInitial, IRInitial,
                   OverlapPrevious, DifferencePrevious, FreqPrevious, IRPrevious,
                   HighestFreq, HighestIR, LowestFreq, LowestResidual]
    ...
  End
End
```

Mode Tracking

The original tracking methods focus on obtaining as accurate as possible a normal mode for the system. This class of tracking methods focuses either on accuracy of the mode, or obtaining modes with particular vibrational character:

TrackingMethod [OverlapInitial, DifferenceInitial, FreqInitial, OverlapPrevious, DifferenceInitial, FreqPrevious, IRPrevious, HighestFreq, HighestIR, LowestFreq, LowestResidual]

OverlapInitial is the default tracking method. Here, we choose the mode which resembles most closely the guess mode that was initially supplied b_1^m . This is done by choosing the mode which has the greatest overlap with the initial guess vector. This method allows us to direct the optimization towards modes that e.g. involve particular atoms or include particular bending/stretching vibrations.

OverlapPrevious instead chooses the mode which resembles closest the approximate mode of the previous iteration Q_k^m . This procedure allows a bit more flexibility in the optimization. Since we essentially “forget” about earlier iterations, this procedure allows the optimization to correct errors in the initial guess. (It is possible for instance that the initial guess included 2 different bond stretches which do not mutually occur in the true modes. This method will then converge quicker to a mode involving only 1 of these stretches, whereas `OverlapInitial` will take a much larger number of iterations to achieve this, if it does so at all.) Do note that this means that the final mode that you obtain does not necessarily represent the mode you initially supplied.

DifferenceInitial works the same as `OverlapInitial`, except that it chooses the mode which has the smallest norm for the difference vector between the initial mode and the approximate normal modes of this iteration. The use of the difference vector prioritizes deviations in the dominant parts of the vibrational character. E.g. if a mode consists primarily of a CO stretch, plus some minor vibrations in a carbon backbone, it may be desired to prioritize getting the correct force constant for the dominant CO stretch. This is achieved using these difference vector methods. In general, overlap methods still work well in these situations, and the use of difference methods should only be necessary in extreme cases.

DifferencePrevious is also the same as `DifferenceInitial` except for the use of the difference vector norm as the selection criterion.

FreqInitial chooses the mode with the frequency closest to that of the initial guess. This allows us to direct the tracking towards modes in a particular frequency region of the spectrum. Note that convergence for these frequency-based methods is slightly slower since the character of the mode itself is not included in the selection criteria, allowing for larger differences in the modes between iterations.

FreqPrevious is similar to `FreqInitial` except that we choose the mode with the frequency closest to that of the previous iteration. This allows the optimization more freedom to move away from the frequency region of the initial guess, and thus allows to correct somewhat for poor initial guesses.

HighestFreq chooses the mode with the highest frequency. This method can be used if it is desired to track particular characteristic high-frequency vibrations.

LowestResidual chooses the mode which has the smallest norm for the residual vector (see the 'Convergence' section below.) This method only focuses on obtain the most accurate mode, regardless of vibrational character or where it lies in the spectrum. This method should generally only be used as a pre-conditioner if you have very little information on what the normal modes should look like. (Since it is basically a non-directed optimization.) This method will then try and find the normal mode closest to your guess. The approximate normal mode obtained this way will most likely not have converged yet, but should give you an indication of what the normal modes may look like. You can use these modes to refine your initial guess, and then do a new Mode Tracking run using any of the other tracking parameters to obtain the desired mode. Although this strategy is possible, it is generally recommended to use an approximate method to get an initial guess for the normal modes instead (as shown in the *examples* (page 371)).

Intensity Tracking

This class of methods focuses on tracking modes based on their intensity in e.g. the infrared spectrum, rather than focusing on getting a mode with a particular type of vibration.

TrackingMethod [IRInitial, IRPrevious, HighestIR] `IRInitial` chooses the mode with the IR intensity closest to that of the initial guess. This constrains the optimization to modes which are IR active, a property that may be lost when using mode tracking update methods.

`IRPrevious` similarly chooses the mode with the IR intensity closest to that of the previous iteration. This allows the method some more flexibility in varying the intensity of the vibration, and thus works better if the initial guess is not that good.

`HighestIR` chooses the mode with the highest IR intensity. This option can be used to find the modes associated with sharp peaks in the IR spectrum.

With Intensity Tracking, we essentially add an additional requirement to the modes: they must have a particular IR intensity. This constrained search has different convergence characteristics than conventional mode tracking, which you should take into account when setting up the mode tracking calculations.

- The majority of modes will have near-zero IR intensity. If we use a near-zero IR intensity mode as our initial guess, and request `IRInitial` or `IRPrevious`, then we could be tracking any of one of these. Conversely, convergence behavior will be poor since the generated basis modes are essentially random. If you are trying to obtain a high IR-intensity mode, use an IR-susceptible mode.

Note: In our conventional work-flow, we recommend starting mode tracking or refinement calculations from a set of approximate normal modes obtained from a semi-empirical or force-field method. Note however, that these method often do not produce accurate IR intensities. When selecting the initial guess mode, do **not** use the `IRRange` or related options in the `ModeSelect` block. This will cause you to miss vibrations which were incorrectly labeled with low IR intensity, or vice versa. Instead, rely on chemical intuition to identify the modes which contain commonly IR active vibrational components (such as C-O or N-H stretches). You can use `AMSSpectra` in the GUI to visualize the vibrational modes, to help you in this process.

- To allow the intensity tracking procedure to converge faster, it is recommended to use the `IRPrevious` tag instead of the `IRInitial` tag. As discussed earlier, the former allows more flexibility in the optimization procedure, which counters the rigidity imposed by the intensity constraint. Intensity tracking methods often need this additional flexibility in generating guess modes to converge to the desired modes.
- **Poor Initial Guesses:** During each iteration, we still use the mode tracking methods to generate new basis modes. These basis modes try to expand the span of the basis with respect to the vibrational character of the modes. Note that this expansion does not guarantee that we will expand the basis specifically in the sub-span of IR-susceptible vibrations. If the initial guess for intensity tracking is correct, we already start our search in the sub-span vicinity of the normal modes. Basis expansion is then more efficient and there is a high chance that new guess modes sample the IR characteristic vibrations. For intensity tracking it is therefore discouraged to use poor initial guess modes.
- `HighestIR` is considered a “pure” intensity tracking method, in that it is used specifically to target characteristics of the IR spectrum irrespective of the underlying vibrational character. Consequently, the normal mode character can vary a lot between iterations. In order to assure that the procedure converges to the desired modes, it is recommended to use sufficiently strict tolerances (see the *Convergence* section). If the tolerances are too lax, the program may consider the modes to be “good enough” based on residual minimization, even though there may be another mode with a higher IR intensity. For this reason it is generally recommended to use `ToleranceForNorm` values 1 order of magnitude lower than the default, or around `0.00005`.

Input: Selecting modes

It is possible to track multiple modes in a single Mode Tracking calculation. The Mode Tracking task will then run the Mode Tracking algorithm for each mode in order.

The initial guess for the mode which will be tracked can be supplied in several ways. This is governed by `ModeInputFormat`:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeTracking
  NormalModes
    ModeInputFormat [File | Inline | Hessian]
    ModeFile string
    ModeInline # Non-standard block. See details.
    ...
  End
  ModeSelect
  ...
  End
  MassWeighInlineMode [True | False]
End
End
```

ModeInputFormat [**File** | **Inline** | **Hessian**]

Inline will make the module read the mode from the input file. If this option is selected, you can supply the mode in the `ModeInline` block. It is possible to supply multiple modes by adding additional `ModeInline` blocks. The modes are given with one line for the x,y,z-displacement per atom, and in the same order, as the `Atoms` block in `System`:

```
ModeTracking
  TrackedMode Inline
  ModeInline
    0.00000000  0.00000000  -0.03815965
   -0.18888544  0.00000000  0.30281066
    0.18888544  0.00000000  0.30281066
  End
  ModeInline
    0.00000000  0.00000000  -0.02243153
    0.32132452  0.00000000  0.17800237
   -0.32132452  0.00000000  0.17800237
  End
  ...
End
```

File will make the module read modes from an AMS or engine output file, specified by `ModePath`. Modes generated using DFTB can be read from the `dftb.rkf` file and optimised using Mode Tracking for example. When this option is selected, all the vibrational modes present in the file are read first. The `ModeSelect` block then specifies for which of these modes you want to perform the Mode Tracking calculation.

Hessian will generate modes as the eigenvectors of the approximate Hessian selected for the preconditioner in `HessianGuess`. This also allows modes to be generated for Hessians obtained from external programs. `ModeSelect` specifies which of the generated vibrational modes are selected for Mode Tracking.

- Settings for the `ModeSelect` block are discussed on the [main page](#) (page 207).

MassWeighInlineMode [**True** | **False**] decides whether the initial guess modes need to be mass-weighted (default True). As discussed above, Mode Tracking uses mass-weighted normal modes. In most cases, the normal modes are given in regular Cartesian coordinates however. By setting `MassWeighInlineMode true`, these Cartesian modes are converted into mass-weighted modes by the program. If you supply a mass-weighted mode through the `ModeInline` block however, you do not need the program to do the mass-weighting, and you should set `MassWeighInlineMode false`.

Input: Convergence

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ModeTracking
  ModeTracking
    ToleranceForNorm float
    ToleranceForResidual float
    ToleranceForBasis float
  End
End
```

In order to guide the Mode Tracking procedure, several convergence criteria are used:

ToleranceForNorm float is the absolute tolerance for convergence of the norm of the residual vector. The residual vector is a vector containing the error for each element of the normal mode, and we use the norm as a measure for the total error. If the total error is smaller than this threshold, we consider the mode to be a true normal mode and we stop iterating. Since the value of this norm depends on the length of the residual vector hence the number of atoms in the system, this tolerance is scaled internally to the number of atoms. `0.0005` is used as a

default value for which most systems will converge to reasonably accurate modes in not too many iterations. If you want a more accurate approximation, you can decrease this value by e.g. 1 order of magnitude. (Consider running using the default settings, and reading the norm at convergence from the logfile. The new norm can be chosen to be lower than this value to ‘force’ the method into another iteration.)

ToleranceForResidual float is the absolute tolerance for the maximum component of the residual vector. Particularly in larger systems, where the vibration may be dominated by a small number of atoms, the error associated with the vibration of the majority of atoms may be small (the scaled residual norm will be small). The error for the atoms involved in the vibration may be comparatively large then, which is why we also check convergence for the maximum component of the error. Note that both the norm and this max. error are checked simultaneously. By varying strictness of the criteria for the norm and the max. error separately, you can prioritize either the total vibration or more localized character.

ToleranceForBasis float checks that the basis mode generated in the previous iteration, through the (Jacobi-)Davidson method, contributes to the approximate normal mode. Since the approximate mode is taken as a linear combination of the basis modes, its linear expansion coefficient must be larger than this tolerance.

The iterative procedure is stopped in one of two cases. Either both the residual criteria are achieved, in which case the mode is deemed to be converged and the program exits normally. Alternatively, the basis criterion is met in which case a warning is broadcast indicating that the desired level of accuracy of the mode may not have been reached yet, but the basis has stopped expanding. The default values for these parameters should be applicable for most cases, but can be adjusted if needed. If stricter criteria are required, it is recommended to adjust both `ToleranceForNorm` and `ToleranceForResidual`.

6.2.7 Selecting modes

Mode Scanning, Mode Refinement and Mode Tracking as well as VG-FC Vibronic-Structure, VG-FC Vibronic-Structure Refinement and VG-FC resonance Raman all require a set of normal modes to operate on. For Mode Scanning these are the modes that you want to calculate the properties of, for Mode Refinement these modes form the basis modes, and for Mode Tracking these are the initial guess modes. For the VG-FC based methods these modes are the modes responsible for the vibronic coupling to the electronic excitation (in VG-FC Vibronic-Structure Refinement they are refined first).

Note: VG-FC Vibronic-Structure Tracking does not require any normal modes and as such does not support the `ModeSelect` (nor does it support the `NormalModes` block for that matter).

These methods provide options to load a large set of modes, after which the program will filter out the modes of interest. This is done according to the keys set in the `ModeSelect` block.

Note: The `ModeSelect` block is part of the `NormalModes` block of the Vibrational Analysis input. All Vibrational Analysis methods share this block, with the exception of VG-FC Vibronic-Structure Tracking. The methods for obtaining the set of modes that we will filter can differ per method. Particularly Mode Tracking features a lot of additional options, and the vibronic variants feature more specialized options.

Below is an overview of all the available options for the `ModeSelect` block as they appear in the basic vibrational analysis tools. The vibronic variants are discussed in more detail on their respective documentation pages.

The options below are not mutually exclusive.

```
ModeSelect
  DisplacementBound float
  FreqAndIRRange float_list
  FreqRange float_list
  Full Yes/No
```

(continues on next page)

```
HighFreq integer
HighIR integer
IRRange float_list
ImFreq Yes/No
LargestDisplacement integer
LowFreq integer
LowFreqNoIm integer
LowIR integer
ModeNumber integer_list
End
```

ModeSelect**DisplacementBound****Type** Float**Description** Vibronic Structure (Refinement), Resonance Raman: Select all modes with a dimensionless oscillator displacement greater than the specified value.**FreqAndIRRange****Type** Float List**Unit** cm-1 and km/mol**Recurring** True**Description** Specifies a combined frequency and IR intensity range within which all modes will be selected. First 2 numbers are the frequency range, last 2 numbers are the IR intensity range.**FreqRange****Type** Float List**Unit** cm-1**Recurring** True**Description** Specifies a frequency range within which all modes will be selected. 2 numbers: an upper and a lower bound. Calculating all modes higher than some frequency can be achieved by making the upper bound very large.**Full****Type** Bool**Default value** No**GUI name** All modes**Description** Select all modes. This only make sense for Mode Scanning calculations.**HighFreq****Type** Integer**GUI name** # High frequencies**Description** Select the N modes with the highest frequencies.**HighIR****Type** Integer**GUI name** # High IR

Description Select the N modes with the largest IR intensities.

IRRange

Type Float List

Unit km/mol

Recurring True

Description Specifies an IR intensity range within which all modes will be selected. 2 numbers: an upper and a lower bound.

ImFreq

Type Bool

Default value No

GUI name All imaginary frequencies

Description Select all modes with imaginary frequencies.

LargestDisplacement

Type Integer

Description Vibronic Structure (Refinement), Resonance Raman: Select the N modes with the largest VG-FC displacement.

LowFreq

Type Integer

GUI name # Low frequencies

Description Select the N modes with the lowest frequencies. Includes imaginary modes which are recorded with negative frequencies.

LowFreqNoIm

Type Integer

GUI name # Low positive frequencies

Description Select the N modes with the lowest non-negative frequencies. Imaginary modes have negative frequencies and are thus omitted here.

LowIR

Type Integer

GUI name # Low IR

Description Select the N modes with the smallest IR intensities.

ModeNumber

Type Integer List

GUI name Mode numbers

Description Indices of the modes to select.

6.2.8 Thermodynamics (ideal gas)

The following thermodynamic properties are calculated by default whenever normal modes are computed: entropy, internal energy, constant volume heat capacity, enthalpy and Gibbs free energy. Translational, rotational and vibrational contributions are calculated for entropy, internal energy and constant volume heat capacity.

The results are written to the output file (section: “Statistical Thermal Analysis”) and to the engine binary results file (section: “Thermodynamics”).

The thermodynamic properties are computed assuming an ideal gas, and electronic contributions are ignored. The latter is a serious omission if the electronic configuration is (almost) degenerate, but the effect is small whenever the energy difference with the next state is large compared to the vibrational frequencies. The thermal analysis is based on the temperature dependent partition function. The energy of a (non-linear) molecule is (if the energy is measured from the zero-point energy)

$$\frac{E}{NkT} = \frac{3}{2} + \frac{3}{2} + \sum_j^{3N-6} \left(\frac{h\nu_j}{2kT} + \frac{h\nu_j}{kT(e^{h\nu_j/(kT)} - 1)} \right) - \frac{D}{kT}$$

The summation is over all harmonic ν_j , h is Planck’s constant and D is the dissociation energy

$$D = D_0 + \sum_j \frac{h\nu_j}{2}$$

Contributions from low (less than 20 1/cm) frequencies to entropy, heat capacity and internal energy are excluded from the total values, but they are listed separately (so the user can add them if they wish).

As an alternative to outright excluding low-frequency contributions, a correction scheme is available that is based on interpolating between harmonic oscillator and free rotor values⁷⁸ (Li/Head-Gordon and Grimme). It can greatly reduce the impact of the inaccuracies of the harmonic oscillator model on thermodynamic properties at these low frequencies. The scheme corrects vibrational contributions to entropies, internal energies and constant volume heat capacities. This correction is applied automatically and its results are printed separately (in the text output, the corrected terms are marked with the symbol (c)). When applied, the correction considers all real frequencies, including those less than 20 1/cm.

The interpolation for a corrected thermodynamic property f at pressure p and temperature T in terms of harmonic oscillator terms f_{HO} , free rotor terms f_{FR} , and interpolator terms x for each harmonic oscillator frequency ν_j is:

$$f(p, T) = \sum_j x(\nu_j) \cdot f_{HO}(p, T, \nu_j) + (1 - x(\nu_j)) \cdot f_{FR}(p, T, \nu_j)$$

$$x(\nu_j) = \frac{1}{1 + \left(\frac{\nu_0}{\nu_j}\right)^\alpha}$$

Where α is an arbitrary exponent and ν_0 is the harmonic oscillator frequency around which x interpolates, with $x = 0.5$ when $\nu_j = \nu_0$ and $x \approx 1.0$ when $\nu_j \gg \nu_0$.

While the free rotor terms used for internal energies and heat capacities are the standard ones, the terms used for entropies have to use the rotors’ moments of inertia μ_{FR} and symmetry σ , which formally cannot be calculated from harmonic frequencies alone. The correction scheme instead estimates each moment of inertia as being of a $\sigma = 1$ free rotor whose first excited state has an energy equal to the given $h\nu_j$. After this, each obtained moment of inertia μ_{FR} is modified by an averaging moment of inertia μ_{av} to avoid grossly overestimating entropies at very small frequencies (less than around 1 1/cm):

$$\mu = \frac{\mu_{FR} \cdot \mu_{av}}{\mu_{FR} + \mu_{av}}$$

Input options

⁷ Yi-Pei Li, Joseph Gomes, Shaama Mallikarjun Sharada, Alexis T. Bell, Martin Head-Gordon, *Improved Force-Field Parameters for QM/MM Simulations of the Energies of Adsorption for Molecules in Zeolites and a Free Rotor Correction to the Rigid Rotor Harmonic Oscillator Model for Adsorption Enthalpies*, J. Phys. Chem. C 2015, 119, 4, 1840-1850 (<https://doi.org/10.1021/jp509921r>)

⁸ Stefan Grimme, *Supramolecular Binding Thermodynamics by Dispersion-Corrected Density Functional Theory*, Chem. Eur. J., 18: 9955-9964 (<https://doi.org/10.1002/chem.201200497>)

```

Thermo
  Temperatures float_list
  Pressure float
  LowFrequencyCorrector
    Alpha float
    Frequency float
    MomentOfInertia float
  End
End

```

Thermo**Type** Block**Description** Options for thermodynamic properties (assuming an ideal gas). The properties are computed for all specified temperatures.**Temperatures****Type** Float List**Default value** [298.15]**Unit** Kelvin**Description** List of temperatures at which the thermodynamic properties will be calculated.**Pressure****Type** Float**Default value** 1.0**Unit** atm**Description** The pressure at which the thermodynamic properties are computed.**LowFrequencyCorrector****Type** Block**Description** Options for the dampener-powered free rotor interpolator that corrects thermodynamic quantities for low frequencies. See DOI:10.1021/jp509921r and DOI:10.1002/chem.201200497.**Alpha****Type** Float**Default value** 4.0**Description** The exponent term used in the dampener.**Frequency****Type** Float**Default value** 100.0**Unit** cm-1**Description** The frequency around which the dampener interpolates between harmonic oscillator and free rotor quantities.**MomentOfInertia****Type** Float

Default value 1e-44**Unit** kg m²**GUI name** Averaging Moment of Inertia**Description** The moment of inertia used to restrict entropy results for very small frequencies (generally around less than 1 cm⁻¹).

Gibbs free energy change for a gas phase reaction

Here an example is given how to calculate the free energy change for a reaction. In the AMS output of a normal modes calculation you can find the electronic bonding energy and nuclear kinetic energies, at room temperature. Example part of the AMS output of a nonlinear molecule:

```

Zero-point energy (Hartree):      0.0333

...
...

Temp                                Transl      Rotat      U
↪Vibrat      Total                                -----
-----
↪--      -----
298.15      Entropy (cal/mol-K):      34.441      11.474      0.
↪137      46.052
Nuclear Internal Energy (kcal/mol):      0.889      0.889      20.
↪941      22.718
Constant Volume Heat Capacity (cal/mol-K):      2.981      2.981      0.
↪565      6.526

Summary of energy terms
                                hartree              eV              kcal/
↪mol              kJ/mol              -----              -----              -----
↪
Energy from Engine:      -0.743995039793930      -20.2451      -466.
↪86      -1953.36
Nuclear Internal Energy:      0.036203917534227      0.9852      22.
↪72      95.05
Internal Energy U:      -0.707791122259703      -19.2599      -444.
↪14      -1858.31
pV/n = RT:      0.000944186013486      0.0257      0.
↪59      2.48
Enthalpy H:      -0.706846936246217      -19.2343      -443.
↪55      -1855.83
-T*S:      -0.021880868282982      -0.5954      -13.
↪73      -57.45
Gibbs free energy:      -0.728727804529199      -19.8297      -457.
↪28      -1913.27

```

The Energy from Engine = -466.86 kcal/mol. It depends on the engine how this energy is calculated. In the ADF and BAND engines the energy is normally calculated with respect to (artificial) spherical averaged neutral atoms.

The Nuclear Internal Energy = zero point energy + 3 kT + small correction term = 22.72 kcal/mol. 3 kT = 3/2 kT for rotation, and 3/2 kT for translation (i.e. 1/2 kT for each degree of freedom). The small correction term is a term due to

the vibration partition function, depending on the temperature not only the ground state vibrational levels are occupied, see also the previous discussion.

The Internal Energy $U = \text{Energy from Engine} + \text{Nuclear Internal Energy} = -466.86 + 22.72 = -444.14$ kcal/mol. Gas phase $pV/n = RT = 8.314472 * 298.15 / 4184 = 0.59$ kcal/mol. The enthalpy $H = U + pV = -444.14 + 0.59 = -443.55$ kcal/mol. The Gibbs free energy $G = H - TS = -443.55 - 298.15 * 46.052 / 1000 = -457.28$ kcal/mol.

For a calculation of the free energy change for reaction (ΔG), you will have to do this for the reactant and product molecules, and add and subtract these energies, for each molecule proportional to the number of molecules that take place in the reaction. Application of ADF for obtaining enthalpy, entropy and Gibbs free energy can for instance be obtained in Refs.^{9,10}.

6.2.9 Moments of inertia

In case normal modes are computed in AMS, AMS also reports the moments of inertia of the molecule in units of amu bohr² (amu = atomic mass unit) and its corresponding principal axes.

6.2.10 Partial Vibrational Spectra (PVDOS)

The Partial Vibrational Spectra (also known as PVDOS) is computed by default whenever normal modes are requested. The PVDOS $P_{I,n}$ for atom I and normal mode n is defined as:

$$P_{I,n} = \frac{m_I |\vec{\eta}_{I,n}|^2}{\sum_J m_J |\vec{\eta}_{J,n}|^2}$$

where m_I is the nuclear weight of atom I , and $\vec{\eta}_{I,n}$ is the displacement vector for atom I in normal mode n .

Tip: The Partial Vibrational Spectra (PVDOS) can be visualized using the **AMSspectra** GUI module (**Vibrations** → **Partial Vibrational Spectra (PVDOS)**). When plotting a partial vibrational spectrum, the IR intensity of normal modes is scaled by the corresponding PVDOS of the selected atoms.

The PVDOS matrix is not printed to the text output, but only saved to the engine binary output (.rkf) in the variable `Vibrations%PVDOS`.

6.3 Phonons

Collective oscillations of atoms around their equilibrium positions, giving rise to lattice vibrations, are called phonons. AMS can calculate phonon dispersion curves within standard harmonic theory, implemented with a finite difference method. Within the harmonic approximation we can calculate the partition function and therefore thermodynamic properties, such as the specific heat and the free energy.

See also:

Example: Phonons for graphene (page 466), *Example: Phonons with isotopes* (page 467), *Example: User-defined Brillouin zone for phonon dispersion* (page 469) and *silicon lattice optimization and phonons tutorial*

The calculation of phonons is enabled in the `Properties` block.

⁹ M. Swart, E. Rösler, and F. M. Bickelhaupt, *Proton affinities of maingroup-element hydrides and noble gases: Trends across the periodic table, structural effects, and DFT validation*, *Journal of Computational Chemistry* 27, 1486 (2006) (<https://doi.org/10.1002/jcc.20431>)

¹⁰ M. Swart, and F. M. Bickelhaupt, *Proton Affinities of Anionic Bases: Trends Across the Periodic Table, Structural Effects, and DFT Validation*, *Journal of Chemical Theory and Computation* 2, 281 (2006) (<https://doi.org/10.1021/ct0502460>).

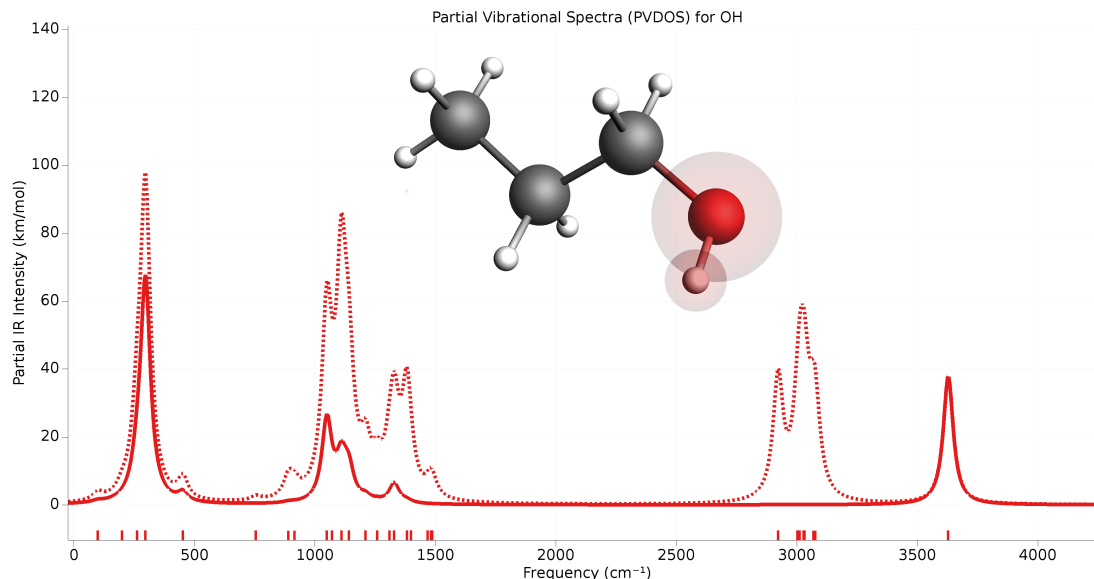


Fig. 6.1: Example of partial vibrational spectrum (PVDOS). The dotted line is the full IR spectrum of 1-propanol. The solid line is the PVDOS-scaled IR spectrum of the OH group (IR spectrum computed using GFN1-xTB).

```
Properties
  Phonons Yes/No
End
```

Note: Phonon calculations should be performed on optimized geometries, **including the lattice vectors**. This can be done by either using an already optimized system as input, or by combining the phonon calculation with the *geometry optimization task* (page 47) (you should set the `GeometryOptimization%OptimizeLattice` input option to `True`).

The details of the phonon calculations are configured in the `NumericalPhonons` block:

```
NumericalPhonons
  SuperCell # Non-standard block. See details.
  ...
End
  StepSize float
  DoubleSided Yes/No
  Interpolation integer
  NDosEnergies integer
  AutomaticBZPath Yes/No
  BZPath
    Path # Non-standard block. See details.
    ...
  End
End
Parallel
  nCoresPerGroup integer
  nGroups integer
  nNodesPerGroup integer
End
```

(continues on next page)

(continued from previous page)

End

NumericalPhonons**SuperCell****Type** Non-standard block**Description** Used for the phonon run. The super lattice is expressed in the lattice vectors. Most people will find a diagonal matrix easiest to understand.

The most important setting here is the super cell transformation. In principle this should be as large as possible, as the phonon bandstructure converges with the size of the super cell. In practice one may want to start with a 2x2x2 cell and increase the size of the super cell until the phonon band structure converges:

```
NumericalPhonons
  SuperCell
    2 0 0
    0 2 0
    0 0 2
  End
End
```

By default the phonon dispersion curves are computed for the standard path though the Brillouin zone (see <https://doi.org/10.1016/j.commatsci.2010.05.010>). One can request the a different path using the following keywords (for an example of how to specify a user-defined path see *Example: User-defined Brillouin zone for phonon dispersion* (page 469)):

```
NumericalPhonons
  AutomaticBZPath Yes/No
  BZPath
    Path # Non-standard block. See details.
    ...
  End
End
End
```

NumericalPhonons**AutomaticBZPath****Type** Bool**Default value** Yes**GUI name** Automatic BZ path**Description** If True, compute the phonon dispersion curve for the standard path through the Brillouin zone. If False, you must specify your custom path in the [BZPath] block.**BZPath****Type** Block**Description** If [NumericalPhonons%AutomaticBZPath] is false, the phonon dispersion curve will be computed for the user-defined path in the [BZPath] block. You should define the vertices of your path in fractional coordinates (with respect to the reciprocal lattice vectors) in the [Path] sub-block. If you want to make a jump in your path (i.e. have a discontinuous path), you need to specify a new [Path] sub-block.**Path**

Type Non-standard block

Recurring True

Description A section of a k space path. This block should contain multiple lines, and in each line you should specify one vertex of the path in fractional coordinates. Optionally, you can add text labels for your vertices at the end of each line.

Other keywords in the `NumericalPhonons` block modify the details of the numerical differentiation procedure and the accuracy of the results:

NumericalPhonons

StepSize

Type Float

Default value 0.04

Unit Angstrom

Description Step size to be taken to obtain the force constants (second derivative) from the analytical gradients numerically.

DoubleSided

Type Bool

Default value Yes

Description By default a two-sided (or quadratic) numerical differentiation of the nuclear gradients is used. Using a single-sided (or linear) numerical differentiation is computationally faster but much less accurate. Note: In older versions of the program only the single-sided option was available.

Interpolation

Type Integer

Default value 100

Description Use interpolation to generate smooth phonon plots.

NDosEnergies

Type Integer

Default value 1000

Description Nr. of energies used to calculate the phonon DOS used to integrate thermodynamic properties. For fast compute engines this may become time limiting and smaller values can be tried.

The numerical phonon calculation supports AMS' *double parallelization* (page 21), which can perform the calculations for the individual displacements in parallel. This is configured automatically, but can be further tweaked using the keys in the `NumericalPhonons%Parallel` block:

```
NumericalPhonons
  Parallel
    nCoresPerGroup integer
    nGroups integer
    nNodesPerGroup integer
  End
End
```

NumericalPhonons

Parallel**Type** Block**Description** Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.**nCoresPerGroup****Type** Integer**GUI name** Cores per group**Description** Number of cores in each working group.**nGroups****Type** Integer**GUI name** Number of groups**Description** Total number of processor groups. This is the number of tasks that will be executed in parallel.**nNodesPerGroup****Type** Integer**GUI name** Nodes per group**Description** Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

6.4 (Resonance) Raman

6.4.1 Raman

In this method the Raman scattering spectrum is calculated from the geometrical derivatives of the frequency-dependent polarizability. Engine ADF is required. Raman scattering intensities and depolarization ratios for all or a selected number of molecular vibrations at a certain laser frequency can be calculated. The Raman scattering calculation is very similar to an IR intensity calculation. In fact, all IR output is automatically generated as well. At all distorted geometries the dipole polarizability tensor is calculated. This is time-consuming and is only feasible for small molecules.

```
Properties
  Raman Yes/No
End
```

```
Raman
  IncidentFrequency float
  FreqRange float_list
End
```

If a `FreqRange` is included the Raman intensities are calculated for a range of vibrational frequencies only. Using this option is a fast alternative for calculating all Raman intensities.

Note that in order to change the nuclear step size that is used in calculating the numerical derivative of the polarizability in case of `FreqRange` one should use `VibrationalAnalysis%Displacement` and `NumericalDiffer-`

entiation%NuclearStepSize otherwise. A larger value for the nuclear step size may be needed since it is harder to calculate the polarizability with enough precision than, for example, the dipole moment.

Properties

Raman

Type Bool

Default value No

Description Requests calculation of Raman intensities for vibrational normal modes.

Raman

IncidentFrequency

Type Float

Default value 0.0

Unit eV

Description Frequency of incident light.

FreqRange

Type Float List

Unit cm-1

Recurring True

GUI name Frequency range

Description Specifies a frequency range within which all modes will be scanned. 2 numbers: an upper and a lower bound.

6.4.2 Resonance Raman: excited-state finite lifetime

Resonance Raman spectroscopy uses incident light with a wavelength close to that of an electronic transition. In this method (Ref.¹¹) the resonance Raman-scattering (RRS) spectra is calculated from the geometrical derivatives of the frequency-dependent polarizability. Engine ADF is required. The polarizability derivatives are calculated from resonance polarizabilities by including a finite lifetime (phenomenological parameter) of the electronic excited states.

```
Raman
  FreqRange float_list
  IncidentFrequency float
  LifeTime float
End
```

Raman

FreqRange

Type Float List

Unit cm-1

Recurring True

GUI name Frequency range

¹¹ L. Jensen, L. Zhao, J. Autschbach and G.C. Schatz, *Theory and method for calculating resonance Raman scattering from resonance polarizability derivatives*, Journal of Chemical Physics 123, 174110 (2005) (<https://doi.org/10.1063/1.2046670>)

Description Specifies a frequency range within which all modes will be scanned. 2 numbers: an upper and a lower bound.

IncidentFrequency

Type Float

Default value 0.0

Unit eV

Description Frequency of incident light.

LifeTime

Type Float

Default value 0.0

Unit hartree

Description Specify the resonance peak width (damping) in Hartree units. Typically the lifetime of the excited states is approximated with a common phenomenological damping parameter. Values are best obtained by fitting absorption data for the molecule, however, the values do not vary a lot between similar molecules, so it is not hard to estimate values. A typical value is 0.004 Hartree.

It is similar to the simple excited-state gradient approximation method (see next section) if only one electronic excited state is important, however, it is not restricted to only one electronic excited state. In the limit that there is only one possible state in resonance the two methods should give more or less the same results. However, for many states and high-energy states and to get resonance Raman profiles (i.e., Raman intensities as a function of the energy of the incident light beam) this approach might be more suitable. The resonance Raman profiles in this approach are averaged profiles since vibronic coupling effects are not accounted for.

6.4.3 Resonance Raman: VG-FC

According to a the time-dependent picture of resonance-Raman (RR) scattering the relative intensities of RR scattering cross sections are, under certain assumptions, proportional to the square of the excited-state energy gradients projected onto the ground-state normal modes of the molecule (see Ref.¹²). For an alternative implementation of RR scattering using a finite lifetime of the excited states, and a discussion of some of the differences, see the previous section. Engine ADF or DFTB is required.

The vertical gradient Franck-Condon (VG-FC) method, also called the Independent Mode Displaced Harmonic Oscillator (IMDHO) model, we use to calculate vibrationally resolved absorption spectra can also be applied to the calculation of resonance Raman spectra. In resonance Raman spectroscopy a molecule is excited from its ground state to some electronically excited state. After a short period of time, the molecule then relaxes back to its electronic ground state. However, when doing so, it might end up in a different vibrational state than it started off in. The result is an energy difference between the incident and emitted photon. One can then plot the intensity for different energy differences to produce what is known as a Raman spectra. Resonance Raman spectroscopy uses incident light with a wavelength close to that of an electronic transition.

AMS supports the calculation of such spectra by modeling the vibronic coupling of electronic transitions using the VG-FC model. This model is discussed also on the *Vibronic-Structure* (page 234) documentation page. Here we will discuss the modifications necessary to use the VG-FC model for resonance Raman spectroscopy. It is worth noting that this VG-FC resonance Raman application does not support the mode selective options. As a result the VG-FC Resonance Raman application will always first perform a full frequency analysis to obtain its normal modes.

¹² J. Neugebauer, E.J. Baerends, E. Efremov, F. Ariese and C. Gooijer, *Combined Theoretical and Experimental Deep-UV Resonance Raman Studies of Substituted Pyrenes*, *Journal of Physical Chemistry A* 109, 2100 (2005) (<https://doi.org/10.1021/jp045360d>)

Theory

While the basic theory behind the VG-FC model is explained in detail on the *Vibronic-Structure* (page 234) documentation page, we will briefly summarize the most important points here, as well as the modifications necessary for its application to resonance Raman spectroscopy. It applies the harmonic approximation to both the ground state and excited state PES and then goes on to assume that neither frequency changes nor normal mode rotations occur. Thus the excited state PES is a shifted version of the ground state PES. We do not include temperature effects (so all initial states will be ground states) and work at the Franck-Condon point. Under these assumptions, the Raman polarizability of a particular excited state n , for a transition between initial and final vibrational states I and F can be written as:

$$(\alpha_{n,ij})_{F \leftarrow I} = \mu_{n,i} \mu_{n,j} \int_0^\infty \langle F | I_n(t) \rangle e^{i[\omega - (E_{n,0} - E_{m,0})]t} \cdot e^{-\Gamma t} dt$$

Here, i, j label the components of the polarizability tensor and $\langle F | I_n(t) \rangle$ denotes the overlap of the initial state I , propagated along the excited state PES with the final state F . Under the *assumptions of the VG-FC model* (page 224), this overlap is equal to:

$$\langle F | I_n(t) \rangle = \prod_{j=1}^{N_{modes}} \left\{ \frac{(-1)^{m_j} \Delta_{n,j}^{m_j}}{2^{m_j/2} m_j!} (1 - e^{-i\omega_j t})^{m_j} \right\} \exp \left[-\frac{\Delta_{n,j}^2}{2} (1 - e^{-i\omega_j t}) \right]$$

Where the m_j denote the excitation number of mode j in final state F . For a more detailed discussion, we refer to¹³. The only parameters that appear in our expression are the dimensionless oscillator displacements $\Delta_{n,j}$ that represent displacement of the excited state PES along normal mode j . Under the simplifying assumptions of the VG-FC, these can be obtained from the ground state normal modes and a single excited state gradient. The Raman intensity is then proportional to the square of the polarizabilities:

$$\sigma(\omega)_{F \leftarrow I} \propto \sum_{i,j} \left| \sum_n (\alpha_{n,ij})_{F \leftarrow I} \right|^2$$

A spectrum is then generated by including various different final states F , which are defined by different combinations of normal mode excitation numbers, and assigning a relative intensity to each transition equal to the above expression. AMS only supports spectra which display relative intensities so the results are plotted in arbitrary units and are normalized such that the largest peak reaches an intensity of 1.

Input

The calculation setup for resonance Raman spectra largely proceeds as it does for *Absorption Spectra* (page 234). We need a set of ground state normal modes as well as an excited state gradient. The former are calculated at the start using the selected AMS engine, or, in case the user has a pre-calculated set of normal modes, these can be read from a .rkf file using the `ModeFile` key in the `NormalModes` sub-block. In this latter case, the engine is not used. The `ModeSelect` block can be used to select specific modes from the full set of normal modes for which the spectrum should be calculated. For details see the *Mode Select* (page 207) documentation on the main page. If one simply wants the spectrum for the full set of normal modes, the `Full` key in the `ModeSelect` block can be set to `True`. The excited state information is passed to the application via the `ExcitationSettings` block.

Another point to note is that since our states are labeled by discrete indices we will be calculating stick spectra (which can be homogeneously broadened in `amspectra`). By contrast, the absorption spectra produced by `VibronicStructure` are raw x,y data. Due to this difference in nature of the Raman spectrum compared to the absorption spectrum, this method uses the `ResonanceRaman` block for input options related to its spectrum (as opposed to the `Absorption-Spectrum` block).

The `ExcitationSettings` block is discussed on the *Vibronic-Structure* (page 241) page. One important difference with the latter is that Resonance Raman calculations are supported for more than one excitation at once. This is more

¹³ T. Petrenko and F. Neese, *Analysis and prediction of absorption band shapes, fluorescence band shapes, resonance Raman intensities, and excitation profiles using the time-dependent theory of electronic spectroscopy* The Journal of Chemical Physics 127, 164319 (2007) (<https://doi.org/10.1063/1.2770706>)

important for the case of Raman spectra as the intensity associated with a set of transitions is not equal to the sum of their individual intensities (we sum over electronic states n before we square the polarizabilities). Here we will address settings specific to the Raman spectrum, all of which can be found in the `ResonanceRaman` block. A short example of how a typical input file might look is included at the end of this section.

```
Task VibrationalAnalysis
VibrationalAnalysis
  Task ResonanceRaman
  ResonanceRaman
    IncidentFrequency float
    LifeTime float
    RamanOrder integer
    RamanRange float_list
    MaximumStates integer
  End
  ...
End
```

IncidentFrequency float Frequency of incident light.

LifeTime float sets the value of Γ (in Hartree) that controls the exponential damping in our integral. This phenomenological parameter can be interpreted as the (inverse) life time of the Raman excited state and can be used to help the results agree with experiment. The default value of $4.5e-4$ is on the low end of reasonable values but should provide a good starting point for most cases.

RamanOrder integer determines the set of final states and overtones to be included in the spectrum. It is an integer and the application considers only final states such that the sum of excitation numbers of all normal modes is less than or equal to this number. Setting this to 1 means we only include the fundamental band.

RamanRange float_list this keyword specifies the frequency range (in cm^{-1}) the Raman shift is restricted to lie in. This prevents us from including excessively many states and overtones for high frequency modes. The default is $[0, 2000] cm^{-1}$ but this can be changed to whatever is desired.

MaximumStates integer Expert key. Due to the combinatorial explosion of included final states that occurs for combinations of large values of the raman order, large molecules and wide spectrum ranges, there is a maximum number of final states that can be included in the spectrum. This is to prevent the program from using excessive amounts of memory/computation times. The user can set this number using the `MaximumStates` key but this should be done with caution.

Finally we give an example of a typical `VibrationalAnalysis` block for a resonance Raman calculation. This also gives an idea of how the settings that were not explicitly mentioned above work:

```
VibrationalAnalysis
  Type ResonanceRaman
  NormalModes
    ModeSelect
      Full True
    End
  End
  ExcitationSettings
    ExcitationInfo File
    ExcitationFile ./your_excitation/dftb.rkf
    Singlet
      A 1 2 4
    End
  End
  ResonanceRaman
    RamanOrder 3
```

(continues on next page)

(continued from previous page)

```
RamanRange 0.0 3000.0
End
End
```

6.5 VROA: (Resonance) vibrational Raman optical activity

The normal and resonance VROA spectra are calculated from geometric derivatives of the different generalized polarizabilities obtained using linear response theory which may include a damping term to account for the finite lifetime. Engine ADF is required. These polarizabilities are the electric dipole - electric dipole polarizability, the electric dipole - magnetic dipole polarizability, and the the electric dipole - electric quadrupole polarizability. For resonance VROA one should include a finite lifetime.

```
Properties
  VROA Yes/No
End
```

```
Raman
  FreqRange float_list
  IncidentFrequency float
  LifeTime float
End
```

Properties

VROA

Type Bool

Default value No

Description Requests calculation of VROA for vibrational normal modes.

Raman

FreqRange

Type Float List

Unit cm-1

Recurring True

GUI name Frequency range

Description Specifies a frequency range within which all modes will be scanned. 2 numbers: an upper and a lower bound.

IncidentFrequency

Type Float

Default value 0.0

Unit eV

Description Frequency of incident light.

LifeTime

Type Float

Default value 0.0

Unit hartree

Description Specify the resonance peak width (damping) in Hartree units. Typically the lifetime of the excited states is approximated with a common phenomenological damping parameter. Values are best obtained by fitting absorption data for the molecule, however, the values do not vary a lot between similar molecules, so it is not hard to estimate values. A typical value is 0.004 Hartree.

6.5.1 Engine ADF

In the ADF engine a method is implemented to calculate both on- and off-resonance vibrational Raman optical activities (VROAs) of molecules using time-dependent density functional theory, see Ref.¹⁴. This is an extension of a method to calculate the normal VROA by including a finite lifetime of the electronic excited states in all calculated properties. The method is based on a short-time approximation to Raman scattering and is, in the off-resonance case, identical to the standard theory of Placzek. The normal and resonance VROA spectra are calculated from geometric derivatives of the different generalized polarizabilities obtained using linear response theory which includes a damping term to account for the finite lifetime. Gauge-origin independent results for normal VROA have been ensured using either the modified-velocity gauge or gauge-included atomic orbitals. In ADF2016 the velocity gauge tensors required for the calculation of VROA are now correctly calculated with the life time damping parameter. With these complex tensors fixed, resonance VROA intensities are now origin invariant in the velocity gauge, see also Ref.¹⁵.

6.6 VCD: Vibrational Circular Dichroism

Vibrational circular dichroism (VCD) is the differential absorption of left and right circularly polarized infrared light by vibrating molecules. Most engines can be used to calculate VCD with the approximate Atomic polar tensor (APT) model. Engine ADF is required for the more accurate analytical VCD.

```
Properties
  VCD Yes/No
End
```

Properties

VCD

Type Bool

Default value No

Description Requests calculation of VCD for vibrational normal modes.

VCDtools (page 301) is a program that can be used to do an analysis of the VCD spectrum. *VCDtools* (page 301) can be used with the AMS-GUI module AMSspectra.

¹⁴ L. Jensen, J. Autschbach, M. Krykunov, and G.C. Schatz, *Resonance vibrational Raman optical activity: A time-dependent density functional theory approach*, *Journal of Chemical Physics* 127, 134101 (2007) (<https://doi.org/10.1063/1.2768533>)

¹⁵ D.V. Chulhai and L. Jensen, *Simulating Surface-Enhanced Raman Optical Activity Using Atomistic Electrodynamics-Quantum Mechanical Models*, *Journal of Physical Chemistry A* 118, 9069 (2014) (<https://doi.org/10.1021/jp502107f>)

6.6.1 Atomic polar tensor (APT) model

In the so-called atomic polar tensor (APT) model the atomic axial tensors (AATs) can be calculated from electric dipole gradients. Note that the APT model may not be very reliable for predicting VCD bands and its implementation should not be blindly applied beyond a quick assessment. Results using the engine DFTB can be found in¹⁶.

For the engines BAND and DFTB only the APT model can be used. In case of the engine ADF the default is to calculate the VCD analytically, see next section. One can calculate VCD using the APT model with the ADF engine if one includes:

```
NormalModes
  Hessian Numerical
End
```

6.6.2 Analytical VCD in ADF

In the ADF engine the VCD intensities are calculated using Stephens' equations for VCD. For the calculation of the atomic axial tensors (AATs), analytical derivatives techniques and London atomic orbitals (the so called GIAO) are employed. As a result the calculated rotational strengths are origin independent, and therefore the common origin gauge is used¹⁷.

New in AMS2020 is that one can calculate analytical VCD also for open-shell systems in a spin-unrestricted calculation.

Calculation of the AATs requires an analytical frequencies calculation. This limits the choice of functionals that can be used for VCD calculations.

The accuracy of the vibrational rotational strengths are determined by the accuracy of the harmonic force field, atomic polar tensors (APTs) and AATs. The most critical parameter being the harmonic force field. Thus, for a fair comparison with experimental data, accurate geometries and functionals that yield accurate force fields (e.g. BP86, OLYP, etc) should be used. Our tests showed that the BP86 functional in combination with TZP basis sets is always a safe choice. For a comparison of VCD spectra calculated with various functionals (e.g BP86, OLYP, BLYP, B3PW91 and B3LYP) see⁷. Regarding the geometries, we recommend the following strict settings, 10^{-4} for the geometry convergence of the gradients, and BeckeGrid quality good. The default settings should be used for the calculation of the frequencies.

By default, only the vibrational rotational strengths are printed in the AMS output file. For a deeper insight regarding the origin of the VCD intensity of a given normal mode one can use the auxiliary program *VCDtools* (page 301). *VCDtools* (page 301) can be used with the ADF-GUI module ADFspectra.

6.7 Vibrational Polarizabilities

If IR intensities are available it is possible to calculate the pure vibrational component for static electric polarizabilities¹⁸ of the system. The tensor can be expressed as a sum-over-state that runs over all normal vibrational modes j :

$$\alpha_{\alpha,\beta}^{vib} = \frac{2}{\hbar} \sum_j \frac{1}{\omega_j} \langle 0 | \mu_\alpha | j \rangle \langle j | \mu_\beta | 0 \rangle$$

Where Q_j are the normal mode coordinates, ω_j are the normal modes angular frequencies, and the bracket notation is used for the system's vibrational states. The full polarizability tensor is printed in atomic units along with the isotropic average of the tensor.

¹⁶ T.Q. Teodoro, M.A.J. Koenis, R. Ruger, S.E. Galembeck, W.J. Buma, V.P. Nicu, L. Vissche, *Use of Density Functional Based Tight Binding Methods in Vibrational Circular Dichroism*, *Journal of Physical Chemistry A* 122, 9435 (2018) (<https://doi.org/10.1021/acs.jpca.8b08218>)

¹⁷ V.P. Nicu J. Neugebauer S.K. Wolff and E.J. Baerends, *A vibrational circular dichroism implementation within a Slater-type-orbital based density functional framework and its application to hexa- and hepta-helicenes*, *Theoretical Chemical Accounts* 119, 245 (2008) (<https://doi.org/10.1007/s00214-006-0234-x>)

¹⁸

M. J. Cohen, A. Willetts, R. D. Amos, and N. C. Handy, *Vibrational contributions to static polarizabilities and hyperpolarizabilities*, *Journal of Chemical Physics* 100, 4467 (1994) (<https://doi.org/10.1063/1.474503>)

VIBRATIONALLY RESOLVED ELECTRONIC SPECTRA

7.1 AH-FC: Adiabatic Hessian Franck-Condon

Electronic spectra, such as absorption, emission, phosphorescence, and ionization, may contain a vibrational structure.

In the Adiabatic Hessian Franck-Condon (AH-FC) method one needs to do a frequency calculation both at the ground state as well as the excited state of interest. The model makes the following assumptions:

- 1. It employs the adiabatic (Born-Oppenheimer) approximation and treats the nuclei as moving in an effective potential defined by the electronic configuration.
- 2. It works at the Franck-Condon (FC) point and assumes that the transition occurs at the ground state equilibrium structure for absorption and at the excited state equilibrium structure for emission.
- 3. It applies the harmonic approximation to both the ground and excited state potential energy surfaces.

Franck-Condon factors can be calculated for the transition between the two electronic states, which can be done with the *FCF Module* (page 225), described below. These Franck-Condon factor can then be used to predict the relative intensities of absorption or emission lines in the electronic spectra. Note that the Herzberg-Teller effect is not taken into account.

In the vertical gradient Franck-Condon (VG-FC) method some extra assumptions are made compared to the AH-FC method. This approach is particularly effective for large molecules as it shows linear scaling with the number of normal modes.

- See the documentation of the *VG-FC method* (page 234).

7.1.1 FCF module: Franck-Condon Factors

fcf is an auxiliary program which can be used to calculate Franck-Condon factors from two vibrational mode calculations¹. The program assumes that the starting vibrational wavefunction is in the ground state, as is the case for most spectroscopic experiments performed at room temperature.

fcf requires an ASCII input file where the user specifies the .rkf files from two vibrational mode calculations, carried out for two different electronic, spin or charge states of the same molecule. These calculations can be either numerical or analytical.

fcf produces a (binary) KF file TAPE61, which can be inspected using the KF utilities. Furthermore, *fcf* writes the frequencies, vibrational displacements and electron-phonon couplings for both states too the standard output, including any error messages.

In AMS2022 the algorithm for the calculation of the Franck-Condon factors has been changed in order to improve the precision, increase the speed, and lower the memory requirements.

¹ J.S. Seldenthuis, H.S.J. van der Zant, M.A. Ratner and J.M. Thijssen, *Vibrational Excitations in Weakly Coupled Single-Molecule Junctions: A Computational Analysis*, ACS Nano 2, 1445 (2008) (<https://doi.org/10.1021/nn800170h>)

Theory

Franck-Condon factors are the squares of the overlap integrals of vibrational wave functions. Given a transition between two electronic, spin or charge states, the Franck-Condon factors represent the probabilities for accompanying vibrational transitions. As such, they can be used to predict the relative intensities of absorption or emission lines in spectroscopy or excitation lines in transport measurements.

When a molecule makes a transition to another state, the equilibrium position of the nuclei changes, and this will give rise to vibrations. To determine which vibrational modes will be active, we first have to express the displacement of the nuclei in the normal modes:

$$\mathbf{k} = \mathbf{L}'^T \mathbf{m}^{1/2} (\mathbf{B}_0 \mathbf{x}_0 - \mathbf{x}'_0)$$

Here, \mathbf{k} is the displacement vector, \mathbf{L} is the normal mode matrix, \mathbf{m} is a matrix with the mass of the nuclei on the diagonal, \mathbf{B} is the zero-order axis-switching matrix and \mathbf{x}_0 is the equilibrium position of the nuclei. For free molecules, depending on symmetry constraints, the geometries of both states may have been translated and/or rotated with respect to each other. To remove the six translational and rotational degrees of freedom, we can center the equilibrium positions around the center of mass and rotate one of the states to provide maximum overlap. The latter is included with the zero-order axis-switching matrix \mathbf{B} , implemented according to².

When we have obtained the displacement vector, it is trivial to calculate the dimensionless electron-phonon couplings. They are given by:

$$\lambda = (\hbar/2)^{1/2} \mathbf{k}$$

Here, $\hbar = 2\pi\omega/h$ is a vector containing the reduced frequencies.³ The Huang-Rhys factor \mathbf{g} is related to λ as:

$$\mathbf{g} = \lambda^2$$

The reorganization energy per mode is

$$\mathbf{E} = (h/2\pi) * \omega \lambda^2$$

When the displacement vector \mathbf{k} , the reduced frequencies \hbar and \hbar' , and the Duschinsky rotation matrix $\mathbf{J} = \mathbf{L}'^T \mathbf{B}_0 \mathbf{L}$ have been obtained, the Franck-Condon factors can be calculated using the two-dimensional array method of Ruhoff and Ratner³.

There is one Franck-Condon factor for every permutation of the vibrational quanta over both states. Since they represent transition probabilities, all Franck-Condon factors of one state which respect to one vibrational state of the other state must sum to one. Since the total number of possible vibrational quanta, and hence the total number of permutations, is infinite, in practice we will calculate the Franck-Condon factors until those sums are sufficiently close to one. Since the number of permutations rapidly increases with increasing number of vibrational quanta, it is generally possible to already stop after the sum is greater than about two thirds. The remaining one third will be distributed over so many Franck-Condon factors that their individual contributions are negligible.

In the limiting case of one vibrational mode, with the same frequency in both states, the expression for the Franck-Condon factors of transitions from the ground vibrational state to an excited vibrational state are given by the familiar expression:

$$|l_{0,n}|^2 = e^{-\lambda^2} \lambda^{2n} / n!$$

² G.M. Sando and K.G. Spears, *Ab Initio Computation of the Duschinsky Mixing of Vibrations and Nonlinear Effects*, *Journal of Physical Chemistry A* 105, 5326 (2001) (<https://doi.org/10.1021/jp004230b>)

³ P.T. Ruhoff and M.A. Ratner, *Algorithms for computing Franck-Condon overlap integrals*, *International Journal of Quantum Chemistry* 77, 383 (2000) ([https://doi.org/10.1002/\(SICI\)1097-461X\(2000\)77:1%3C383::AID-QUA383%3E3.0.CO;2-0](https://doi.org/10.1002/(SICI)1097-461X(2000)77:1%3C383::AID-QUA383%3E3.0.CO;2-0))

Algorithm

The algorithm for the calculation of the FC integrals is based on the work by Santoro et al.⁴ which is here summarized. There are in principle infinite FC factors that should be computed in order to achieve 100% convergence in the spectrum. This number is reduced by dividing the vibrational into classes.

A class is defined based on the number of simultaneously excited vibrational modes, thus a class 3 state has exactly 3 modes which are simultaneously excited, while all the remaining modes have zero quanta. The *fcf* program first evaluates the class 1 e 2 FC up to a fairly large vibrational quantum number and uses these results to infer how much each mode should be excited for the calculation of the integrals involving states of higher classes. We refer to the original paper for the details of the algorithm.

The convergence of the results after each class can be estimated by summing all FC factors, which should converge to 1 in the limit of a complete set. The program is terminated when the maximum allowed class is reached, when there is little gain from one class to the next, or when a sufficient convergence criterion is met. It should be noted that if one is interested in the overall shape of the spectrum then in most cases it isn't necessary to reach a convergence that is close to 100%.

Input

The input for *fcf* is keyword-oriented and is read from the standard input. *fcf* recognizes several keywords, but only the states have to be specified to perform the calculation. All input therefore contains at least the following lines:

```
$AMSBIN/fcf << eor
  STATE1 state1
  STATE2 state2
eor
```

The spectrum is always calculated from the ground vibrational state belonging to the potential energy surface specified by *state1* to the vibronic states belonging to *state2*. Documentation for all keys of *fcf*:

```
$AMSBIN/fcf << eor
  State1 state1
  State2 state2
  Lambda float
  Modes first last
  Rotate [True | False]
  Translate [True | False]
  NumericalQuality ["Basic" | "Normal" | "Good" | "Excellent"]
  Prescreening
    Class1 integer
    Class2 integer
    MaxClass integer
    MaxFCI integer
  End
  Spectrum FreqMin FreqMax NFreq
    LineShape ["Stick" | "Gaussian" | "Lorentzian" ]
    SpcMin float
    SpcMax float
    SpcLen integer
    HWHM float
  End
  Printing
    Verbose
```

(continues on next page)

⁴ F. Santoro, R. Improta, A. Lami, J. Bloino, V. Barone, *Effective method to compute Franck-Condon integrals for optical spectra of large molecules in solution*, J. Chem. Phys. 126, 084509 (2007) (<https://doi.org/10.1063/1.2437197>)

```

FCFThresh float
End
eor

```

Convergence**Type** Float**Description** Minimum fraction of the FC factors sum to be calculated**Lambda****Type** Float**Default value** 0.0**GUI name** Minimum coupling**Description** Optional. The minimum value of the electron-phonon coupling for a mode to be taken into account in the calculation. Together with the MODES option, this provides a way to significantly reduce the total number of Franck-Condon factors. As with the MODES option, always check if the results do not change too much.**Modes****Type** Integer List**Default value** [0, 0]**Description** Optional. The first and last mode to be taken into account in the calculation. By default, all modes are taken into account. This option can be used to effectively specify an energy range for the Franck-Condon factors. When using this option, always check if the results (electron-phonon couplings, ground state to ground overlap integral, average sum of Franck-Condon factors, etc.) do not change too much.**NumericalQuality****Type** Multiple Choice**Default value** Normal**Options** [0-0, Basic, Normal, Good, Excellent]**Description** Set the quality of several technical aspects of an FC calculation, including details for the prescreening, the amount of computed integrals, the maximum integral class evaluated, as well as the convergence criteria.**Printing****Type** Block**Description** Optional. Printing Options.**FCFThresh****Type** Float**Default value** 0.01**GUI name** FC factor threshold**Description** The minimum value for the printing of a FC factor.**Verbose****Type** Bool

Default value No

GUI name Verbose printing

Description Increase output verbosity.

Rotate

Type Bool

Default value Yes

Description Recommended to be used. Rotate the geometries to maximize the overlap of the nuclear coordinates.

Spectrum

Type Block

Description Optional. Controls the details of the spectrum calculation

HWHM

Type Float

Default value 100.0

Description Half-Width at Half-Maximum for the spectral lineshape function

LineShape

Type Multiple Choice

Default value Stick

Options [Stick, Gaussian, Lorentzian]

Description Type of lineshape function

SpcLen

Type Integer

Default value 2001

Description Number of points in the spectrum

SpcMax

Type Float

Default value 9500.0

Description Maximum absolute energy difference between the states relative to the 0-0 transition

SpcMin

Type Float

Default value -500.0

Description Minimum absolute energy difference between the states relative to the 0-0 transition

Type

Type Multiple Choice

Default value Absorption

Options [Absorption, Emission]

Description Type of spectrum

State1

Type String

Description Filename of the result files of a numerical or analytical frequency calculation for the first (initial) state.

State2

Type String

Description Filename of the result files of a numerical or analytical frequency calculation for the second (final) state.

Translate

Type Bool

Default value Yes

Description Recommended to be used. Move the center of mass of both geometries to the origin.

Only a few keys from the .rkf file are used for the calculation of the Franck-Condon factors. Disk space usage can be significantly reduced by extracting just these keys from the .rkf file before further analysis. The following shell script will extract the keys from the KF file specified by the first argument and store them in a new KF file specified by the second argument using the *cpkf* utility:

```
#!/bin/sh
cpkf $1 $2 General Molecule Vibrations
```

Result: TAPE61

After a successful calculation, *fcf* produces a TAPE61 KF file. All results are stored in the Fcf section:

contents of TAPE61	comments
lambda	the minimum value of the electron-phonon coupling
translate, rotate	whether the TRANSLATE and ROTATE options were specified in the input
natoms	number of atoms in the molecule
mass	atomic mass vector (m)
xyz1, xyz2	equilibrium geometries of both states (x ₀ and x ₀ ')
b0	zero-order axis-switching matrix matrix (B ₀)
nmodes	number of vibrational modes with a non-zero frequency
gamma1, gamma2	reduced frequencies of both states (Γ and Γ')
lmat1, lmat2	mass-weighted normal modes of both states (L and L')
jmat	Duschinsky rotation matrix (J)
kvec1, kvec2	displacement vectors for both states (k and k' , kvec1 is used for the calculation of the Franck-Condon factors)
lambda1, lambda2	electron-phonon couplings for both states (λ and λ')
i0	ground state to ground state overlap integral ($I_{0,0}$)

In addition to producing a binary TAPE61 file, *fcf* also writes the frequencies, displacement vectors and electron-phonon couplings for both states to the standard output.

7.1.2 FCF example absorption and fluorescence

In this example it is assumed that the molecule has a singlet ground state S_0 , and the interesting excited state is the lowest singlet excited state S_1 . First one needs to do a ground state geometry optimization, followed by a frequency calculation. For the ground state frequency calculation we will use `AMS_JOBNAME=S0`. Next one needs to do an excited state geometry optimization. Here it is assumed that the lowest singlet excited state S_1 is of interest:

```
AMS_JOBNAME=S1_GEO $AMSBIN/ams <<eor
...
Task GeometryOptimization
Engine ADF
...
Excitation
  Onlysing
  Lowest 1
End
ExcitedGO
  State A 1
  Singlet
End
EndEngine
eor
```

To get the frequencies for this excited state, numerical frequencies need to be calculated, at the optimized geometry of the first excited state:

```
AMS_JOBNAME=S1 $AMSBIN/ams <<eor
...
LoadSystem
  File S1_GEO.results/adf.rkf
End
Task SinglePoint
Properties
  NormalModes True
End
Engine ADF
...
Excitation
  Onlysing
  Lowest 1
End
ExcitedGO
  State A 1
  Singlet
End
EndEngine
eor
```

Next for the absorption spectrum, we look at excitations from the lowest vibrational state of the electronic ground state to the vibrational levels of the first singlet excited state S_1 ($S_1 \leftarrow S_0$), using the *FCF program* (page 225), which calculates the Franck-Condon factors between the vibrational modes of the two electronic states, with input

```
$AMSBIN/fcf << eor
STATE1 S0.results/adf.rkf
STATE2 S1.results/adf.rkf
TRANSLATE
ROTATE
eor
```

See *the description of FCF program* (page 225) for more details.

For the fluorescence spectrum, we look at excitations from the lowest vibrational state of the first singlet excited state S_1 to the vibrational levels of the singlet ground state S_0 ($S_1 \rightarrow S_0$). Input for the *FCF program* (page 225) is in this case:

```
$AMSBIN/fcf << eor
STATE1 S1.results/adf.rkf
STATE2 S0.results/adf.rkf
TRANSLATE
ROTATE
eor
```

Note that the FCF program calculates the spectrum relative to the 0-0 transition. Thus one should add to spectrum calculated with FCF the difference in energy of the lowest vibrational state of the ground state S_0 and the lowest vibrational state of the electronically singlet excited state S_1 .

7.1.3 FCF Example phosphorescence

In this example it is assumed that the molecule has a singlet ground state S_0 , and the interesting excited state is the lowest triplet excited state T_1 . Emission from a triplet state to a singlet state is spin forbidden, however, due to spin-orbit coupling such transitions may occur. In the following we assume that the geometry of the triplet excited state is not influenced much by spin-orbit coupling.

First one needs to do a the ground state geometry optimization, followed by a frequency calculation, using `AMS_JOBNAME=S0`. Next one needs to do an excited state geometry optimization of the lowest triplet excited state, followed by a frequency calculation.

```
AMS_JOBNAME=T1 $AMSBIN/ams <<eor
...
Task GeometryOptimization
Properties
  NormalModes True
End
Engine ADF
  Unrestricted
  SpinPolarization 2.0
EndEngine
eor
```

For the phosphorescence spectrum, we look at excitations from the lowest vibrational state of the first triplet excited state T_1 to the vibrational levels of the singlet ground state S_0 ($T_1 \rightarrow S_0$). Input for the *FCF program* (page 225) is in this case:

```
$AMSBIN/fcf << eor
STATE1 T1.results/adf.rkf
STATE2 S0.results/adf.rkf
TRANSLATE
ROTATE
eor
```

Note that the FCF program calculates the spectrum relative to the 0-0 transition. Thus one should add to spectrum calculated with FCF the difference in energy of the lowest vibrational state of the ground state S_0 and the lowest vibrational state of the electronically triplet excited state T_1 .

Zero field splitting (ZFS) and the radiative rate constants (i.e. radiative phosphorescence lifetimes) could be calculated with spin-orbit coupled ZORA time-dependent density functional theory (ZORA-TDDFT). With the ADF engine spin-

orbit coupling can be treated self-consistently (i.e. non perturbatively) during both the SCF and TDDFT parts of the computation.

An alternative to the use of the unrestricted formalism to calculate the lowest triplet excited state is to use the TDDFT formalism:

```
AMS_JOBNAME=T1_GEO $AMSBIN/ams <<eor
...
Task GeometryOptimization
Engine ADF
  Excitation
    Onlytrip
    Lowest 1
  End
  ExcitedGO
    State A 1
    Triplet
  End
EndEngine
eor
```

To get the frequencies for this excited state, numerical frequencies need to be calculated, at the optimized geometry of the first excited state.

```
AMS_JOBNAME=T1 $AMSBIN/ams <<eor
...
LoadSystem
  File T1_GEO.results/adf.rkf
End
Task SinglePoint
Properties
  NormalModes True
End
Engine ADF
...
  Excitation
    Onlytrip
    Lowest 1
  End
  ExcitedGO
    State A 1
    Triplet
  End
EndEngine
eor
```

7.1.4 Density of States computed with AH-FC method

The FCF module can also be used to evaluate the density of states ρ that enters the expression of the rate constant for a number of transfer phenomena based on Fermi's Golden Rule:

$$\mathbf{k} = \frac{2\pi}{\hbar} J^2 \rho$$

To calculate the transfer rate from a donor molecule to an acceptor molecule it is sufficient to employ the FCF code as described above to evaluate the emission spectrum of the donor and the absorption spectrum of the acceptor. In fact, it

can be shown⁵ that the expression for the density of states can be written as:

$$\rho = \frac{1}{\hbar} \int_{-\infty}^{+\infty} F^D(\omega) F^A(\omega) d\omega$$

Where F denotes the Franck-Condon spectrum calculated by the FCF code, specifically the absorption for the acceptor and the emission for the donor.

The convolution may be easily calculated by using the PLAMS library.

7.2 VG-FC: Vertical Gradient Franck-Condon

Electronic spectra, such as absorption, emission, phosphorescence, and ionization, may contain a vibrational structure.

In the vertical gradient Franck-Condon (VG-FC) method some extra assumptions are made compared to the Adiabatic Hessian Franck-Condon (AH-FC) method. VG-FC is also called the Independent Mode Displaced Harmonic Oscillator (IMDHO) model. The AH-FC model (used in the *FCF Module* (page 225)) makes the following assumptions:

- 1. It employs the adiabatic (Born-Oppenheimer) approximation and treats the nuclei as moving in an effective potential defined by the electronic configuration.
- 2. It works at the Franck-Condon point and assumes that the transition occurs at the ground state equilibrium structure for absorption and at the excited state equilibrium structure for emission.
- 3. It applies the harmonic approximation to both the ground and excited state potential energy surfaces.

The VG-FC model makes following additional assumptions:

- 4. It assumes the excited state PES has the same shape as that of the ground state, but it is displaced from it, i.e. both states have the same normal modes and frequencies but different equilibrium geometries.
- 5. The excited state equilibrium structure is found from a Newton-Raphson step from the ground state geometry using the excited state gradient at this point.

Under these simplifying approximations we can reduce the ingredients necessary for a spectrum calculation to an excited state gradient and a set of ground state normal modes. Furthermore it uses a time-domain description of the absorption cross-section (this introduces no further approximations) so we do not need any explicit Franck-Condon factors as is done in the *FCF Module* (page 225). This approach is particularly effective for large molecules as it shows linear scaling with the number of normal modes. Further details on how to use this method, and the VG-FC model in general can be found below.

The approximations we make remove the need for an excited state geometry optimization and frequency analysis. This means the most expensive step in a typical calculation is actually the ground state frequency analysis. The ability of Mode Tracking to generate a set of approximate normal modes, without performing a full frequency analysis can be applied to the calculation of vibrationally resolved optical spectra. This is exactly what is done in *Vibronic-Structure Tracking* (page 236). On the other hand, the ability of Mode Refinement to refine entire spectral regions at once means this method can be transferred to calculating vibrationally resolved optical spectra from a select number of (vibronically active) approximate normal modes. This idea is applied in *Vibronic-Structure Refinement* (page 237). Under suitable assumptions, the computational cost of calculating an approximation of the vibronic-structure can be reduced significantly through the use of these two methods, allowing for application to large molecules inaccessible to more detailed methods. While they are clearly best suited for these large molecules, they can also serve as an efficient method to obtain quick, first approximations for more moderately sized molecule.

With the VG-FC model one can calculate the 0-0 energy difference between the ground state and excited state. In this VG-FC method the vibrationally resolved emission spectrum will be a mirror image of the vibrationally resolved absorption spectrum, in which the 0-0 transitions are the same.

⁵ X. de Vries *High energy acceptor states strongly enhance exciton transfer between metal organic phosphorescent dyes*, *Nature Communications* 11, 1292 (2020) (<https://doi.org/10.1038/s41467-020-15034-0>)

Note: The VG-FC model uses certain approximations which may not always be valid. Something to look out for that may affect the reliability of VG-FC results are large changes in conformation upon excitation. In this case the normal modes of the excited state may be completely different from those of the ground state, at which point the model is not expected to produce reliable results. Should non-adiabatic effects become important, the BO approximation could potentially break down as well. In these cases the *FCF Module* (page 225) may provide a more suitable alternative to the VG-FC model.

See also:

Tutorials: [Resonance Raman](#), [Vibrationally resolved electronic spectra with ADF](#), [Vibrationally resolved electronic spectra with DFTB](#)

7.2.1 Theory

Here we will introduce the theory behind the model used to compute vibronic couplings. We use the so-called Vertical Gradient Franck-Condon (VG-FC) method, also called Independent Mode Displaced Harmonic Oscillator model (IMDHO). The VG-FC model as used here works as follows: The PES in the ground state is assumed parabolic (the harmonic approximation). Upon excitation, we assume that the only change to the PES that occurs is a shift in origin (i.e. no stretching or rotation of the parabolic well). This means, both the normal modes and their frequencies remain the same in both the ground and excited state. The result is that a spectrum can be calculated using only a single excited state gradient at the optimized ground state geometry. Hence we avoid the expensive excited state geometry optimization and frequency analysis used by methods such as the *FCF Module* (page 225).

Moving to a slightly more detailed discussion, we can start with an expression for the absorption cross-section in terms of a sum over contributions from different Franck-Condon factors, each homogeneously broadened with an assumed Lorentzian of linewidth Γ . For excitation from the vibrational ground state of electronic state m , to electronic state n we get the following expression (Hartree atomic units are used throughout):

$$\sigma_{n \leftarrow m}(\omega) = \frac{4\pi\omega}{3c} |\mu_{mn}|^2 \sum_{l_{n,1}} \dots \sum_{l_{n,N_{modes}}} \frac{\Gamma \prod_{i=1}^{N_{modes}} |\langle l_{n,i} | 0_{m,i} \rangle|^2}{\left(E_{n,0} + \sum_i^{N_{modes}} \omega_i l_{n,i} - E_{m,0} - \omega \right)^2 + \Gamma^2}$$

Here the μ_{mn} is the transition dipole moment and the $\prod_{i=1}^{N_{modes}} |\langle l_{n,i} | 0_{m,i} \rangle|^2$ denote the Franck-Condon factors for excitation from the vibrational ground state to the vibrationally excited state of the excited state PES, with quantum numbers $l_{n,i}$. This sum-over-states formulation is what is also used to compute the spectrum in the *FCF Module* (page 225). While efficient pre-screening and thresholding techniques can make this method applicable to moderately sized molecules, it is still quite expensive for large molecules. We can derive an expression which is equivalent to the one above, but which enjoys significant computational benefits. This is done by writing the cross-section as an integral over time:

$$\sigma_{n \leftarrow m}(\omega) = \frac{4\pi\omega}{3c} |\mu_{mn}|^2 \text{Re} \int_0^\infty \langle i | i_n(t) \rangle e^{i[\omega + E_{m,0}]t} \cdot e^{-\Gamma t} dt$$

Here, $\langle i | i_n(t) \rangle$ denotes the overlap of the initial state, propagated along the excited state PES with itself at time $t = 0$. This expression is still completely general, however, using the *assumptions of the VG-FC model* (page 224), this overlap admits a simple closed form expression:

$$\langle i | i_n(t) \rangle = \prod_{j=1}^{N_{modes}} \exp \left[-\frac{\Delta_{n,j}^2}{2} (1 - e^{-i\omega_j t}) \right] e^{-iE_{n,0}t}$$

This expression can be derived by different methods and admits a few interpretations, the details of which we will not go into here. The interested reader is referred to reference¹. Instead we will focus on its numerical implementation. The

¹ J.R. Reimers, K.R. Wilson and E.J. Heller, *Complex time dependent wave packet technique for thermal equilibrium systems: Electronic spectra* The Journal of Chemical Physics 79, 4749 (1983) (<https://doi.org/10.1063/1.445618>)

great computational advantage of this expression is that it scales only weakly with the number of degrees of freedom. Compare this with the sum-over-states formalism above, where the number of FCF's needed to have a converged sum proliferates for large molecules and the advantage becomes clear.

The $\Delta_{n,j}$ appearing in the expression are the dimensionless normal mode displacements at the equilibrium geometry in state n, compared to state m along normal mode j which has angular frequency ω_j . They represent the change in origin of the PES along a particular normal mode. These are the parameters which control the shape of the spectrum. Under the assumptions we listed above they can be calculated from the excited state energy gradient at the ground state equilibrium structure as:

$$\Delta_j = \frac{q_j^m \cdot \nabla_m E}{\omega_j^{3/2}}$$

Where we have suppressed the n subscript. The gradient is with respect to mass weighted coordinates and the q_j^m denote the mass-weighted normal modes.

Essentially, we use the (assumed) parabolic shape of the PES in the harmonic approximation along each of the normal modes to determine the displacement from the gradient projection along that mode. An important consequence of the simplified VG-FC model is that the Franck-Condon factors can be expressed in closed form:

$$|\langle l_i | 0_i \rangle|^2 = \frac{\left(\frac{\Delta_i}{2}\right)^2}{l_i!} e^{-\frac{\Delta_i^2}{2}}$$

Modes with the largest displacement are then expected to also have the largest impact on the structure of the vibrational progression in the spectrum. This gives us an obvious candidate for a tracking method to be used with the Mode Tracking protocol. This approach is taken in the *Vibronic-Structure Tracking* (page 236) module.

Theory: Vibronic-Structure Tracking

Vibronic-structure tracking (VST) is a method for obtaining quick and approximate vibrationally resolved optical spectra for larger sized molecules. It is based on the mode-tracking algorithm and works by tracking those modes that are expected to have the largest impact on the vibronic-structure of the spectrum. Its AMS implementation follows that in reference [Page 325, 1](#).

The modes that are tracked by the mode tracking routine are used to generate a UV/vis spectrum. This is done using the Vertical Gradient Franck-Condon (VG-FC) method, also called the Independent Mode Displaced Harmonic Oscillator (IMDHO) model as described on the *Vibronic-Structure* (page 234) page. This model reduces the necessary TD-DFT calculations to a single excited state gradient performed at the ground state equilibrium geometry. At this point it is typically the ground state frequency analysis which becomes the bottleneck for large molecules. Through the use of Mode Tracking we can circumvent this step and calculate only those modes which will significantly impact the vibronic fine structure. This yields a very cheap and efficient method for obtaining vibrationally resolved optical spectra.

The use of Mode Tracking within the context of vibronic-structure calculations proceeds as follows: from an initial guess for a normal mode, we construct a new basis vector which we hope will improve the quality of our initial guess. We then iteratively expand the basis by refining those modes which have the largest impact on the vibronic fine structure. We keep iterating until we deem the spectrum to be converged. We'll address the technical details of this procedure in this section.

Let us first consider how we can gauge which modes will have a large impact on our spectrum. Over on the *Vibronic-Structure* (page 234) page, we showed that according to the VG-FC model, the Franck-Condon factors can be written as:

$$|\langle l_i | 0_i \rangle|^2 = \frac{\left(\frac{\Delta_i}{2}\right)^2}{l_i!} e^{-\frac{\Delta_i^2}{2}}$$

This expression implies modes with large displacements Δ_j will have the largest Franck-Condon factors. Thus, we expect that modes with large oscillator displacements will contribute most strongly to the vibronic fine structure of the spectrum.

This suggests a tracking method in addition to those described in the *Mode Tracking* (page 199) documentation. Namely, to track the mode with the largest Δ_j . This is the only setting for the `TrackingMethod` supported by Vibronic-Structure Tracking and is automatically set when choosing Vibronic-Structure Tracking as the Vibrational Analysis type. As a reminder, the oscillator displacements can be obtained from the assumed parabolic shape of the excited state PES and the known excited state gradient:

$$\Delta_j = \frac{q_j^m \cdot \nabla_m E}{\omega_j^{3/2}}$$

This expression for our normal mode displacements suggests that a reasonable guess for a hypothetical normal mode with a large effect on the spectrum is given by the normalized excited state gradient, as this maximizes the projection.

The choice of preconditioner is of course an important one. While better preconditioners such as the Jacobi-Davidson method can lead to fast and tightly directed convergence of the modes, this may not be ideal in the case of Vibronic-Structure Tracking, as we are not necessarily focused on obtaining converged modes but rather obtaining a converged spectrum. By default the method does not use any preconditioner for generating normal modes from the residual vectors to allow the procedure to more freely explore the entire space of modes. This means that the new basis vector produced on each iteration is the (normalized) residual vector of that iteration's selected mode. Note that this is different from using the Davidson method with an identity matrix as guess for the Hessian. The user is still able to use any of the pre-conditioning options provided by the stand-alone mode tracking method, however we suggest the user uses the default \mathbb{I} (for identity) as the `UpdateMethod`. This also conveniently means no approximate Hessian is required.

It is important to choose a suitable convergence criterion. When using Vibronic-Structure Tracking, the aim is to get an approximation of the progression in the spectrum. The convergence of the modes then takes a backseat to the convergence of the spectrum. Although the two usually go hand in hand, requiring that all modes be converged in the usual mode-tracking sense is likely to be far too restrictive. Thus the convergence criterion used for VST is the following: at every iteration, the previous iteration's spectrum is subtracted from the new one. The absolute difference is then integrated on the requested frequency range. Convergence is achieved once the so-obtained number drops below a pre-set convergence threshold. The result is that it may not be the case that all modes are exact normal modes yet, however further refinement will have a limited effect on the resulting spectrum, for example due to these modes having very small Franck-Condon factors.

Convergence according to this criterion is affected by the other options that the user chooses, see the section on how the adiabatic excitation energy is calculated.

Theory: Vibronic-Structure Refinement

Vibronic-Structure Refinement takes the idea of Mode Refinement, and applies it to the calculation of vibrationally resolved optical spectra. Under the assumptions of the Vibronic-Structure application, the most time-consuming step becomes the calculation of the ground state normal modes. However, we may not be interested in all normal modes that contribute to the Vibronic fine structure of a spectrum. By using Mode Refinement we can limit ourselves to the spectral region of interest, or to modes which we expect to have the largest impact on the fine structure. The details of the Mode Refinement protocol can be found on the relevant *documentation page* (page 196).

Theory: Adiabatic excitation energy

The last aspect we will comment on here is the calculation of the adiabatic excitation energy. The number we get from an excited state calculation is the vertical excitation energy (ΔE_{vert}), this number is generally unobservable in spectra. The more interesting quantity is the adiabatic excitation energy (ΔE_{ad}). The former is the difference in energy between the two PES'es at the ground state geometry, the latter is the difference in energy between the ground and excited state vibrational ground states. Since we assumed both PES'es to have the same frequencies, the zero-point energy of the two states are the same and hence, the adiabatic energy difference is the same as the 0-0 energy difference (ΔE_{0-0}). This is simply the difference between the bottom of the two PES'es. It can be reconstructed from the excited state gradients

projected onto our normal modes, as well as their frequencies. For a molecule with N modes we obtain:

$$\Delta E_{ad} = \Delta E_{vert} - \sum_j^{N_{modes}} \frac{1}{2} \omega_j \Delta_j^2$$

Where the sum represents the reorganization energy stored in the excited oscillator modes. Depending on the desired information, one can use two different representations of the spectrum. The first is to simply plot the spectrum against an energy range with the ground state energy as an offset. This would represent a true absorption spectrum that can be compared directly with experiment. However, the energy difference $\Delta E_{vert} - \Delta E_{ad}$ in the VG-FC model is reconstructed only from the ground state equilibrium structure and can thus be somewhat unreliable. If the user is primarily interested in the shape of the spectrum, using the 0-0 excitation energy as an offset may be a more suitable choice. The latter is the default setting in AMS, but the method supports both options.

Note that in case of a Vibronic-structure tracking (VST) calculation we only have access to a small set of approximate normal modes, we will have an approximation of ΔE_{ad} that changes from iteration to iteration as new normal modes are introduced and the old normal modes are refined. If a spectrum relative of the 0-0 energy is requested, the shift caused by the iterative convergence of ΔE_{ad} is not taken into account, although it will still have some effect on the spectrum as it also appears in the integral that defines the spectrum. If one is interested in a converged approximation of ΔE_{0-0} it may be more reliable to provide an absolute frequency range for the spectrum as the shift in the peak locations will then also affect convergence.

7.2.2 Input: Vibronic-Structure all modes

As mentioned, we need both a set of ground state normal modes as well as an excited state gradient. All the normal modes are calculated using the AMS engine that was selected, or, in case the user has a pre-calculated set of normal modes, these can be read from a .rkf file using the `ModeFile` key in the `NormalModes` sub-block. In this latter case, the engine is not used. One can then use the keys in the `ModeSelect` block to filter out specific modes, or, simply select all modes using the `Full` key in this block. For further details on how to use the `Mode Select` block for more specialized selection options, see the *Mode Select* (page 207) documentation. As for the excited state information, this is passed to the application via the `ExcitationSettings` block. Additionally there are (optional) settings related to the appearance of the spectrum under the `AbsorptionSpectrum` block. For an overview of the input options see the list of keys at the end of this page.

For completeness we provide an example of what the user input may look like:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type VibronicStructure
  NormalModes
    # Select all modes present in the .rkf file
  ModeSelect
    Full True
  End
End
ExcitationSettings
  ExcitationInfo File
  ExcitationFile ./your_excitation.t21
  Singlet
    B1.u 2
  End
End
AbsorptionSpectrum
  LineWidth 100.0
  AbsorptionRange -500.0 4000.0
End
End
```


7.2.3 Input: Vibronic-Structure Tracking

VST is notably the only Vibrational Analysis task that does not support the `NormalModes` block as no initial normal modes are necessary. The excited state gradient fills this role instead. Furthermore, the recommended default of using the identity matrix as a preconditioner means that no approximate Hessian is required either.

One thing to note regarding the Mode Tracking settings is that VST features a convergence criterion not present in standard Mode Tracking. The tolerance for the convergence of the spectrum is set using the `ToleranceForSpectrum` keyword in the `ModeTracking` block. The default is set to 0.01 and should be sufficient for most purposes, but *restarting* (page 239) with a lower value may improve the reliability of the convergence.

Note: The usual Mode Tracking tolerances are still present in addition to the spectral tolerance mentioned above. This is so we do not track modes that have already converged. Instead, once a mode is converged in the usual mode tracking sense, we switch to the next mode that satisfies our tracking criterion. The defaults should normally apply, but may be loosened a bit to allow for more free subspace exploration.

A typical Vibronic-Structure Tracking run may be setup as follows:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type VibronicStructureTracking
  # Select our excited state energy+gradient from a previous calculation
  ExcitationSettings
    ExcitationInfo File
    ExcitationFile ./your_excitation.t21
  End
  # Tuning how our spectrum will look
  AbsorptionSpectrum
    LineWidth 250.0
    AbsorptionRange -500.0 6000.0
  End
  ModeTracking
    UpdateMethod I
  End
End
```

Input: Restarting VST

The Vibronic-Structure Tracking task is fully restartable from a previously completed VST run. The main reason why it may be useful to perform a restart is related to the way the spectrum is generated. Most modules/applications in AMS that calculate a spectrum usually produce a stick spectrum. This stick spectrum is then convoluted against either a gaussian or lorentzian of specified width or area. This allows one to tweak the homogeneous broadening post-calculation to improve agreement with experiments. VST operates differently, in that the Lorentzian linewidth is specified at the start of the calculation as an essential input parameter. If upon convergence it becomes clear that a different linewidth would have been better suited for the spectrum at hand, one can restart the calculation with this new linewidth. The program then computes a new spectrum using these new settings and repeats the last iteration of the previous run. The latter is done because the linewidth directly influences the convergence (larger linewidths tend to converge more easily as the features are not as sharply resolved). If the spectrum does not change after the first iteration the program terminates as usual and the new spectrum is now available to the user. However, if this additional iteration does not pass the convergence test, the program keeps iterating until the spectrum converges for this new linewidth.

In addition to changing the linewidth post-calculation, the user is also free to change the spectral range that is to be computed as well as its resolution through the `FrequencyGridPoints` keywords. Alternatively, the tolerance used may be lowered if tighter convergence is required. Importantly however, none of the previous run's input settings are

retrieved upon restart, so any settings the user doesn't want to change have to be same in the new run script as in the old. The easiest way to restart is to simply re-use the previous run's runscript under a new name and then changing the relevant settings.

The restart functionality is controlled by the `RestartPath` keyword. One simply states the path to a previous calculation's `.rkf` file from which the relevant data is to be read. The `.rkf` file of any VST runs contains a section labeled `VSTRestart` which contains the data needed to restart from that run. Restarting is then a simple one-liner in the `VibrationalAnalysis` block:

```
VSTRestartFile ./previous_run.results/ams.rkf
```

7.2.4 Input: Vibronic-Structure Refinement

Vibronic-Structure Refinement (VSR) assumes that the modes relevant to the vibronic-structure are, at least in an approximate sense, known a priori. The VSR method takes these approximate modes and refines them via the Mode Refinement algorithm. The approximate normal modes should thereby span a subspace containing the exact normal modes and, the more similar they are to the exact mode, the better they allow to reproduce the spectrum of a full ground state frequency analysis. Naturally, the refinement becomes more accurate with increasing dimensionality of the spanned subspace, although this increases the computational costs. In any case, the subspace needs to contain those modes that are most relevant for the vibronic progression for the entire approach to work, which leads to the question, how do we select such modes?

This is done using familiar `ModeSelect` block from the mode selective analysis tasks. While all the usual options are available, for which further details can be found on the *Vibrational Analysis* (page 207) page, there are two selection methods that are geared specifically towards VSR. Within the VG-FC model, the parameters defining the effect a mode will have on the spectrum are the oscillator displacements Δ_j . We can determine these values from the projection of the approximate normal modes onto the gradient in combination with their respective frequencies. We are then interested in those modes with the largest displacement. To select these, two options are available:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type VibronicStructureRefinement
  NormalModes
    ModeSelect
      LargestDisplacement integer
      DisplacementBound float
      ...
    End
  ...
End
...
End
```

LargestDisplacement integer sets an integer value N , to select the N modes with the largest displacements as calculated within the VG-FC model. This method limits the total number of modes we refine and thus places an upper bound on the computational cost required by the method, but it does not ensure that all relevant modes have been selected. In particular there may still be modes with large displacements that have been omitted and as such peaks or progressions may be missing from the spectrum.

DisplacementBound float Alternatively this selects all approximate modes with a displacement greater than the supplied lower bound. An appropriate choice for this value ensures all modes which visibly affect the spectrum (at least at the lower level of theory used to produce the approximate modes) are included in the subspace basis used for Mode Refinement. The displacements Δ_j are dimensionless and the largest ones will typically be of order one. Based on this, a value of 0.01 for this parameter will generally select all relevant modes. This of course comes at the trade-off that for general molecules it is not known how many such modes there will be and the computational cost may be larger than expected. But, if one is not discouraged by this, this will of course yield the most accurate

results. Values up to 0.05 may still provide reasonable results while minimizing computation times. Using larger linewidths (AbsorptionSpectrum%LineWidth) for the homogeneous broadening can help to correct for the non-resolved modes.

The calculation setup for Vibronic-Structure Refinement is essentially the same as that for Vibronic-Structure, the only difference being that the modes that we provide will first be refined, before a spectrum is computed. A detailed description is given on the *Vibronic-Structure* (page 234) page. A typical VSR calculation can be setup as follows:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type VibronicStructureRefinement
  # Select our normal modes from a previous calculation
  NormalModes
    ModeFile ams.rkf
    ModeSelect
      # select all modes with VG-FC displacements over 0.01
      DisplacementBound 0.01
    End
  End
  # Select our excited state energy+gradient from a previous calculation
  ExcitationSettings
    ExcitationInfo File
    ExcitationFile ./your_excitation.t21
    # Select second singlet excitation with symmetry label A
    Singlet
      A 2
    End
  End
  # Tuning how our spectrum will look
  AbsorptionSpectrum
    LineWidth 250.0
    AbsorptionRange -500.0 6000.0
  End
End
```

7.2.5 Input: Excited State

Both the excited state gradient at the ground state equilibrium structure as well as the vertical excitation energy are necessary to obtain a spectrum. These can be provided by most TD-DFT programs, including ADF. Unfortunately, the AMS driver does not yet support computing these properties on the fly. As a result they are currently required as user input. One can use ADF or DFTB to compute them and then either read them from the produced output file, or copy and paste them to an inline input block.

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ...
  ExcitationSettings
    ExcitationInputFormat [File | Inline]
    ExcitationFile string
    EnergyInline float
    GradientInline # Non-standard block. See details.
    ...
  End
  Singlet # Non-standard block. See details.
  ...
End
```

(continues on next page)

(continued from previous page)

```

    Triplet # Non-standard block. See details.
    ...
  End
End
End

```

ExcitationInputFormat [**File** | **Inline**] this keyword is used to specify whether the gradient and energy are to be read from a kf file or if one chooses to use the inline block for them. Currently, no TD-DFT engine is implemented in the AMS driver. Furthermore, ADF uses the old tape21 format for its output which is quite different from the more streamlined AMS format. The `inline` option allows one to bypass any possible confusion here. The `File` option requires the specification of the specific excitation to read, which we will discuss below.

GradientInline is the block where the gradient can be specified if the inline option is selected. The format can be either a N by 3 block (N rows, 3 columns) or a 3N long column vector if one happens to have a gradient in this format. The gradient values should be in the unit Hartree/Bohr.

EnergyInline **float** is used to specify the excitation energy. This will just be a single floating point number (in Hartree).

The resulting input would look like:

```

Task VibrationalAnalysis
VibrationalAnalysis
  Type ...
  ...
  ExcitationSettings
    ExcitationInfo Inline
    # Excited state gradient for transhexatriene 14 atoms x 3 coordinates (to be
    ↪provided in Hartree/Bohr)
    GradientInline
      -0.03786125      0.01786798      0.00003833
        0.05322148      -0.00798712     -0.00004152
      -0.06658803      0.01373495      0.00004727
        0.06656379      -0.01374825      0.00002398
      -0.05318451      0.00799875     -0.00002097
        0.03783718      -0.01786722      0.00001362
        0.00382226      0.00327391      0.00001046
      -0.00046176     -0.00499971     -0.00003583
        0.00014312      0.00534412     -0.00001335
        0.00011081     -0.00558254     -0.00002107
      -0.00011074      0.00558350     -0.00000933
      -0.00014517     -0.00534330      0.00000839
      -0.00381513     -0.00327314     -0.00000248
        0.00046796      0.00499807      0.00000250
    End
    # The vertical excitation energy is simply a float (to be provided in Hartree)
    EnergyInline 0.17062882
  End
End

```

ExcitationFile **string** If `ExcitationInputFormat` is set to `File` one also has to set the `ExcitationFile` keyword to provide a path to the file from which the info should be read.

Singlet or **Triplet** In case the excited state information should be read directly from a file, one should specify which excitation AMS should read. This is done analogously to how this is done for excited state gradients in ADF. One chooses either the `Singlet` or `Triplet` blocks (for singlet-singlet or singlet-triplet excitations respectively). Once such a block is chosen, a line containing the symmetry label, followed by the number of the excitation of that symmetry. As for the symmetry labels, the notational convention used can be found in the [ADF manual appendix](#)

on symmetry labels. If symmetry was disabled, either explicitly by the user or when using TD-DFTB which does not support symmetry, when calculating the excited state properties, the symmetry label A should be used. Vibronic-structure calculations are only supported for one excitation at a time.

The resulting input block looks something like this:

```
ExcitationSettings
  ExcitationInputFormat File
  ExcitationFile ./ExcitedState.results/myengine.rkf
  Singlet
  A 1
  End
End
```

7.2.6 Input: Producing the spectrum

To go from normal modes to an actual spectrum, we have to solve the integral that we introduced in the first section, the details of which will be discussed here.

For long times, the integrand is dominated by the exponential damping term. We can define a suitable cut-off by demanding that this damping term be smaller than some threshold. As mentioned, the integral is evaluated using a Chebyshev quadrature. The number of Chebyshev nodes used for the integral can then be determined from this integration limit and the time step size. This time step size should be large enough to accurately represent the highest frequencies that are present in the highly oscillatory integrand. The Nyquist frequency can be used as a guide here: the highest frequency should be represented by at least two samples each period. Note however, that in principle there is no upper bound to the frequencies present in the integrand due to the fact that modes can be excited to arbitrarily high energy levels. Fortunately, the Franck-Condon factors will quickly act to dampen these high frequencies, restricting their significance. The user may either supply a time step size directly or leave this up to the program to determine. If the latter is chosen the highest relevant frequency is estimated by assuming that oscillator excitations are relevant up to about twice the Huang-Rhys parameter (which follow directly from the displacements). This default should in most cases be sufficient to produce a converged integral.

The keywords associated with the different input parameters are collected under the `AbsorptionSpectrum` block. It contains the following keys:

```
Task VibrationalAnalysis
VibrationalAnalysis
  Type ...
  ...
  AbsorptionSpectrum
    AbsorptionRange float_list
    FrequencyGridPoints integer
    LineWidth float
    SpectrumOffset [absolute | relative]
  End
End
```

LineWidth float sets the lorentzian line width and thus has a large impact on the appearance of the final spectrum.

It may be used to improve the agreement of the computed spectrum with experiment. Another purpose that the linewidth may serve is that some low frequency modes may not be represented very accurately within the VG-FC model. However, these modes do not result in particularly distinct vibronic progressions but rather cause an unspecific broadening of existing peaks. Applying a homogeneous peak broadening by increasing the value of Γ may be an effective (albeit a little ad hoc) way of resolving such issues, should they occur. The default value is 200cm^{-1} but it is recommended to do some experimentation with this value.

AbsorptionRange float_list keyword specifies the frequency range (in cm^{-1}) that is to be computed by VST.

SpectrumOffset [**absolute** | **relative**] specifies whether the range provided by the `AbsorptionRange` keyword is relative to the 0-0 excitation energy (`Relative`), or relative to the vertical excitation energy (`Absolute`). Due to the limited accuracy of the VG-FC model at predicting ΔE_{0-0} the default is `Relative` with a `AbsorptionRange` of `[-500,4000]`.

FrequencyGridPoints **integer** sets the number of points we use on our frequency grid. It is set to 400 by default which generally produces a smooth looking spectrum.

The current implementation of VG-FC vibronic-structure supports only spectra for one excitation at a time. The spectrum is normalized such that the highest peak is equal to 1 in arbitrary units. For this reason the prefactor of the integral is irrelevant and transition dipole moments do not affect the appearance of the spectrum.

DIPOLE MOMENT, POLARIZABILITY, BOND ORDERS, ORBITAL ENERGIES

This page in the AMS manual describes the calculation of the dipole moment, the polarizability, and bond orders.

```
Properties
  DipoleMoment Yes/No
  Polarizability Yes/No
  BondOrders Yes/No
End
```

Note that because these properties are tied to a particular point on the potential energy surface, they are found on the *engine output files* (page 19). Note also that the properties are not always calculated in every PES point that the AMS driver visits during a calculation. By default they are only calculated in *special* PES points, where the definition of special depends on the *task* (page 45) AMS is performing: For a *geometry optimization* (page 47) properties would for example only be calculated at the final, converged geometry. This behavior can often be modified by keywords special to the particular running task.

8.1 Charges, Dipole Moment, Polarizability

```
Properties
  Charges Yes/No
  DipoleMoment Yes/No
  DipoleGradients Yes/No
  Polarizability Yes/No
End
```

Properties

Charges

Type Bool

Default value No

Description Requests the engine to calculate the atomic charges.

DipoleMoment

Type Bool

Default value No

Description Requests the engine to calculate the electric dipole moment of the molecule. This can only be requested for non-periodic systems.

DipoleGradients**Type** Bool**Default value** No**Description** Requests the engine to calculate the nuclear gradients of the electric dipole moment of the molecule. This can only be requested for non-periodic systems.**Polarizability****Type** Bool**Default value** No**Description** Requests the engine to calculate the polarizability tensor of the system.

8.2 Bond orders & Molecule detection

Many engines can determine bond orders between atoms. For engines based on force fields, these might just be the bond orders used internally by the force field, while for quantum mechanical engines the bond orders are usually determined by analyzing the results of the quantum mechanical calculation, e.g. the electronic density. We refer users to the manuals of the respective engine for details.

If bond orders are requested but the engine does not implement a method for determining bond orders, a bond guessing algorithm will be used instead (see also [BondOrders block](#) (page 246)). The bond guessing algorithm (which is also used by the graphical user interface to guess bonds) uses inter-atomic distances and atomic valences to guess the bond orders.

You can request bond orders to be calculated in the `Properties` input block:

```
Properties
  BondOrders Yes/No
End
```

Properties**BondOrders****Type** Bool**Default value** No**Description** Requests the engine to calculate bond orders.

For MM engines these might just be the defined bond orders that go into the force-field, while for QM engines, this might trigger a bond order analysis based on the electronic structure. For engines that do not have a bond order analysis method, a bond guessing algorithm will be used. See also the input options in the `BondOrders` block.

More options can be specified in the `BondOrders` block:

```
BondOrders
  Method [Engine | Guess | EngineWithGuessFallback]
End
```

BondOrders**Method****Type** Multiple Choice**Default value** EngineWithGuessFallback

Options [Engine, Guess, EngineWithGuessFallback]

Description How to compute the bond orders when they are requested via the ‘Properties%BondOrders’ key.

‘Engine’: let the engine compute the bond orders. The specific method used to compute the bond orders depends on the engine selected, and it may be configurable in the engine’s input. Note: the calculation may stop if the engine cannot compute bond orders.

‘Guess’: Use a bond guessing algorithm based on the system’s geometry. This is the same algorithm that is used by the Graphical User Interface to guess bonds.

‘EngineWithGuessFallback’: let the engine compute the bond orders (same as in ‘Engine’ option) but if the engine did not produce any bond orders, use the bond guessing algorithm as a fallback option.

Based on the bond orders, the AMS driver can analyze the atomic connectivity graph in order to determine which sets of atoms together constitute molecules. This allows for example to monitor the changes in molecular composition during a reactive molecular dynamics calculation. For *molecular dynamics* (page 90) calculations this option is enabled by default. For other *tasks* (page 45) the molecular analysis can explicitly be requested in the Properties block.

```
Properties
  Molecules Yes/No
End
```

Properties

Molecules

Type Bool

Default value No

Description Requests an analysis of the molecular components of a system, based on the bond orders calculated by the engine.

Details of the molecule detection are configured in a dedicated block:

```
Molecules
  AdsorptionSupportRegion string
  BondOrderCutoff float
End
```

Molecules

Type Block

Description Configures details of the molecular composition analysis enabled by the Properties%Molecules block.

AdsorptionSupportRegion

Type String

GUI name Adsorption support region

Description Select region that will represent a support for adsorption analysis. Adsorbed molecules will receive an ‘(ads)’ suffix after name of the element bonded to the support. Such elements will be listed separate from atoms of the same element not bonded to the support, for example, HOH(ads) for a water molecule bonded to a surface via one of its H atoms.

BondOrderCutoff

Type Float

Default value 0.5

Description Bond order cutoff for analysis of the molecular composition. Bonds with bond order smaller than this value are neglected when determining the molecular composition.

8.3 Bond guessing algorithm

The algorithm to determine bond orders purely from atomic positions, which is used if `BondOrders%Method = Guess`, is roughly as follows:

- Each chemical element has a maximal number of bonds (`connectors` property taken from the PLAMS `PeriodicTable` class) and a covalent radius.
- Calculate interatomic distances
- Determine bond orders between all non-metal atoms
- Add bonds to any isolated H atoms (these bonds do not count towards the maximal number of bonds for an element).
- Find central atoms of common anions like carbonate, nitrate, sulfate, phosphate, and arsenate
- Add bonds between metal atoms and all other atoms, except the ones from the previous step
- Delete metal-metal bonds and metal-hydrogen bonds if the metal is bonded to enough electronegative atoms and not enough metal atoms. This means that the metal is likely a cation.

The calculated bonds are useful for visualization, but not necessarily for setting up ForceField simulations.

The bond orders to metal atoms are always 1.

Note: The problem of finding molecular bonds for a given set of atoms in space does not have a general solution, especially considering the fact the chemical bond in itself is not a precisely defined concept. For every method, no matter how sophisticated, there will always be corner cases for which the method produces disputable results. Moreover, depending on the context (area of application) the desired solution for a particular geometry may vary. The algorithm used here gives good results for geometries that are not very far from the optimal geometry, especially consisting of lighter atoms. All kinds of organic molecules, including aromatic ones, usually work very well. Problematic results can emerge for transition metal complexes, transition states, incomplete molecules etc.

Warning: This method works reliably only for geometries representing complete molecules. If some atoms are missing (for example, a protein without hydrogens) the resulting set of bonds would usually contain more bonds or bonds with higher order than expected.

A version of this algorithm is also implemented in the PLAMS `Molecule.guess_bonds()` method.

8.4 Orbital energies, HOMO-LUMO gap

Ab-initio or semiempirical engines, such as ADF or DFTB, internally compute molecular orbital energies and occupations (see *Summary of engine capabilities* (page 252)). This information is printed to the AMSResults section of the text output and is stored in the AMSResults section of the binary engine results.

Example of molecular orbitals information printed to the text output:

```
-----
Molecular orbitals info
-----
```

```
n orbitals:           8
n spin:               1

HOMO (eV):           -13.5919
LUMO (eV):           -4.2036
HOMO-LUMO gap (eV):  9.3883
```

Index	Energy (eV)	Occupation
8	12.3038	0.000
7	9.4801	0.000
6	-1.3196	0.000
5	-4.2036	0.000 < LUMO
4	-13.5919	2.000 < HOMO
3	-14.8182	2.000
2	-16.6543	2.000
1	-20.6183	2.000

n spin: 1 in case of spin-restricted or spin-orbit calculations, 2 in case of spin-unrestricted calculations.

Occupations: in case of spin-unrestricted calculations the occupation numbers will be in the range 0-2. In case of spin-restricted calculation or spin-orbit calculations, the the occupation numbers will be in the range 0-1.

Note: In case of **fractional occupation** (i.e. non-integer occupations numbers), the definition of HOMO and LUMO is somewhat ill defined.

If fractional occupations are detected, a message will be printed to the text output.

The logical variable `AMSResults%fractionalOccupation` in the engine .rkf results file indicates whether fractional occupation was detected.

Here, we use the following convention:

- The HOMO is the highest-energy orbital for which `occupation[iOrbital] > occupied_threshold`. The LUMO is HOMO+1.
- if `occupation[LUMO] < unoccupied_threshold` we have integer occupations.
- if `occupation[LUMO] > unoccupied_threshold` we have we have **fractional occupations**

where `occupied_threshold = 0.9 * max_occupation`, `unoccupied_threshold = 0.1 * max_occupation` (max occupation = 2 for spin-restricted calculations and 1 for spin-unrestricted or spin-orbit calculations)

In case of spin-unrestricted calculation, the “smallest HOMO-LUMO gap” is the smallest HOMO-LUMO gap irrespective of spin (i.e. $\min(\text{LUMO}) - \max(\text{HOMO})$).

The molecular orbital information is generally automatically computed by engines supporting it.

You can explicitly request this in the input via the following keyword:

```
Properties
  OrbitalsInfo Yes/No
End
```

Properties

OrbitalsInfo

Type Bool

Default value No

Description Basic molecular orbitals information: orbital energies, occupations, HOMO, LUMO and HOMO-LUMO gap.

If you explicitly request `OrbitalsInfo` to be computed, but the engine cannot compute it, AMS will stop with an error.

Molecular orbital information can only be calculated in case of non-periodic systems.

See also:

In [PLAMS](#), you can use dedicated getters to extract this information from [AMSResults](#).

ENGINES

The engines are the core of the Amsterdam Modeling Suite: While the AMS driver steers the calculation over the potential energy surface in e.g. a *geometry optimization* (page 47) or *molecular dynamics* (page 90) calculation, the engines calculate energies and gradients and in this way *define* the PES on which the driver works.

```
Engine header
```

Engine

Type Block

Description The input for the computational engine. The header of the block determines the type of the engine.

The engine used for an AMS calculation is selected and configured with the special `Engine` block in the AMS input:

```
Engine DFTB
... input for the DFTB engine ...
EndEngine
```

Here the type of engine, e.g. `DFTB` as in the example above, is specified on the line that opens the block. Note that the `Engine` block ends with `EndEngine`, and is in this way different from all the other blocks in the AMS input, which close just with `End`. The content of the engine block is what we call the “engine input”. Generally the engine input consists of a series of blocks and keywords, and looks just like the AMS driver input. However, many engines have a lot of options and keywords, which are documented in a separate engine manual. In other words: This AMS driver manual documents all the keywords outside of the `Engine` block, while the individual engine manuals document the contents of the engine block.

9.1 Available engines

The following engines are available in the 2023.1 release of the Amsterdam Modeling Suite:

- **ADF** A DFT engine particularly strong in understanding and predicting structure, reactivity, and spectra of molecules.
- **BAND** An atomic-orbital based DFT engine aimed at periodic systems (crystals, slabs, chains) but supporting also molecular systems.
- **DFTB** An engine implementing Density Functional based Tight-Binding, a fast approximation to DFT.
- **ReaxFF** An engine for modeling chemical reactions with atomistic potentials based on the reactive force field approach.
- **MLPotential** Machine learning potentials (machine learning force fields).

- **ForceField** An engine implementing classical non-reactive force fields such as UFF (a non-reactive force field covering the entire periodic table).
- **GFNFF** The GFNFF force field
- **Hybrid** Hybrid engine, for embedding and QM/MM calculations that combine multiple engines.
- **MOPAC** An engine wrapping the MOPAC code, a general-purpose semiempirical molecular orbital package for the study of solid state and molecular structures and reactions.
- **External (page 254)** A flexible scripting interface that allows advanced users to use external modeling programs as engines in AMS.
- **LennardJones (page 258)** A simple toy engine implementing a Lennard-Jones potential.

9.2 Summary of engine capabilities

Some options/properties can only be computed in combination with some of the engines (i.e., not all engines support all features). These tables summarize the capabilities of the engines of the Amsterdam Modeling Suite:

Table 9.1: Engine support for AMS driver options

Feature	ADF	BAND	DFTB	ReaxFF	MLPot.	Force-Field	MOPAC	GFNFF
All elements available	✓	✓	✓ ²			✓ ³	✓	✓
<i>Non-periodic systems</i> (page 31)	✓	✓	✓	✓	✓ ⁴	✓	✓	✓
<i>1D periodic systems</i> (page 31)		✓	✓	✓		✓	✓	
<i>2D periodic systems</i> (page 31)		✓	✓	✓		✓	✓	
<i>3D periodic systems</i> (page 31)		✓	✓	✓	✓ [?]	✓	✓	✓
Charged molecular systems	✓	✓	✓	✓		✓	✓	✓
External electric field	✓	✓	✓				✓	
External point charges	✓	✓	✓					

² All elements are available for the GFN1-xTB model, but other DFTB parameter sets are not parametrized for all elements.

³ All elements are available with UFF (universal force field), but other force fields are not parametrized for all elements.

⁴ MLPotential backends may support non-periodic and/or 3D-periodic calculations.

Table 9.2: Engine support for AMS driver properties

Feature	ADF	BAND	DFTB	ReaxFF	MLPot.	Force-Field	MOPAC	GFNFF
<i>Atomic charges</i> (page 245)	✓	✓	✓	✓		✓	✓	✓
<i>Bond orders</i> (page 246) ¹	✓		✓	✓		✓	✓	✓
<i>Orbital energies</i> (page 248)	✓	✓	✓				✓	
<i>HOMO-LUMO gap</i> (page 248)	✓	✓	✓				✓	
<i>Dipole gradients</i> (page 245)	✓	✓	✓				✓	✓
<i>Dipole moment</i> (page 245)	✓	✓	✓				✓	✓
<i>Elastic tensor</i> (page 184)		✓	✓	✓	✓	✓	✓	✓
<i>Gradients / Forces</i> (page 179)	✓	✓	✓	✓	✓	✓	✓	✓
<i>Hessian</i> (page 180)	✓	✓	✓	✓	✓	✓	✓	✓
<i>Infrared spectra</i> (page 189)	✓	✓	✓				✓	✓
<i>Molecule detection</i>	✓		✓	✓		✓	✓	✓
<i>Normal modes</i> (page 189)	✓	✓	✓	✓	✓	✓	✓	✓
<i>PES point character</i> (page 180)	✓	✓	✓	✓	✓	✓	✓	✓
<i>Phonons</i> (page 213)		✓	✓	✓	✓	✓	✓	✓
<i>Polarizability</i> (page 245)	✓							
<i>Raman</i> (page 217)	✓							
<i>Stress tensor</i> (page 183)		✓	✓	✓	✓	✓	✓	✓
<i>Thermodynamic properties</i> (page 209)	✓	✓	✓	✓	✓	✓	✓	✓
<i>VCD</i> (page 223)	✓	✓	✓				✓	
<i>VROA</i> (page 222)	✓							

Note: The features/options in the following tables are **engine-specific**, and are described in the corresponding engine's manual. The input for these options should be specified in the *Engine block* (page 9) section of the input file.

¹ If the engine does not support the calculation of bond orders, a bond guessing algorithm will be used instead. See *Bond Orders* (page 246).

Table 9.3: Engine-specific capabilities

Feature	ADF	BAND	DFTB	ReaxFF	MLPot.	Force-Field	MOPAC	GFNFF
EFG	✓ (doc)	✓ (doc)						
Electronic transport	✓ (doc)	✓ (doc)	✓ (doc)					
Energy decomposition analysis	✓ (doc)	✓ (doc)						
ESR/EPR	✓ (doc)							
Hyperpolarizabilities	✓ (doc)							
NMR	✓ (doc)							
pKa							✓ (doc)	
Solvation models	✓ (doc)	✓ (doc)	✓ (doc)				✓ (doc)	
Spin-polarization	✓ (doc)	✓ (doc)	✓ (doc)				✓ (doc)	
UV-VIS optical spectra	✓ (doc)		✓ (doc)					

Table 9.4: Engine-specific capabilities for periodic systems

Feature	ADF	BAND	DFTB	ReaxFF	MLPot.	ForceField	MOPAC
Density of states (DOS)		✓ (doc)	✓ (doc)				
Dielectric function		✓ (doc)					
Effective mass		✓ (doc)	✓ (doc)				
Electronic band structures		✓ (doc)	✓ (doc)				
k-space sampling		✓ (doc)	✓ (doc)				
X-ray form factors		✓ (doc)					

9.3 External programs as engines

The AMS driver allows running external programs as an engine. In this way users can combine the functionality in the AMS driver (tasks and PES point properties) with the energies and gradients of any molecular modeling program they have access to. For example, the graphical user interface supports setting up **VASP** as an external engine to the AMS driver.

In general, the interfacing between the AMS driver and the external program has to be done by the user in form of a small script, which allows users to hook up any external program without access to the source code of AMS. The graphical user interface of the Amsterdam Modeling Suite can then be used to analyze the results of these calculations.

An external engine is specified with `Engine External`. The keyword `Execute` is used to specify the command that is run to execute the external program:

```
Engine External
  Execute /path/to/my_interface_script.sh
EndEngine
```


The command can in principle be anything, as it will just be executed as is by the system shell. However, it should not use relative paths (e.g. to files in the directory where the input file is). We recommend writing the interfacing script in Python and using the Python interpreter that ships with AMS:

```
Engine External
  Execute "$AMSBIN"/amspython /path/to/my_python_interface_script.py
EndEngine
```

AMS then starts running and for every geometry prepares a folder in which the external engine is supposed to run. This is the folder in which the interface script specified with the `Execute` key is executed (so any relative paths are relative to that folder). AMS puts two files into this folder:

```
system.xyz
request.json
```

The `system.xyz` just contains the geometry AMS wants the external engine to calculate. It is an *extended format XYZ file* (page 477) with the `VEC1`, `VEC2`, `VEC3` extension at the end for periodic systems, e.g. diamond would look like this:

```
2
C      -0.51292147   -0.51292147   -0.51292147
C       0.51292147    0.51292147    0.51292147
VEC1   0.00000000    2.05168587    2.05168587
VEC2   2.05168587   -0.00000000    2.05168587
VEC3   2.05168587    2.05168587    0.00000000
```

The `request.json` file is just a small JSON file that specifies what exactly AMS wants the external engine to calculate:

```
{
  "title": "GOSTep28",
  "quiet": false,
  "gradients": true,
  "stressTensor": false,
  "hessian": true,
  "dipoleMoment": false,
  "properties": true,
  "prevResults": "GOSTep27"
}
```

The job of the interfacing script is now to read these files, run the external program and convert its output into a format understood by AMS. Generally these are simple text files with the name of the property and the extension `.txt`. The bare minimum the interfacing script needs to produce is the file `energy.txt` containing a single number, i.e. the total energy in atomic units (Hartree). Other properties are optional, and it is easiest to go through the `request.json` entries one by one to see what AMS might request and what the interfacing script could produce in response.

title Just a title for this particular engine run. It can be passed on to the external program if desired, or can just be ignored.

quiet Whether AMS wants the external engine to write to standard output. This can be ignored in principle, but that might lead to really incomprehensible text output files of AMS if the external engine has to be called many times, e.g. for numerical derivatives.

gradients Whether or not to calculate nuclear gradients. The interface script should put the gradients in a file called `gradients.txt` with `nAtoms` lines of 3 real numbers each, in atomic units, i.e. Hartree/Bohr. Note that AMS wants the gradients, not forces (beware the - sign!).

stressTensor Whether to calculate the stressTensor for periodic systems. Should be written to `stresstensor.txt` in atomic units.

hessian Whether to calculate the Hessian, that is just the second derivative of the energy with respect to the nuclear coordinates, *without* applying any mass weighing to it. If the Hessian has been calculated, it should be put in `hessian.txt` as a 3 nAtoms x 3 nAtoms matrix in atomic units.

dipoleMoment If true, calculate the dipole moment and put it in `dipolemoment.txt` in atomic units, in one line with three numbers.

properties This is set to true if AMS considers this “geometry” important and wants the engine to calculate further properties that the user might be interested in. In practice this is set to “true” for e.g. the final converged step in a geometry optimization, so that the user can then let the engine calculate e.g. the band structure, which one would not want to do at all the steps *during* the optimization. AMS can’t do anything with the properties that the engine might calculate, but the files will remain on disk for people to inspect them.

prevResults This is the title of a previous similar calculation that the engine has already performed. These results can be accessed in `./$prevResults/`, so for the example above `GOSTep28` can access the results from the previous step in the geometry optimization in `./GOSTep27/`. This is just the directory in which the interfacing script was run when the `title` field was set to `GOSTep27`, so files that were written back then are still accessible. They can in principle be used to restart for example the SCF of the engine from step to step. Of course all of that has to be done by the interfacing script. The AMS driver does not know anything about how to restart the external program and can only point the interfacing script to the right location.

That is really all there is to the external engine: AMS prepares a folder with `system.xyz` and `request.json` and runs the user’s interfacing script in there, which has to take care of preparing the input for the external engine, running it, and putting the results in the text files that AMS expects, e.g. `gradients.txt`.

Note for properties that are in one way or another derivatives of the energy, it is generally ok if the external engine does not calculate what was requested by the AMS driver in `request.json`. If AMS requests, for example, the gradients from the external engine, but then does not find the `gradients.txt` in the directory after the interfacing script has run, it will just assume that the engine was not capable of calculating the gradient analytically. AMS will then just do the gradient numerically by rerunning the external engine for displaced geometries, reading only the energy from `energy.txt`. In this sense it is only absolutely required for the external engine to produce the energy, the rest can be done numerically by AMS if required. It is of course best to let the engine do as much as possible, especially if it implements analytical derivatives. Note that currently AMS can not calculate the Hessian numerically for engines that do not provide gradients. This is just a technical limitation, as it is of course possible to do a second derivative numerically, but it is just not implemented in AMS yet. (And it would also be a very slow way to calculate a Hessian.)

In addition to the `Execute` keyword that specifies the interfacing script, it is also possible to use the `ExecuteAtEnd` keyword to specify another command to be run at the end of the calculation, for example after the last step of a geometry optimization or molecular dynamics simulation. This command is run in the results directory.

Moreover, the `Engine External` block can also contain some information about the capabilities of the external engines:

```
Engine External
  Execute {...}
  ExecuteAtEnd {...}
  Supports
    DipoleMoment      {true|false}
    PeriodicityNone   {true|false}
    PeriodicityChain  {true|false}
    PeriodicitySlab   {true|false}
    PeriodicityBulk   {true|false}
  End
EndEngine
```

The normal engines that come with AMS (e.g. DFTB and BAND) produce the engine output files with extension `.rkf` in the results directory, see [here](#) (page 19). These files are also produced when an external engine is used and the information on them (anything related to the shape of the PES at that point, e.g. normal modes, phonons, ...) can be visualized normally with the graphical interface. In addition to each engine output `.rkf` file, external engines will also

produce a correspondingly named folder per engine file, which is just the working directory of the interfacing script for that particular invocation of the external program. These folders just contain the full output of the external program and anything that the interfacing script might have produced. In this way users still have access to all results from the external program, even if these results were not communicated back to the AMS driver.

This last point is probably best illustrated with a simple example. Consider the following job that uses an external engine to do a linear transit calculation of ethane, going from the staggered to the eclipsed configuration, calculating normal modes at all converged points along the path:

```

AMS_JOBNAME=ethane_torsion $AMSBIN/ams << EOF

Task PESScan

System
  Atoms
    C      0.00000000      0.00000000      0.76576000
    C      0.00000000      0.00000000     -0.76576000
    H     -0.88668938      0.51193036      1.16677000
    H      0.88668938      0.51193036      1.16677000
    H      0.00000000     -1.02386071      1.16677000
    H      0.00000000      1.02386071     -1.16677000
    H     -0.88668938     -0.51193036     -1.16677000
    H      0.88668938     -0.51193036     -1.16677000
  End
End

PESScan
  CalcPropertiesAtPESPoints True
  ScanCoordinate
    nPoints 5
    Dihedral 3 1 2 6 60.0 0.0
  End
End

Properties
  NormalModes True
End

Engine External
  ...
EndEngine

EOF

```

If we run this job and look into the results folder, we will find the standard `ams.log` and `ams.rkf` as well as the usual engine result files `PESPoint(1).rkf` to `PESPoint(5).rkf`. Just as if we had used one of the native AMS engines, like DFTB. Each of these files can be opened in AMSspectra to visualize the normal modes for this particular point. For an external engine we additionally have one folder per engine file, so for this example we would have `PESPoint(1)/` to `PESPoint(5)/`. These are the folders in which the interfacing script ran for these particular points, so they contain all the native output files of the external program.

9.4 Toy engines

The AMS driver comes with a simple built-in toy engine that implements a Lennard-Jones potential. This can sometimes be useful for testing, as many properties of the Lennard-Jones gas/liquid/solid can be calculated analytically and compared to the results from AMS. Note that the potential is exactly the same for all elements, i.e. the N-N bond has exactly the same strength as the He-He bond.

The Lennard-Jones engine only has three keywords, which define the shape of the potential:

```
Engine LennardJones
  RMin  float
  Eps   float
  Cutoff float
EndEngine
```

Cutoff

Type Float

Default value 15.0

Unit Angstrom

Description The distance at which the interaction is truncated.

Eps

Type Float

Default value 1.0

Unit Hartree

Description The depth of the potential well.

RMin

Type Float

Default value 1.0

Unit Angstrom

Description The distance of the potential minimum.

9.5 Engine add-ons

Engine add-ons can be used to augment the results returned from an engine.

9.5.1 Dispersion corrections

For engines that do not natively support Grimme's D3 and D4 dispersion corrections, the `D3Dispersion` and `D4Dispersion` engine add-ons can be used to add such corrections.

```
EngineAddons
  D3Dispersion
    Damping [BJ | Zero]
  Enabled Yes/No
```

(continues on next page)

(continued from previous page)

```

Functional string
a1 float
a2 float
s6 float
s8 float
sr6 float
End
D4Dispersion
Enabled Yes/No
Functional [...]
Verbosity [Silent | Normal | Verbose | VeryVerbose]
a1 float
a2 float
s6 float
s8 float
s9 float
End
End

```

EngineAddons**D3Dispersion****Type** Block**Description** This block configures the add-on that adds the Grimme D3 dispersion correction to the engine's energy, gradients, and stress tensor.**Damping****Type** Multiple Choice**Default value** BJ**Options** [BJ, Zero]**Description** Type of damping: BJ (Becke-Johnson) or Zero. BJ is recommended for most applications.**Enabled****Type** Bool**Default value** No**Description** Enables the D3 dispersion correction addon.**Functional****Type** String**Default value** PBE**Description** Use the D3 parameterization by Grimme for a given xc-functional. Accepts the same values as the `-func` command line option of the official `dftd3` program. Note: the naming convention is different from elsewhere in the AMS suite. For example, BLYP should be called `b-lyp`.**a1****Type** Float**Description** The `a1` parameter. Only used if Damping is set to BJ. If set, it overwrites the `a1` value for the chosen functional.

a2**Type** Float**Description** The a2 parameter. Only used if Damping is set to BJ. If set, it overwrites the a2 value for the chosen functional.**s6****Type** Float**Description** The s6 parameter, global scaling parameter. If set, it overwrites the s6 value for the chosen functional.**s8****Type** Float**Description** The s8 parameter. If set, it overwrites the s8 value for the chosen functional.**sr6****Type** Float**Description** The sr6 parameter. Only used if Damping is set to Zero. If set, it overwrites the sr6 value for the chosen functional.**D4Dispersion****Type** Block**Description** This block configures the addon that adds the Grimme D4(EEQ) dispersion correction to the engine's energy, gradients, stress tensor and Hessian.**Enabled****Type** Bool**Default value** No**Description** Enables the D4 dispersion correction addon.**Functional****Type** Multiple Choice**Default value** PBE**Options** [HF, BLYP, BPBE, BP86, BPW, LB94, MPWLYP, MPWPW91, OLYP, OPBE, PBE, RPBE, REVPBE, PW86PBE, RPW86PBE, PW91, PW91P86, XLYP, B97, TPSS, REVTPSS, SCAN, B1LYP, B3LYP, BHLYP, B1P86, B3P86, B1PW91, B3PW91, O3LYP, REVPBE0, REVPBE38, PBE0, PWP1, PW1PW, MPW1PW91, MPW1LYP, PW6B95, TPSSH, TPSS0, X3LYP, M06L, M06, OMEGAB97, OMEGAB97X, CAM-B3LYP, LC-BLYP, LH07TSVWN, LH07SSVWN, LH12CTSSIRPW92, LH12CTSSIFPW92, LH14TCALPBE, B2PLYP, B2GPPLYP, MPW2PLYP, PWPB95, DSDBLYP, DSDPBE, DSDPBEB95, DSDPBEP86, DSDSVWN, DODBLYP, DODPBE, DODPBEB95, DODPBEP86, DODSVWN, PBE02, PBE0DH, DFTB(3ob), DFTB(mio), DFTB(pbc), DFTB(matsci), DFTB(ob2), B1B95, MPWB1K, REVTPSSH, GLYP, REVPBE0DH, REVTPSS0, REVDSDPBEP86, REVDSDPBEPBE, REVDSDBLYP, REVDODPBEP86, B97M, OMEGAB97M, R2SCAN]**Description** Use the D4 parameterization by Grimme for a given xc-functional.**Verbosity****Type** Multiple Choice

Default value Silent

Options [Silent, Normal, Verbose, VeryVerbose]

Description Controls the verbosity of the dftd4 code. Equivalent to the `-silent` and `-verbose` command line switches of the official dftd4 program.

a1

Type Float

Description The a1 parameter, see D4 article. The physically reasonable range for a1 is [0.0,1.0]. If set, it overwrites the a1 value for the chosen functional.

a2

Type Float

Description The a2 parameter, see D4 article. The physically reasonable range for a2 is [0.0,7.0]. If set, it overwrites the a2 value for the chosen functional.

s6

Type Float

Description The s6 parameter, see D4 article. The physically reasonable range for s6 is [0.0,1.0]. If set, it overwrites the s6 value for the chosen functional.

s8

Type Float

Description The s8 parameter, see D4 article. The physically reasonable range for s8 is [0.0,3.0]. If set, it overwrites the s8 value for the chosen functional.

s9

Type Float

Description The s9 parameter, see D4 article. If set, it overwrites the s9 value for the chosen functional.

9.5.2 Pressure

Pressure can be included using the following keyword (this can only be used for **3D periodic systems**):

```
EngineAddons
  Pressure float
End
```

EngineAddons

Pressure

Type Float

Default value 0.0

Unit GPa

Description Add a hydrostatic pressure term to the engine's energy and stress tensor. Can only be used for 3D periodic boundary conditions.

The engine's energy will include the following extra term: $P \cdot V$, where V is the volume of the unit cell. The engine's stress tensor will include the following extra term: $P \cdot \mathbb{I}$, where \mathbb{I} is the identity matrix. This can only be used for 3D periodic boundary conditions (i.e. bulk). The energy and stress tensor printed in output and written to the `.rkf` binary file will include these extra terms (i.e. the printed stress tensor is the sum of the internal stress and the external stress due to pressure).

When studying the effect that pressure has on the structure and properties of your system, one should generally start by *optimizing the structure* (page 47) **including the lattice vectors** under pressure. Properties such as *phonons* (page 213) or *elastic tensor* (page 184) can then be computed at the relaxed geometry. If you are investigating phase transitions under pressure (or if you simply expect some symmetry breaking) you should disable symmetry and/or perturb the initial geometry of your system.

See also:

Example: Periodic lattice optimization under pressure (page 373)

Warning: If you want to include pressure in *molecular dynamics* (page 90) calculations, you should not use this engine addon, but use the MD-specific pressure option.

9.5.3 Non-isotropic external stress

An **non-isotropic external stress tensor** can be included by using the following keywords:

```
EngineAddons
  ExternalStress
    StressTensorVoigt float_list
    UpdateReferenceCell Yes/No
  End
End
```

EngineAddons

ExternalStress

Type Block

Description This block configures the addon that adds external stress term to the engine's energy and stress tensor.

StressTensorVoigt

Type Float List

Unit a.u.

GUI name External stress tensor

Description The elements of the external stress tensor in Voigt notation. One should specify 6 numbers for 3D periodic system (order: *xx,yy,zz,yz,xz,xy*), 3 numbers for 2D periodic systems (order: *xx,yy,xy*) or 1 number for 1D periodic systems.

UpdateReferenceCell

Type Bool

Default value No

Description Whether or not the reference cell should be updated every time the system changes (see documentation).

The energy and stress tensor printed in output and written to the `.rkf` binary file already include the corresponding extra terms, i.e. the printed stress tensor is the sum of the internal stress and the input-specified external stress.

When studying the effect that an external stress has on the structure and properties of your system, one should generally start by *optimizing the structure* (page 47) **including the lattice vectors** under the external stress (depending on the magnitude of the applied external stress, you might have to adjust the *stress energy per atom convergence threshold* (page 48)). If your system is symmetric, you should **disable symmetry** when optimizing structures under external stress. Be aware that the geometry optimization might go completely astray (e.g. the material will break apart) if you apply a) too large shear stress or b) too large tension stress (too large negative stresses for the diagonal values).

Following this paper⁵ from Parrinello and Rahman, the extra energy term due to a non-isotropic external stress⁶ is defined with respect to a *reference unit cell*, which in our case is the unit cell at the beginning of the simulation. If, during the simulation, large deformations of the unit cell occur, the above mentioned energy expression is only approximately consistent with the stress tensor. This affects the calculation differently depending on whether the stress tensor is computed by the engine or by AMS via numerical differentiation: a) If the stress tensor is computed directly by the engine, for large unit-cell deformations the energy might increase during the optimization; b) If the stress tensor is computed by AMS via numerical differentiation, the actual final value of the stress tensor might not match perfectly the external stress specified in the input (for large cell deformations, this error can be in the order of 10%).

After the optimization under external stress is converged, it is therefore good practice to validate the results. To do this, you should compute the *stress tensor* (page 183) at the optimized geometry by performing a *single point calculation* (page 45) **without** applying the external stress. The values in the computed stress tensor should have opposite sign compare to the external stress applied during the optimization. If the values differ too much, then you can run a second geometry optimization under external stress starting from the optimized geometry.

See also:

Example: Boron nitride optimization under external stress (page 376)

An alternative option is to set the key `ExternalStress%UpdateReferenceCell` to `True`; this will update the reference unit cell at every optimization step, effectively changing the definition of the energy expression at every geometry optimization step. The energy might not consistently go down during the optimization, but the resulting internal stress will match much better the applied external stress. This option should only be used during geometry optimizations (i.e. it should not be used when computing properties such as the elastic tensor).

See also:

Example: Graphene optimization under external stress (page 378)

9.5.4 Atom energies

This add-on adds an element-dependent energy for each atom in a system, effectively applying an energy shift. It does not affect any other property.

```
EngineAddons
  AtomEnergies # Non-standard block. See details.
  ...
End
End
```

⁵ M. Parrinello, and A. Rahman, *Polymorphic transitions in single crystals: A new molecular dynamics method*, Journal of Applied Physics 52, 7182 (1981) (<https://doi.org/10.1063/1.328693>)

⁶ The energy term due to a non-isotropic external stress is:

$$E_{\text{stress}} = p_h(V - V_0) + \frac{1}{2}V_0\text{Tr}[(\sigma - p_h\mathbb{I})(h_0^T)^{-1}h^T h h_0^{-1} - \mathbb{I}]$$

where: σ is the external stress tensor, p_h is the hydrostatic pressure associated with σ (i.e. the average of the diagonal elements of σ), V is the volume of the unit cell (for 2D periodic systems this is the area of the cell, and for 1D periodic systems is the length of the cell), V_0 is the volume of the *reference unit cell*, h are the lattice vectors in matrix form, h_0 are the lattice vectors of the reference unit cell in matrix form and \mathbb{I} is the identity matrix.

EngineAddons**Type** Block**Description** This block configures all the engine add-ons.**AtomEnergies****Type** Non-standard block**Description** Add an element-dependent energy per atom. On each line, give the chemical element followed by the energy (in atomic units).

The below example will add -0.5 Hartree for every H atom and -5.0 Hartree for every C atom in the system to the total energy. The add-on will ignore any atoms of other elements:

```
EngineAddons
  AtomEnergies
    H -0.5
    C -5.0
  End
End
```

9.5.5 Restraints

A restraint is potential energy function (a spring) attached to a certain coordinate, for example, an interatomic distance, the minimum of the potential energy being at the specified optimal value. A restraint can have one or two parameters: a ForceConstant and, for some types, a F(Inf) value. The ForceConstant parameter corresponds to second derivative of the restraint potential energy $\frac{d^2V(x)}{dx^2}$ for any x (harmonic restraints) or only at $x = 0$ (other restraints). Here, x is a deviation from the restraint's optimal value.

Geometry restraints can be added using the following input block:

```
Restraints
  Profile [Harmonic | Hyperbolic | Erf | GaussianWell]
  fInfinity float
  Distance atomIdx1 atomIdx2 OptValue ForceConstant {Profile} {fInfinity}
  Angle
  Dihedral
  SumDist
  DifDist
End
```

The shape of the restraint potential function is defined by its profile type (Harmonic, Hyperbolic, Erf) and the appropriate parameter(s). The Harmonic profile is most suitable for geometry optimizations but may result in very large forces that can be problematic in molecular dynamics. For MD simulations the Hyperbolic or Erf may be more suitable because the restraint force is bounded by a user-defined value. A Harmonic restraint is defined as $V(x) = C \frac{x^2}{2}$. A Hyperbolic restraint is defined as $V(x) = a(\sqrt{1 + (bx)^2} - 1)$. An Erf restraint is defined as $V(x) = a(bx \cdot \operatorname{erf}(bx) + \frac{e^{-(bx)^2} - 1}{\sqrt{\pi}})$, which corresponds to an indefinite integral of the error function $\frac{dV(x)}{dx} = ab \cdot \operatorname{erf}(bx)$. The a and b parameters are calculated from the FInfinity and ForceConstant values. The Erf profile is very similar to Hyperbolic however its derivative converges to F(Inf) much faster.

There is a special restraint type, GaussianWell, that should only be used with MD BondBoost because it has a negligible force at large deviations. It is defined as $V(x) = a(1 - e^{-bx^2})$. Here, instead of the force constant and the asymptotic force value, the two parameters define the depth and the width of the well, respectively.

The following keys define global parameters for all restraints.

Restraints**Profile****Type** Multiple Choice**Default value** Harmonic**Options** [Harmonic, Hyperbolic, Erf, GaussianWell]**GUI name** Default restraint profile**Description** Select the default type of restraint profile.

The harmonic profile is most suitable for geometry optimizations but may result in very large forces that can be problematic in molecular dynamics.

For MD simulations the Hyperbolic or Erf may be more suitable because the restraint force is bounded by a user-defined value.

A per-restraint profile type can be specified after the ForceConstant value on the corresponding restraint line.

FInfinity**Type** Float**Default value** 1.0**GUI name** Default F(inf)**Description** Specify the default asymptotic value for the restraint force for the Hyperbolic and Erf profiles, in Hartree/Bohr or Hartree/radian.

A per-restraint value can be specified after the profile type on the corresponding restraint line.

The following keys define individual restraints. The force constant, profile type and the F(Inf) value can be set for each restraint individually.

Restraints**Distance****Type** String**Recurring** True**Description** Specify two atom indices followed by the distance in Angstrom and, optionally, by the ForceConstant (default is 1.0 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the distance between the two specified atoms at the given value. For periodic systems this restraint follows the minimum image convention.**Angle****Type** String**Recurring** True**Description** Specify three atom indices *i j k* followed by an angle in degrees and, optionally, by the ForceConstant (default is 0.3 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the *i-j-k* angle at the given value. For periodic systems this restraint follows the minimum image convention.**Dihedral****Type** String**Recurring** True

Description Specify four atom indices *i j k l* followed by an angle in degrees and, optionally, by the ForceConstant (default is 0.1 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the *i-j-k-l* dihedral angle at the given value. For periodic systems this restraint follows the minimum image convention.

DifDist

Type String

Recurring True

Description Specify four atom indices *i j k l* followed by the distance in Angstrom and, optionally, by the ForceConstant (default is 1.0 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the difference $R(ij)-R(kl)$ at the given value. For periodic systems this restraint follows the minimum image convention.

SumDist

Type String

Recurring True

Description Specify four atom indices *i j k l* followed by the distance in Angstrom and, optionally, by the ForceConstant (default is 1.0 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the sum $R(ij)+R(kl)$ at the given value. For periodic systems this restraint follows the minimum image convention.

A default value for the force constant depends on the restraint type: 1.0 Hartree/Bohr for Distance, SumDist and DifDist, 0.3 Hartree/radian for Angle and 0.1 Hartree/radian for Dihedral.

Below is an example if the Restraints block.

```
Restraints
  Profile Hyperbolic      # Change the default profile type
  fInfinity 10.0          # Change the asymptotic value for the restraint force away_
  ↪from optimum
# Type   Atoms   OptValue  FC   Profile  F(Inf)
Distance 1 2     5.0       1.0  Erf      1.0
Angle    1 2 3     90.0
Dihedral 4 1 2 3 180.0    0.1
# The next two together are equivalent to imposing two distance restraints: R(23) to_
  ↪0.85 Angstrom and R(14) to 0.65 Angstrom
SumDist  1 4 2 3   1.5     # Keep R(14)+R(23) as close to 1.5 Angstrom as possible
DifDist  1 4 2 3   0.2     # Keep R(14)-R(23) as close to 0.2 Angstrom as possible
End
```

9.5.6 Wall potential

This add-on adds an inward repulsive potential around the origin of the form

$$E_{\text{wall}}(r) = k \log(1 + \exp(-b(R - r)))$$

where the prefactor *k*, the radius *R*, and the gradient *b* are parameters, and *r* is the distance to the origin. The potential is time-independent and spherical. Inside the radius *R*, values for potential and forces are near zero. Outside of *R*, the potential exerts a nearly constant inward pointing force of $k \cdot b$ on each mass point⁷.

⁷ S. Grimme, *Exploration of Chemical Compound, Conformer, and Reaction Space with Meta-Dynamics Simulations Based on Tight-Binding Quantum Chemical Calculations*, *Journal of Chemical Theory and Computation* 15, 2847-2862 (2019) (<https://doi.org/10.1021/acs.jctc.9b00143>)

```

EngineAddons
  WallPotential
    Enabled Yes/No
    Gradient float
    Prefactor float
    Radius float
  End
End

```

EngineAddons**Type** Block**Description** This block configures all the engine add-ons.**WallPotential****Type** Block**Description** This block configures the addon that adds a spherical wall potential to the engine's energy and gradients.**Enabled****Type** Bool**Default value** No**Description** Enables the wall potential addon. When enabled, a spherical wall of radius [Radius] around the origin will be added. The force due to the potential will decay exponentially inside the wall, will be close to [Prefactor*Gradient] outside and exactly half of that at the wall.**Gradient****Type** Float**Default value** 10.0**Unit** 1/Angstrom**Description** The radial gradient outside the sphere.**Prefactor****Type** Float**Default value** 0.01**Unit** Hartree**Description** The multiplier for the overall strength of the potential.**Radius****Type** Float**Default value** 30.0**Unit** Angstrom**Description** The radius of the sphere, wherein the potential is close to zero.

10.1 ChemTraYzer

10.1.1 General information

The ChemTraYzer scripts, developed in the [Leonhard group](https://www.ltt.rwth-aachen.de/cms/LTT/Forschung/Forschung-am-LTT/Modellierung-und-Design-molekularer-Syst/Aktuelle-Projekte/~kqbf/ChemTraYzer/lidx/1/) (https://www.ltt.rwth-aachen.de/cms/LTT/Forschung/Forschung-am-LTT/Modellierung-und-Design-molekularer-Syst/Aktuelle-Projekte/~kqbf/ChemTraYzer/lidx/1/) at Aachen University, provide a methodology for deducing quantitative reaction models from reactive molecular dynamics (MD) simulations by identifying, quantifying, and evaluating elementary reactions of MD trajectories.

For usage with AMS, the scripts have been slightly modified and use RDKit instead of the openbabel-bindings. The original paper, Automated Discovery of Reaction Pathways, Rate Constants, and Transition States Using Reactive Molecular Dynamics Simulations, can be found [here](http://dx.doi.org/10.1021/acs.jctc.5b00201) (http://dx.doi.org/10.1021/acs.jctc.5b00201).

10.1.2 Graphical user interface

See the [combustion ReaxFF tutorial](#) .

10.1.3 Command line execution

1. Open a terminal:

- on Linux: Ctrl+Alt+T usually works, otherwise browse your application menus
- on Windows: double click `adf_command_line.bat` in your ADF installation directory (e.g. `C:/ADF2016.106`), enter 'sh' to go to a shell

2. cd into the directory where your trajectories are located with the terminal

3. Assuming your trajectory file is located in directory called `jobname.results`, running ChemTraYzer is a two step procedure

- run the processing step (with default values)

```
$AMSBIN/amspython $AMSHOME/scripting/standalone/chemtrayzer/processing_scm.py  
jobname.results
```

- run the analysis step (with default values)

```
$AMSBIN/amspython $AMSHOME/scripting/standalone/chemtrayzer/analyzing_scm.py  
jobname.results
```

You will probably want to adjust the settings. A list of all available options is shown by calling the scripts without arguments, e.g. `$AMSBIN/amspython $AMSHOME/scripting/standalone/chemtrayzer/analyzing_scm.py`

10.1.4 Results

ChemTraYzer creates several output files, the most relevant ones being:

reac.spec.tab

1st line: indices of the species, e.g. S1;S2;S3;etc...

2nd line: SMILES of the species, e.g. ;C;CC;CCO;CCOO;CO;O;[H];etc...

3rd - end: timestep, counts of the species, e.g. 150;0;0;2;... // step 150, current count of S3 == 2

reac.rate.tab

1st line: indices of the reactions, e.g. t [steps];R0;R0*;R1;R1*; // a "*" marks the back reaction

2nd line: the reactions formulated with the species indices, e.g. S0 + S0 + S0 + S13 -> S65; // see reac.spec.tab

3rd line: the reactions formulated with sum formulas, e.g. CH3 + H -> CH4, etc...

4th - ...: timestep; rate constant of the reaction; rate constant of the back reaction; etc...

reac.pic/

folder containing the 2D structures (if obabel was able to create them) `reac.pic/xyz/xyz` files of the species as they first appeared in the trajectory

10.2 ChemTraYzer2

ChemTraYzer2 (CT2) is a tool for post-processing reactive *molecular dynamics* (page 90) (MD) trajectories. The purpose of CT2 is to detect and distinguish the reactive events that occur, construct a database of unique reactions from these events, and then calculate aggregate kinetic and population properties for the trajectory. Practically speaking, CT2 is capable of greatly simplifying MD simulations into a set of useful values such as reaction rate constants¹, net fluxes for all chemical species, and occurrence counts for all reactions. ChemTraYzer2 is the successor of *ChemTraYzer* (page 269).

See also:

The GUI tutorial [Detecting reactions with ChemTraYzer 2: Hydrogen combustion with ReaxFF](#) will show you how to set up and perform a ChemTraYzer2 analysis using the Graphical User Interface.

10.2.1 New in ChemTraYzer2-2023

- trajectory population analysis
- support for trajectories with a non-constant number of atoms
- an improved reaction rates calculator
- additional output files for population statistics

¹ L.C. Kroeger et al., *Assessing Statistical Uncertainties of Rare Events in Reactive Molecular Dynamics Simulations*, *Journal of Chemical Theory and Computation* 13, 3955-3960 (2017) (<http://dx.doi.org/10.1021/acs.jctc.7b00524>)

10.2.2 Important information for using ChemTraYzer2

Bond orders are necessary for post-processing MD trajectories with ChemTraYzer2. CT2 does *not* estimate bond orders but instead uses those computed by the MD engine used to run the simulation. Though most AMS *engines* (page 251) can compute bond orders, there are some that cannot (see *Summary of engine capabilities* (page 252)). CT2 can still be used with these engines, but a bond guessing algorithm must be used to estimate the bond orders. This can be done by specifying the following settings in the MD input.

Important: When preparing MD simulations for use with CT2, it is recommended to set the `BondOrders` variable in the `Properties` block to `Yes`. This will ensure that bond orders are calculated and stored. Depending on the chosen engine's capabilities, either it will supply bond orders or a bond guessing algorithm will be used. More information on this setting can be found in [here](#) (page 244)

The quality of the ChemTraYzer2's analysis depends partially on the quality of the bond orders provided, but it is more dependent on the connectivity information (i.e., whether or not there is a bond between two atoms).

10.2.3 The ChemTraYzer2 algorithm

The following is a summary of the steps taken by ChemTraYzer2 while post-processing a MD trajectory. All of these steps are automatically conducted by ChemTraYzer2, so it is not necessary to understand them in detail in order to use ChemTraYzer2. This section is simply intended to provide the interested user with more technical information about the algorithm.

(1) Identifying all bond breaking and bond forming events in the the MD trajectory

Bond changes are fundamental to chemical reactions, and the first step of ChemTraYzer2 is to analyze the MD trajectory and detect all bond change events that occur. ChemTraYzer2 defines a bond change event as either of the following:

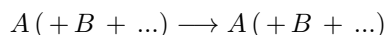
- *Bond formation* – this occurs when the bond order between 2 atoms crosses the `BondFormationThreshold` parameter between 2 MD frames. More specifically, this means the bond order between 2 atoms must be below the `BondFormationThreshold` in one frame and then above it in the subsequent frame.
- *Bond breakage* – this occurs when the bond order between 2 atoms decreases to below the `BondBreakingThreshold`. It is defined analogously to *bond formation*.

(2) Filtering and combining all bond change events into stable reactions using the TStable criterion

Many bond change events in a MD trajectory might represent the formation of short-lived intermediates that do not need to be explicitly included in the complete reaction. These intermediates, though perhaps important to the mechanism, do not affect the overall reactants and products of a reaction and may introduce unwanted complexity to ChemTraYzer2 output. For this reason, the adjustable parameter `TStable` is used to filter out reactive intermediates which exist for an amount of time less than `TStable`. An example of using `TStable` to filter reactions is provided below.

(3) Removing all reactions that have the same reactants and products

It is not uncommon for chemical equilibria to be observed in certain MD trajectories. Certain equilibria occur on a very short time-scale, meaning a series of bond change events may be filtered out using the `TStable` criterion. In these cases, the remaining reaction can have identical molecules on both sides of the reaction, as shown below.



These reactions are removed from the final reaction list as they have no effect on net species fluxes, rate constants, etc.

Note: Reactions that involve bond changes but result in the same molecules will also be filtered. For example, the following proton transfer will not be included in the final reaction list: $\text{H}_3\text{O}^+ + \text{H}_2\text{O} \rightarrow \text{H}_2\text{O} + \text{H}_3\text{O}^+$. Options for

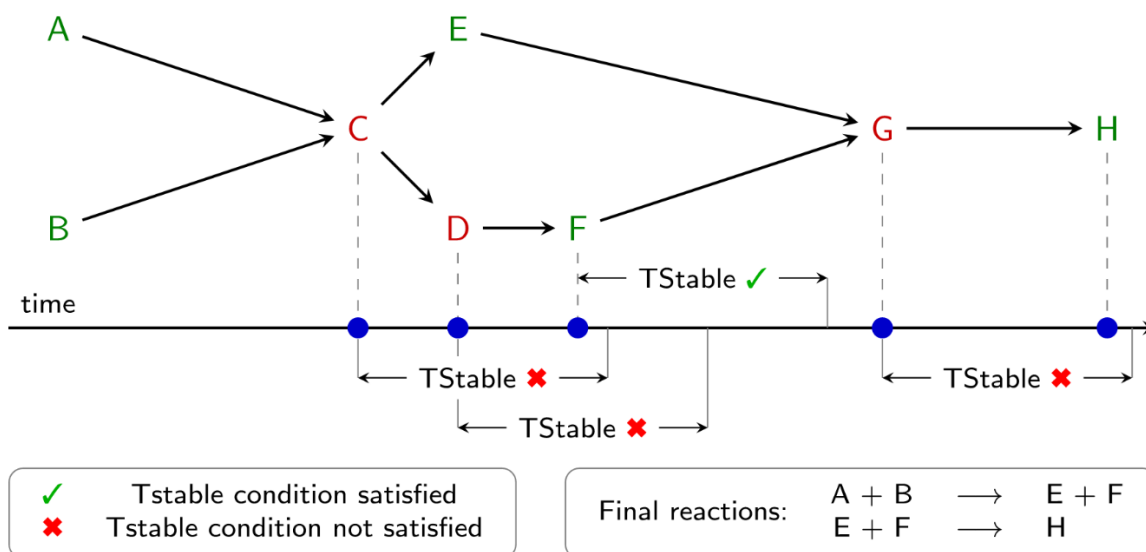


Fig. 10.1: An example of how ChemTraYzer2 filters reaction events based on the `TStable` criterion. In this reaction network, all species in red are determined to be short-lived intermediates and do not appear in the final reactions.

including these reactions will be present in the next version of CT2.

(4) Aggregating equivalent reactions

After the filtering steps are complete, all equivalent reaction events are combined into a set of unique reactions that have occurred in the MD trajectory. More specifically, the *reaction event* $A \rightarrow B$ may have happened multiple times in the trajectory, and each of these will count toward one occurrence of the $A \rightarrow B$ reaction. More detail about determining when two reactions (or molecules) are equivalent is provided in the following section.

10.2.4 Distinguishing reactions with ChemTraYzer2

In ChemTraYzer2, reactions are determined to be equivalent using a very straightforward condition: two reactions (R1 and R2) are equivalent if the sets of reactant/product molecules of R1 and the sets of reactant/product molecules of R2 are equivalent. Comparing reactions in this way requires defining the equivalence of two individual molecules, and this is more challenging to assess. In the original ChemTraYzer, molecule equivalence is determined via a comparison of canonical SMILES strings. Though SMILES can represent a large number of chemical structures, they fall short in representing the complete space of chemical reactions. For this reason, ChemTraYzer2 evaluates each molecule using a subgraph-based descriptor, which is generalizable to the complete reactive chemical space. ChemTraYzer2's subgraph descriptor builds local atomic environments using a breath-first search of each atom in a molecule, evaluates a unique hash value for each atom, and finally sums these hash values to produce a unique hash value for each unique molecule. This is summarized in the figure below.

Note: The current version of the subgraph descriptors do not distinguish stereoisomers

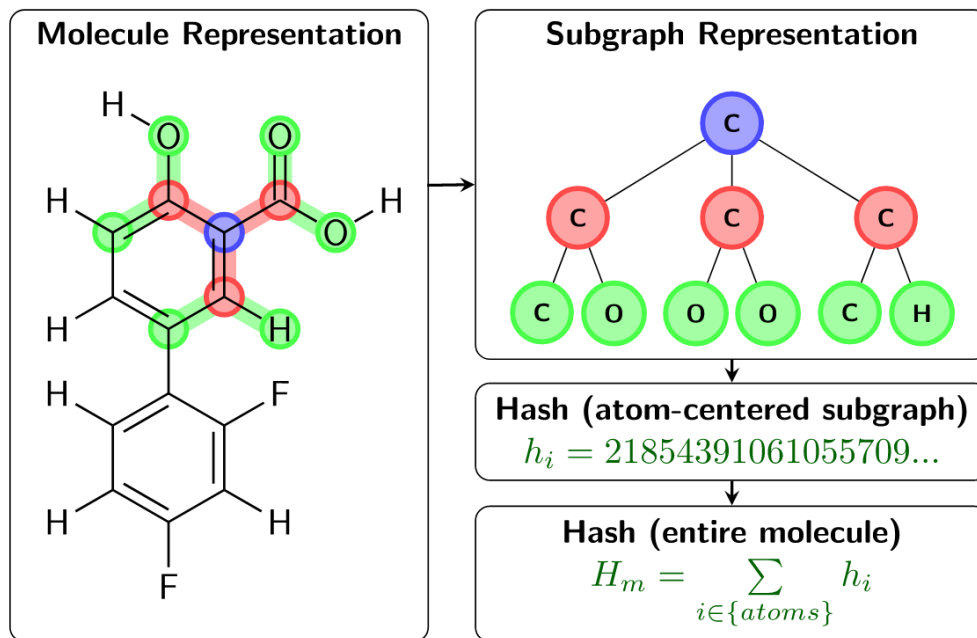


Fig. 10.2: The subgraph-based descriptors used to distinguish molecules in ChemTraYzer2

10.2.5 Using ChemTraYzer2 from the GUI

ChemTraYzer2 is fully supported in the AMS GUI. A thorough description of using the GUI can be found in the [ChemTraYzer2 GUI tutorial](#).

10.2.6 Tips for getting the most out of ChemTraYzer2

The MD simulation

- It is important to ensure the simulation is on a **time scale that is long enough to observe multiple reaction events**. Multiple occurrences of reactions improve the accuracy of calculations of kinetic parameters such as reaction rate constants.
- **The sampling frequency of MD trajectories should be sufficiently small** to observe all important reactions. In AMS MD simulations, this is controlled by the `SamplingFreq` keyword in the `Trajectory` block (see the [Molecular dynamics](#) (page 90) page for more details). If the sampling frequency is too large, important reaction events may not be detected by ChemTraYzer2, which will have an effect on the quality of the reported properties. A rough recommendation would be to set the sampling frequency to at most 10 for a time step of 0.25 fs, but the best value for this parameter depends on the temperature of the simulation.

ChemTraYzer2 Settings

- **Set the `TStable` parameter to an appropriate value.** Typically, the default value will work for many applications. However, the user can adjust this parameter to generate output on the spectrum between *many reactive intermediates* (low `TStable`) and *a summary of only the main reactions* (high `TStable`). Generally, it is best to adjust `TStable` to a level where all important intermediates are long-lived enough to appear in the final output. You may want to perform a few CT2 analysis using different values for `TStable` to see how this affects the results.
- **Set the `BondBreakingThreshold` and `BondFormationThreshold` parameters to appropriate values for the chemical system.** The default values are suitable for most types of systems, but these threshold values may need to be changed in certain cases (e.g., the MD engine calculates bond orders with a systematic error, bonds in the system have partial ionic character, etc.).
- **Set the rate confidence interval `RateConfidence` to adjust bounds for the reaction rate constants.** CT2 assumes the number of observed reactive events are distributed according to a Poisson distribution, where the expected value is used to calculate the reaction rate constant. The confidence interval specifies what ratio of the event counts will fall between the lower and upper bounds, with the condition that both bounds represent an equal number of events. Usually, a confidence interval of 95% is used, which corresponds roughly to 2σ in a normal distribution. For more details about this approach, see [Page 325, 1](#).

10.2.7 Minimal input

This is the minimal input script for performing a chemtrayzer2 analysis of your MD trajectory:

```
#!/bin/sh

$AMSBIN/chemtrayzer2 << EOF
  Trajectory
    Path path/to/the/ams/results/folder
  End
EOF
```

10.2.8 Input options

Several input options can be specified in the chemtrayzer2 input.

The trajectory the user wants to analyze can be specified in the `Trajectory` block:

```
Trajectory
  FinalFrame integer
  FirstFrame integer
  Path string
End
```

Trajectory

Type Block

Description Info regarding the trajectory to analyze.

FinalFrame

Type Integer

Default value -1

Description Last frame of the trajectory to analyze.

FirstFrame

Type Integer

Default value 1

Description First frame of the trajectory to analyze.

Path

Type String

Description The path to ams results dir of an AMS calculation. This folder must contain a ams.rkf file.

Reaction detection options can be specified in the `ReactionDetection` block:

```
ReactionDetection
  BondBreakingThreshold float
  BondFormationThreshold float
  InitialBondThreshold float
  TStable float
End
```

ReactionDetection

Type Block

Description Parameters for the the reaction detection algorithm.

BondBreakingThreshold

Type Float

Default value 0.3

Description The bond-order threshold for bond breaking. If the bond order of a bond goes below this value, the bond is considered broken.

BondFormationThreshold

Type Float

Default value 0.8

Description The bond-order threshold for bond formation. If the bond order between two atoms goes above this value, then this will be considered to be a new bond.

InitialBondThreshold

Type Float

Description The bond-order threshold for determining the connectivity for the first frame of the simulation. If not specified, the value in `BondFormationThreshold` will be used instead.

TStable

Type Float

Default value 10.0

Unit fs

GUI name T stable

Description The minimum time for a molecule to be considered stable.

Options for the analysis of the reactions:

```
Analysis
  PerformAnalysis Yes/No
  RateConfidence float
End
```

Analysis

Type Block

Description Statistical post-detection analysis, includes reaction coefficients calculation.

PerformAnalysis

Type Bool

Default value Yes

Description Determine the reaction rate coefficients and statistical errors for the detected reactions.

RateConfidence

Type Float

Default value 0.9

Description Upper and lower bounds to the rate coefficients will be calculated for this confidence ($0 < \text{confidence} < 1$), assuming a Poisson distribution of the number of reactive events. A value of 0.9 means that the kinetics of 90% of events of one reaction can be described by a coefficient between the bounds.

Options for Output file writing:

```
Output
  CreateLegacyOutput Yes/No
  ShowReactionGraph Yes/No
  WriteEventsPerTime Yes/No
  WriteMolPopulation Yes/No
  WriteReactions Yes/No
  WriteXYZFiles Yes/No
End
```

Output

Type Block

Description Settings for program output and output file generation.

CreateLegacyOutput

Type Bool

Default value No

Description Whether to save the reactions, species, and rates as 'react.react.tab', 'react.spec.tab', and 'react.rate.tab' in the same format as ChemTraYzer 1.

ShowReactionGraph

Type Bool

Default value No

Description Whether or not to show the reaction graph at the end of the calculation. Requires the python library matplotlib to be installed.

WriteEventsPerTime**Type** Bool**Default value** No**Description** Write two .csv files that contain the number of reactions in every frame (`reaction_events_per_time.csv`) and the number of bond changes in every frame (`bond_change_events_per_time.csv`)**WriteMolPopulation****Type** Bool**Default value** No**Description** Write two .csv files: (1) `mol_statistics.csv`, which contains basic population statistics (counts, averages) for each unique species over the entire trajectory; and (2) `mol_population.csv`, which provides the count of each unique species in every frame.**WriteReactions****Type** Bool**Default value** Yes**Description** Write two .csv files that contain information about (1) all unique reactions (`reactions.csv`); and (2) all individual reaction events (`reaction_events.csv`).**WriteXYZFiles****Type** Bool**Default value** No**Description** Write XYZ files (geometries) for detected species and XYZ movies for detected reactions into a subfolder named 'xyz'.

10.2.9 Output

Summarizing reactions

ChemTraYzer2 produces 2 main output files for summarizing reactions, `reaction_events.csv` and `reactions.csv`. These 2 files are produced with the option `WriteReactions` in the `Output` block.

`reaction_events.csv`

This file contains a list of all bond breaking or bond forming events. These events are complete reactions that occur for some specific set of molecules at some specific point in the trajectory. Various important properties are included in this file, a few of which are listed below.

- `Initial frame` – the MD frame at which the bond change event began
- `Final frame` – the MD frame at which the bond change event ended
- `Reactants/Products` – a SMILES-like representation of molecules involved in the reaction
- `Reactants atoms indices/Products atoms indices` – the atom indices of the molecules involved in the reaction

reactions.csv

This file contains aggregate information about all unique reactions that occurred in the trajectory. A few important properties contained in this file are listed below.

- `Rate constant` – the calculated value of the reaction rate constants. Note that the units for the reaction rate depend on the reaction order.
- `Number of events` – the number of times this reaction occurred in the trajectory
- `Reaction event indices` – the indices of all reactive events that are equivalent to this reaction. The indices correspond to indices in the `reaction_events.csv` file.

Reaction frequency

The option `WriteEventsPerTime` in the `Output` block will produce two files that detail the accumulated number of reactions and reaction events per frame over the entire trajectory.

reaction_events_per_time.csv

- `Frame` – the MD frame
- `Time` – the simulation time for the frame
- `Events` the number of reactions that *begin* in the specified frame

bond_change_events_per_time.csv

- `Frame` – the MD frame
- `Time` – the simulation time for the frame
- `Events` the number of bond change events that occur in the specified frame

Molecular population analysis

The option `WriteMolPopulation` in the `Output` block will produce two files that provide summary statistics for each unique molecule in the trajectory as well as population counts for all frames.

mol_statistics.csv

- `Molecule hash` – the hash value used to identify a molecule
- `SMILES` – the SMILES representation of a molecule, should one be available
- `Average count` – the average number of molecule over the entire trajectory
- `Average conc.` – the average concentration (in mol/L) of molecule over the entire trajectory
- `Mann-Kendall value` – a value in the range [-1,1] that indicates whether a molecule behaves more like a reactant (with a maximum value of -1) or a product (with a maximum value of +1). Intermediates are expected to have values around 0.

mol_population.csv

- `Frame` – the MD frame
- `Time` – the simulation time for the frame
- `Count` the number of a particular molecule in a particular frame

Geometry output

The option `WriteXYZFiles` will produce xyz files for each unique molecule and a series of xyz frames for each unique reaction. These files are named according to the molecule and reaction indices and will be placed into a directory called `xyz`.

Additional output files

In addition to the main csv output files, ChemTraYzer2 generates a `gml` (https://en.wikipedia.org/wiki/Graph_Modelling_Language) file (`reaction_network.gml`) containing the full reaction network. At the moment, we don't offer any built-in tool for visualizing or manipulating this file. The savvy user might want to import and analyze the `.gml` file using the `networkx` (<https://networkx.org/>) python library or visualize it with third party graph visualization tools.

10.2.10 References

10.3 Trajectory Analysis

`analysis` is a standalone program that performs analysis of molecular dynamics trajectories created with AMS. It can produce histograms and radial distribution functions. It is used under the hood in `AMSmovie` (**MD Properties** menu bar).

10.3.1 New in Trajectory Analysis-2023

- Intra- and inter-molecular radial distribution functions
- Properties used to compute autocorrelation or mean square displacement can be stored to file
- Manual selection of coordinate unwrapping for autocorrelation or mean square displacement functions

10.3.2 General Input Options

This example computes the oxygen-oxygen radial distribution function of a MD simulation using the analysis utility program:

```
Task RadialDistribution

TrajectoryInfo
  Trajectory
    KFFilename ams.results/ams.rkf
    Range 1 1000 2
  End
```

(continues on next page)

(continued from previous page)

```

End
RadialDistribution
  NBins 1000
  AtomsFrom
    Element O
  End
  AtomsTo
    Element O
  End
End
eor

```

The analysis program reads one or more trajectory files (filename.rkf) from an AMS molecular dynamics (MD) or a Grand Canonical Monte Carlo (GCMC) simulation. The file information is supplied in the `TrajectoryInfo` input block. In this block, a separate `Trajectory` subblock needs to be supplied for each trajectory file. The `Trajectory` subblock contains a mandatory keyword `KFFilename`, and an optional keyword `Range`. The latter contains the initial frame to be read, the final frame to be read, and optionally the stepsize. By default all frames on the trajectory file are read.

```

TrajectoryInfo
  NBlocksToCompare integer
  Trajectory
    KFFilename string
    Range integer_list
    StepSize integer
  End
End

```

TrajectoryInfo**Type** Block**Description** All the info regarding the reading of the trajectory files.**NBlocksToCompare****Type** Integer**Default value** 1**Description** Get an error estimate by comparing histograms for `NBlocks` time blocks of the trajectory.**Trajectory****Type** Block**Recurring** True**Description** All info regarding the reading of a single trajectory file.**KFFilename****Type** String**Default value** ams.rkf**Description** The name of the AMS trajectory file.**Range****Type** Integer List

Description One or two values: start frame, and optionally end frame. By default the first and last frame are read.

StepSize

Type Integer

Default value 1

Description The step size at which frames are read from the RKF (default 1, every frame is read).

All tools in the analysis program provide an option to obtain information on the equilibration of the simulation. If the optional keyword `NBlocksToCompare` in the `TrajectoryInfo` block is set to a value N higher than 1, the trajectory is divided into N blocks, and the analysis results for each block are compared. The variation in the analysis result is provided as a standard deviation.

10.3.3 Radial Distribution Function (RDF)

The Analysis tool computes radial distribution functions $g(r)$ if the `Task` keyword is set to `RadialDistribution`.

```
Task [RadialDistribution | Histogram | AutoCorrelation | MeanSquareDisplacement | ↵
↵AverageBinPlot]
```

Task

Type Multiple Choice

Options [RadialDistribution, Histogram, AutoCorrelation, MeanSquareDisplacement, AverageBin-Plot]

Description The analysis task.

Further details on the radial distribution functions are then set in the `RadialDistribution` block. If more than one `RadialDistribution` block is present in the input, more than one radial distribution function will be computed. The result is printed to output as text, as well as stored in a binary file (plot.kf).

Description

A radial distribution function $g(r)$, or pair correlation function, is a density of distances between particles, relative to the average distance density. The x -axis variable represents a distance r , while the y -axis represents the relative density of that distance. For a complete homogeneous system of particles the $g(r)$ values for the distances between all particles equals 1 everywhere.

Two sets of atoms S_{from} and S_{to} , of length n_{from} and n_{to} respectively, are specified with the keywords `AtomsFrom` and `AtomsTo` in the `RadialDistribution` block. As a result the program computes $n_{\text{from}} * n_{\text{to}}$ distances r_{ij}^s between atom i in S_{from} and atom j in S_{to} for each trajectory frame s out of a total of n_{frames} frames.

A normalized histogram is then computed from these distances, resulting in a function $N(r)$.

$$N(r) = \frac{1}{n_{\text{frames}}} \sum_{s=1}^{n_{\text{frames}}} \sum_{i=1}^{n_{\text{from}}} \sum_{j=1}^{n_{\text{to}}} \delta(r_{ij}^s - r).$$

This histogram is converted to a density, by dividing all values $N(r)$ with the volume $V(r) = 4\pi r^2 dr$ of a sphere-slice at radius r with thickness dr .

The density is further converted to a relative density by dividing with the total density of the system $\rho_{\text{tot}} = \frac{n_{\text{from}} * n_{\text{to}}}{V_{\text{tot}}}$, yielding the final radial distribution function $g(r)$.

$$g(r) = \frac{N(r)}{V(r) * \rho_{\text{tot}}}$$

Options

Non-periodic systems The above equation assumes that the volume V_{tot} of the system is a well-defined quantity. This assumption is correct for systems with 3D periodicity, where the V_{tot} is defined as the volume of the periodic cell. In such a system the value of r can be no larger than r_{max} , the radius of the largest sphere that can be placed inside the periodic cell.

If a system is non-periodic in one or more direction, then the program still computes a $g(r)$, only if the radius r_{max} is supplied by the user with the `Range` keyword in the `RadialDistribution` block. The radius is the second value supplied.

```
RadialDistribution
  Range float_list
End
```

RadialDistribution

Type Block

Recurring True

Description All input related to radial distribution functions.

Range

Type Float List

Description Either one, two, or three real values. If one it is the stepsize. If two, it is the minimum value and the maximum value. If three, it is the minimum value, the maximum value, and the stepsize. The stepsize overrides NBins.

In this case the volume V_{tot} is assumed to be the volume of a sphere with radius r_{max} .

NPT simulations The above equation further assumes that the volume V_{tot} is constant throughout the simulation. The $g(r)$ of the trajectory from an NPT simulation can still be computed, and in this case V_{tot} is the average value of the volume of the periodic cell.

Simulations with varying numbers of atoms The above equation also assumes that n_{from} and n_{to} remain constant throughout the simulation. However, in a Molecular Gun simulation particles can be added to the system, and in a GCMC simulation particles can be both added and removed from the system. Nonetheless, the program still computes a $g(r)$ in these situations.

If the `AtomsFrom` and `AtomsTo` blocks contain element names (supplied with the recurring `Element` keyword), then every time atoms are added to or removed from the system, the sets of atoms \mathbb{S}_{from} and \mathbb{S}_{to} are re-evaluated.

If the `AtomsFrom` and `AtomsTo` blocks contain atom numbers (supplied with the recurring `Atom` keyword), these numbers are updated in the sets \mathbb{S}_{from} and \mathbb{S}_{to} every time atoms are added to or removed from the system. If one of the atoms from the set disappears, the number of distances contributing to the $g(r)$ decreases.

Note: Currently, the values of n_{from} and n_{to} in the normalization factor are taken from the last frame of the simulation.

Warning: If multiple trajectories are supplied, and the number of atoms changes between the end of one trajectory and the beginning of another, this may result in an error in the atom numbers used by the program internally.

Inter- or intra-molecular atom-pairs By default, all $n_{\text{from}} * n_{\text{to}}$ distances are included. Sometimes it can be convenient to view exclusively the distances between atoms within a molecule, or those between different molecules. This can be controlled with the keyword `DistanceTypeSelection` in the `RadialDistribution` block.

```
RadialDistribution
  DistanceTypeSelection [All | InterMolecular | IntraMolecular]
End
```

RadialDistribution**Type** Block**Recurring** True**Description** All input related to radial distribution functions.**DistanceTypeSelection****Type** Multiple Choice**Default value** All**Options** [All, InterMolecular, IntraMolecular]**Description** Select only a certain type of interatomic distances.

10.3.4 Histogram

The Analysis program computes histograms if the `Task` keyword is set to `Histogram`.

```
Task [RadialDistribution | Histogram | AutoCorrelation | MeanSquareDisplacement | ↵
↵AverageBinPlot]
```

Task**Type** Multiple Choice**Options** [RadialDistribution, Histogram, AutoCorrelation, MeanSquareDisplacement, AverageBin-Plot]**Description** The analysis task.

Further details on the histogram need to be specified in the `Histogram` block. If more than one `Histogram` block is present in the input, more than one histogram will be computed. The result is printed to output as text, as well as stored in a binary file (`plot.kf`). By default the histogram contains the number of occurrences of a certain value, but the normalized occurrence is provided if the keyword `Normalized` in the `Histogram` block is specified.

```
Histogram
  Normalized Yes/No
End
```

Histogram**Normalized****Type** Bool**Default value** No**Description** Give the normalized histogram.

Histograms can be computed for every quantity stored on the molecular dynamics trajectory file (`ams.rkf`) in the section `History`. Example quantities are `PotentialEnergy`, `KineticEnergy`, `TotalEnergy`, `Temperature`. In the histogram block, this quantity is selected with the keyword `Variable` in the `Axis` subblock. If more than one `Axis` subblock is present, the dimensionality of the histogram is increased: Three `Axis` subblocks result in a 3D histogram.

For each histogram axis, the number of bins can be selected with the `NBins` keyword in the `Axis` block, in which case the range of values along each axis is automatically determined. The default `NBins` value is 100.

Alternatively, a range and a stepsize can be selected with the keyword `Range` in the `Axis` subblock. The keyword `Range` can contain one, two, or three values: 1: Only a stepsize. 2: A smallest value and a largest value. 3: A smallest value, a largest value, and the stepsize.

```
Histogram
  Axes
    Axis
      NBins integer
      Range float_list
      Variable string
    End
  End
End
```

Histogram**Type** Block**Recurring** True**Description** All input related to histograms.**Axes****Type** Block**Description** Specifications for the histogram axes.**Axis****Type** Block**Recurring** True**Description** Specifications for a single histogram axis.**NBins****Type** Integer**Default value** 100**Description** The number of bins along the histogram axis.**Range****Type** Float List**Description** Either one, two, or three real values. If one it is the stepsize. If two, it is the minimum value and the maximum value. If three, it is the minimum value, the maximum value, and the stepsize. The stepsize overrides NBins.**Variable****Type** String**Description** The quantity along the histogram axis.

10.3.5 Autocorrelation Functions

The Analysis program computes autocorrelation functions (ACF) if the Task keyword is set to AutoCorrelation.

```
Task [RadialDistribution | Histogram | AutoCorrelation | MeanSquareDisplacement | ↵
↵AverageBinPlot]
```

Task

Type Multiple Choice

Options [RadialDistribution, Histogram, AutoCorrelation, MeanSquareDisplacement, AverageBin-Plot]

Description The analysis task.

Further details need to be specified in the AutoCorrelation block. If more than one AutoCorrelation block is present in the input, more than one ACF will be computed. The result is printed to output as text, as well as stored in a binary file (plot.kf).

```
AutoCorrelation
  Atoms
    Atom integer
    Element string
  End
  DataReading [Auto | AtOnce | BlockWise]
  InputValues
    Values float_list
  End
  MaxFrame integer
  NPointsHighestFreq integer
  PerElement Yes/No
  Property [Velocities | DipoleMomentFromCharges | InputValues | ↵
↵DiffusionCoefficient |
    DipoleDerivativeFromCharges | PressureTensor | Viscosity]
  TimeStep float
  UnwrapCoordinates [Auto | Yes | No]
  UseAllValues Yes/No
  VecElements
    Index integer
  End
  WritePropertyToKF Yes/No
End
```

AutoCorrelation

Atoms

Type Block

Description Relevant if Property is set to Velocities, DipoleMomentFromCharges, DipoleDerivativeFromCharges, or DiffusionCoefficient. Atom numbers or elements for the set of atoms for which the property is read/computed. By default all atoms are used.

Atom

Type Integer

Recurring True

Description Atom number.

Element**Type** String**Recurring** True**Description** Element Symbol Atom.**DataReading****Type** Multiple Choice**Default value** Auto**Options** [Auto, AtOnce, BlockWise]**Description** The KF data can be read in and handled once, or blockwise. The former is memory intensive, but mostly faster. If Auto is selected, the data is read at once if it is less than 1 GB, and blockwise if it is more.**InputValues****Type** Block**Description** Relevant if Property is set to InputValues. All input values (a vector on each line) need to be provided in this block, using the keyword Values (possibly multiple times).**Values****Type** Float List**Recurring** True**Description** The values at each step (on a single line)**MaxFrame****Type** Integer**Description** The maximum number of frames for which the autocorrelation function will be computed. The default is half of the number of provided frames.**NPointsHighestFreq****Type** Integer**Default value** 4**Description** The number of points (timesteps) used for the highest frequency displayed in spectrum. This determines up to which frequency the spectrum is displayed. If the spacing between time-steps used for the ACF is 1 fs, then by default the maximum frequency displayed is 0.25 fs⁻¹ (or 8339 cm⁻¹). This corresponds to a (default) value of NPointsHighestFreq of 4. A higher number selected here, will result in a lower maximum frequency returned by the program. The lowest possible value (spectrum up to highest possible frequency) is 2.**PerElement****Type** Bool**Default value** No**Description** Compute ACF for all elements in the system. Any other settings in the block will be used.**Property****Type** Multiple Choice

Default value DipoleDerivativeFromCharges

Options [Velocities, DipoleMomentFromCharges, InputValues, DiffusionCoefficient, DipoleDerivativeFromCharges, PressureTensor, Viscosity]

Description Compute the ACF either from velocities (from rkf), the dipole moment (from coordinates and atomic charges in rkf), the dipole moment derivative (from velocities and atomic charges in rkf), from the pressure tensor (from rkf), or from values specified in input. Selecting DiffusionCoefficient is equivalent to selecting Velocities. The default, DipoleDerivativeFromCharges, results in the computation of an IR spectrum.

TimeStep

Type Float

Description Relevant if Property is set to InputValues. The time separating the entries (in fs). If Property is set to any of the other quantities, it can be read from an RKF file, and the timestep is read from the RKF file as well. The read value then overrides this keyword.

UnwrapCoordinates

Type Multiple Choice

Default value Auto

Options [Auto, Yes, No]

Description If the coordinates are involved in the requested property, those coordinates are wrapped into the box at each time step. If set to true, this keyword unwraps those coordinates so that the trajectory is continuous. If not provided the code uses automatic defaults.

UseAllValues

Type Bool

Default value No

Description By default the same number of values are used for each t-step in the ACF. This has the advantage that all values in the ACF are equally reliable, but it does mean that for the smaller timesteps much of the data is not used. To switch this off and use all data, UseAllValues can be set to true

VecElements

Type Block

Description A set of indices referring to a subset of the property vector. Works in combination with the atoms block. For example, in combination with the property Velocities, the Atoms block allows the selection of a subset of atoms, while the VecElements block allows the selection of a subset of vector elements (e.g. 1 and 2 for the elements x and y). Currently not implemented with InputValues.

Index

Type Integer

Recurring True

Description Element of the property vector.

WritePropertyToKf

Type Bool

Default value No

Description Write the selected property to the KF files for every requested frame

Description

An autocorrelation function $C(t)$ describes the average correlation (overlap) of a (vector) property **A** with itself as a function of time.

$$C(t) = \langle \mathbf{A}(0) \cdot \mathbf{A}(t) \rangle$$

The average runs over all time-intervals $(t_0, t_0 + t), (t_1, t_1 + t), \dots, (t_N, t_N + t)$, with $t_N = t_n - t_m$. Here n is the total number of frames read from the trajectory (as determined in the block `TrajectoryInfo`), and m is the number of discrete t values for which $C(t)$ is computed. The value m can be set with the keyword `MaxFrame`, and defaults to half the total number of frames read. As stated above, the default average runs over the same number of time intervals for each value of t . If `UseAllValues` is selected, the average runs over all available time intervals for each value of t , which is large for small t , and smallest (N) for t_m .

The normalized autocorrelation function $c(t)$ describes the decorrelation of the property with time, and always starts at 1.0 at $t = 0$.

$$c(t) = \frac{\langle \mathbf{A}(0) \cdot \mathbf{A}(t) \rangle}{\langle \mathbf{A}(0) \cdot \mathbf{A}(0) \rangle}$$

In most cases short timescale fluctuations are important, so frequent storage of the desired property is required (when preparing the molecular dynamics simulation, set the `Frequency` keyword in the `Trajectory` block of the `MolecularDynamics` settings low, preferably to 1).

A power spectrum is automatically computed by Fourier transform of the autocorrelation function, and provides information on the frequencies of the signal. When the selected property is the dipole moment or the dipole moment derivative, the power spectrum matches the IR spectrum.

Properties

Autocorrelation functions can be computed for different simulation properties: 1) Dipole moments from coordinates and atomic charges 2) Dipole moment derivatives from velocities and atomic charges 3) Velocities 4) The pressure tensor 5) User provided values. Selecting 6) Diffusion coefficient is equivalent to selecting *Velocities*.

```
AutoCorrelation
  Property [Velocities | DipoleMomentFromCharges | InputValues | ↵
↵DiffusionCoefficient |
          DipoleDerivativeFromCharges | PressureTensor | Viscosity]
End
```

AutoCorrelation

Type Block

Recurring True

Description All input related to auto correlation functions.

Property

Type Multiple Choice

Default value DipoleDerivativeFromCharges

Options [Velocities, DipoleMomentFromCharges, InputValues, DiffusionCoefficient, DipoleDerivativeFromCharges, PressureTensor, Viscosity]

Description Compute the ACF either from velocities (from rkf), the dipole moment (from coordinates and atomic charges in rkf), the dipole moment derivative (from velocities and atomic charges in rkf), from the pressure tensor (from rkf), or from values specified in input. Selecting DiffusionCoefficient is equivalent to selecting Velocities. The default, DipoleDerivativeFromCharges, results in the computation of an IR spectrum.

Some of the properties for which an autocorrelation function can be computed are simply read as is from the trajectory RKF file, but others are quite complex. For example, the dipole moment is a property obtained by reading the coordinates and the atomic charges, multiplying each atomic position vector with the corresponding charge, and then summing over all atoms. With the keyword `WritePropertyToKF` in the `AutoCorrelation` block, the user can choose to store not only the autocorrelation function, but also the property used to produce it.

```
AutoCorrelation
  WritePropertyToKF Yes/No
End
```

AutoCorrelation

Type Block

Recurring True

Description All input related to auto correlation functions.

WritePropertyToKF

Type Bool

Default value No

Description Write the selected property to the KF files for every requested frame

If a property involves atomic coordinates, then this generally means atomic coordinates wrapped into the periodic box at every time step. As a result, coordinates can make seemingly big jumps from one side of the box to another between two consecutive frames. The code is able to unwrap the coordinates, so that all atoms follow a continuous trajectory. For the DipoleMoment property, the wrapped coordinates will be used by default, but an experienced user can determine whether the wrapped or unwrapped coordinates are used with the keyword `UnwrapCoordinates` in the `AutoCorrelation` block.

```
AutoCorrelation
  UnwrapCoordinates [Auto | Yes | No]
End
```

AutoCorrelation

Type Block

Recurring True

Description All input related to auto correlation functions.

UnwrapCoordinates

Type Multiple Choice

Default value Auto

Options [Auto, Yes, No]

Description If the coordinates are involved in the requested property, those coordinates are wrapped into the box at each time step. If set to true, this keyword unwraps those coordinates so that the trajectory is continuous. If not provided the code uses automatic defaults.

Options

With the keyword `MaxFrame` the number of values m in the autocorrelation function ($t = [0, t_1, t_2, \dots, t_m]$) can be set. The default value is half of the total number of frames n read from the trajectory.

A subset of atoms for which the property `A` should be selected/computed can be provided in the block `Atoms`. The block can contain element names (recurring keyword `Element`), or individual atom numbers (recurring keyword `Atom`).

```
AutoCorrelation
  Atoms
    Atom integer
    Element string
  End
End
```

AutoCorrelation

Type Block

Recurring True

Description All input related to auto correlation functions.

Atoms

Type Block

Description Relevant if Property is set to `Velocities`, `DipoleMomentFromCharges`, `DipoleDerivativeFromCharges`, or `DiffusionCoefficient`. Atom numbers or elements for the set of atoms for which the property is read/computed. By default all atoms are used.

Atom

Type Integer

Recurring True

Description Atom number.

Element

Type String

Recurring True

Description Element Symbol Atom.

A subset of vector elements can be provided with the subblock `VecElements`. By default all vector elements found on the RKF file will be used.

```
AutoCorrelation
  VecElements
    Index integer
  End
End
```

AutoCorrelation

Type Block

Recurring True

Description All input related to auto correlation functions.

VecElements

Type Block

Description A set of indices referring to a subset of the property vector. Works in combination with the atoms block. For example, in combination with the property Velocities, the Atoms block allows the selection of a subset of atoms, while the VecElements block allows the selection of a subset of vector elements (e.g. 1 and 2 for the elements x and y). Currently not implemented with InputValues.

Index

Type Integer

Recurring True

Description Element of the property vector.

10.3.6 Mean Square Displacement

The Analysis program computes mean square displacements (MSD) if the Task keyword is set to MeanSquareDisplacement.

```
Task [RadialDistribution | Histogram | AutoCorrelation | MeanSquareDisplacement | ↵
↵AverageBinPlot]
```

Task

Type Multiple Choice

Options [RadialDistribution, Histogram, AutoCorrelation, MeanSquareDisplacement, AverageBin-Plot]

Description The analysis task.

Further details need to be specified in the MeanSquareDisplacement block. If more than one MeanSquareDisplacement block is present in the input, more than one MSD will be computed. The result is printed to output as text, as well as stored in a binary file (plot.kf).

```
MeanSquareDisplacement
  Atoms
    Atom integer
    Element string
  End
  DataReading [Auto | AtOnce | BlockWise]
  InputValues
    Values float_list
  End
  MaxFrame integer
  PerElement Yes/No
  Property [Coords | InputValues | DiffusionCoefficient]
  StartTimeSlope float
  TimeStep float
  UnwrapCoordinates [Auto | Yes | No]
  UseAllValues Yes/No
  VecElements
    Index integer
  End
  WritePropertyToKF Yes/No
End
```

MeanSquareDisplacement

Atoms**Type** Block**Description** Relevant if Property is set to any quantity that is available per atom (Coords, DiffusionCoefficient). Atom numbers or elements for the set of atoms for which the property is read/computed are provided here. By default all atoms are used.**Atom****Type** Integer**Recurring** True**Description** Atom number.**Element****Type** String**Recurring** True**Description** Element Symbol Atom.**DataReading****Type** Multiple Choice**Default value** Auto**Options** [Auto, AtOnce, BlockWise]**Description** The KF data can be read in and handled once, or blockwise. The former is memory intensive, but mostly faster. If Auto is selected, the data is read at once if it is less than 1 GB, and blockwise if it is more.**InputValues****Type** Block**Description** Relevant if Property is set to InputValues. All input values (a vector on each line) need to be provided in this block, using the keyword Values (possibly multiple times).**Values****Type** Float List**Recurring** True**Description** The values at each step (on a single line)**MaxFrame****Type** Integer**Description** The maximum number of frames for which the mean square displacement function will be computed. The default is half of the number of provided frames.**PerElement****Type** Bool**Default value** No**Description** Compute MSD for all elements in the system. Any other settings in this block will be used.**Property**

Type Multiple Choice

Default value Coords

Options [Coords, InputValues, DiffusionCoefficient]

Description Compute the MSD from the property selected here (from rkf). Selecting Diffusion-Coefficient is equivalent to selecting the property Coords.

StartTimeSlope

Type Float

Default value 0.0

Description The MSD has a nonlinear regime at short timescales, and a linear regime at long timescales. To determine the slope, the starting point for the linear regime has to be determined. This keyword sets the starting time in fs. If set to zero, the starttime will be automatically determined.

TimeStep

Type Float

Description Relevant if Property is set to InputValues. The time separating the entries (in fs). If Property is set to any of the other quantities, it can be read from an RKF file, and the timestep is read from the RKF file as well. The read value then overrides this keyword.

UnwrapCoordinates

Type Multiple Choice

Default value Auto

Options [Auto, Yes, No]

Description If the coordinates are involved in the requested property, those coordinates are wrapped into the box at each time step. If set to true, this keyword unwraps those coordinates so that the trajectory is continuous. If not provided the code uses automatic defaults.

UseAllValues

Type Bool

Default value No

Description By default the same number of values are used for each t-step in the MSD. This has the advantage that all values in the MSD are equally reliable, but it does mean that for the smaller timesteps much of the data is not used. To switch this off and use all data, UseAllValues can be set to true

VecElements

Type Block

Description A set of indices referring to a subset of the property vector. Works in combination with the atoms block. For example, in combination with the property Coords, the Atoms block allows the selection of a subset of atoms, while the VecElements block allows the selection of a subset of vector elements (e.g. 1 and 2 for the elements x and y). Currently not implemented with InputValues.

Index

Type Integer

Recurring True

Description Element of the property vector.

WritePropertyToKF

Type Bool

Default value No

Description Write the selected property to the KF files for every requested frame

Description

The mean square displacement $MSD(t)$ describes the average change of a (vector) property \mathbf{A} over time. This property is usually a set of atom coordinate vectors, but the implementation is entirely general.

$$MSD(t) = \langle [\mathbf{A}(0) - \mathbf{A}(t)]^2 \rangle$$

The average runs over all time-intervals $(t_0, t_0 + t)$, $(t_1, t_1 + t)$, ..., $(t_N, t_N + t)$, with $t_N = t_n - t_m$. Here n is the total number of frames read from the trajectory, and m is the number of discrete t values for which $MSD(t)$ is computed. The value m can be set with the keyword `MaxFrame`, and defaults to half the total number of frames read from the trajectory. As stated above, the default average runs over the same number of time intervals for each value of t . If `UseAllValues` is selected, the average runs over all available time intervals for each value of t , which is large for small t , and smallest (N) for t_m .

The most common use of the mean square displacement is for the computation of the diffusion coefficient, in which case the selected property is the set of atom coordinates (`Coords`). The diffusion coefficient is proportionate to the slope of this mean square displacement function, and therefore this slope is automatically computed. The function $MSD(t)$ becomes linear only after an initial time interval, and the user can set this initial time with the keyword `StartTimeSlope`. If not provided, this start time is automatically determined. To allow the user to determine if the linear regime has been sufficiently sampled, the slope of $MSD(t)$ as a function of t is computed as well. If the slope has not converged to a stable value, the user should select a larger value of t_m or continue the molecular dynamics simulation for a longer time.

Properties

Autocorrelation functions can be computed for different simulation properties: 1) Coordinates 2) User provided values. Option 3) Diffusion coefficient is equivalent to option 1).

```
MeanSquareDisplacement
  Property [Coords | InputValues | DiffusionCoefficient]
End
```

MeanSquareDisplacement

Type Block

Recurring True

Description All input related to auto correlation functions.

Property

Type Multiple Choice

Default value Coords

Options [Coords, InputValues, DiffusionCoefficient]

Description Compute the MSD from the property selected here (from rkf). Selecting Diffusion-Coefficient is equivalent to selecting the property Coords.

When read from file, the atomic coordinates will be wrapped inside the periodic box at every time step. As a result, coordinates can make seemingly big jumps from one side of the box to another between two consecutive frames. By default, the coordinates are unwrapped before the computation of the mean square displacement, so that all atoms follow a continuous trajectory. For the experienced users, the option exist to manually determine whether the wrapped or unwrapped coordinates are used with the keyword `UnwrapCoordinates` in the `MeanSquareDisplacement` block.

```
MeanSquareDisplacement
  UnwrapCoordinates [Auto | Yes | No]
End
```

MeanSquareDisplacement

Type Block

Recurring True

Description All input related to auto correlation functions.

UnwrapCoordinates

Type Multiple Choice

Default value Auto

Options [Auto, Yes, No]

Description If the coordinates are involved in the requested property, those coordinates are wrapped into the box at each time step. If set to true, this keyword unwraps those coordinates so that the trajectory is continuous. If not provided the code uses automatic defaults.

Since the coordinates used to compute the mean square displacement often differ from the coordinates as read from the trajectory (they will be unwrapped, so that the trajectory becomes continuous). With the keyword `WritePropertyToKF` in the `MeanSquareDisplacement` block, the user can choose to store not only the mean square displacement results, but also the property used to produce it.

```
MeanSquareDisplacement
  WritePropertyToKF Yes/No
End
```

MeanSquareDisplacement

Type Block

Recurring True

Description All input related to auto correlation functions.

WritePropertyToKF

Type Bool

Default value No

Description Write the selected property to the KF files for every requested frame

Options

A subset of atoms for which the property **A** should be selected/computed can be provided in the block `Atoms`. The block can contain element names (recurring keyword `Element`), or individual atom numbers (recurring keyword `Atom`).

```
MeanSquareDisplacement
  Atoms
    Atom integer
    Element string
  End
End
```

MeanSquareDisplacement

Type Block

Recurring True

Description All input related to auto correlation functions.

Atoms

Type Block

Description Relevant if Property is set to any quantity that is available per atom (Coords, DiffusionCoefficient). Atom numbers or elements for the set of atoms for which the property is read/computed are provided here. By default all atoms are used.

Atom

Type Integer

Recurring True

Description Atom number.

Element

Type String

Recurring True

Description Element Symbol Atom.

A subset of vector elements can be provided with the subblock `VecElements`. By default all vector elements found on the RKF file will be used.

```
MeanSquareDisplacement
  VecElements
    Index integer
  End
End
```

MeanSquareDisplacement

Type Block

Recurring True

Description All input related to auto correlation functions.

VecElements

Type Block

Description A set of indices referring to a subset of the property vector. Works in combination with the atoms block. For example, in combination with the property Coords, the Atoms block allows the selection of a subset of atoms, while the VecElements block allows the selection of a subset of vector elements (e.g. 1 and 2 for the elements x and y). Currently not implemented with InputValues.

Index

Type Integer

Recurring True

Description Element of the property vector.

10.3.7 AverageBinPlot

The Analysis program can plot two arbitrary properties, present on the RKF file, against each other averaged over each bin if the Task keyword is set to AverageBinPlot.

```
Task [RadialDistribution | Histogram | AutoCorrelation | MeanSquareDisplacement | ↵
↵AverageBinPlot]
```

Task

Type Multiple Choice

Options [RadialDistribution, Histogram, AutoCorrelation, MeanSquareDisplacement, AverageBinPlot]

Description The analysis task.

Further details need to be specified in the AverageBinPlot block. If more than one AverageBinPlot block is present in the input, more than one AverageBinPlot will be computed. The result is printed to output as text, as well as stored in a binary file (analysis.kf).

```
AverageBinPlot
  Nbins integer
  Property
    Axis float_list
    Name string
    Region string
    Vector string
  End
  Timestep integer
End
```

AverageBinPlot**Nbins**

Type Integer

Default value 10

Description Number of bins that are plotted

Property

Type Block

Recurring True

Description Property 1**Axis****Type** Float List**Description** If defined the dot_product along this axis will be taken**Name****Type** String**Description** Name of the property**Region****Type** String**Description** Name of the atom region among which the forces will be averaged**Vector****Type** String**Description** is it a vector? yes/no**Timestep****Type** Integer**Default value** 1**Description** Timestep used for the plotting

In the case of plotting the viscosity or friction coefficient, it is sufficient to only specify one property (meaning either `Viscosity` or `FrictionCoefficient`), which will be plotted automatically against the timestep.

10.3.8 Viscosity

The viscosity can be computed from an equilibrated Molecular Dynamics run as the integral over the pressure tensor autocorrelation function.

$$\eta = \frac{1}{10T} \int_{t=0}^{t=t_{max}} \langle \mathbb{P}_{ij}(0) \cdot \mathbb{P}_{ij}(t) \rangle dt$$

The viscosity is computed if the task `AutoCorrelation` is selected, and if in the `AutoCorrelation` block `Viscosity` is selected as the `Property`.

```
$AMSBIN/analysis <<eor
  Task AutoCorrelation
  AutoCorrelation
    Property Viscosity
  End
eor
```

AutoCorrelation**Type** Block**Recurring** True**Description** All input related to auto correlation functions.**Property****Type** Multiple Choice

Default value DipoleDerivativeFromCharges

Options [Velocities, DipoleMomentFromCharges, InputValues, DiffusionCoefficient, DipoleDerivativeFromCharges, PressureTensor, Viscosity]

Description Compute the ACF either from velocities (from rkf), the dipole moment (from coordinates and atomic charges in rkf), the dipole moment derivative (from velocities and atomic charges in rkf), from the pressure tensor (from rkf), or from values specified in input. Selecting DiffusionCoefficient is equivalent to selecting Velocities. The default, DipoleDerivativeFromCharges, results in the computation of an IR spectrum.

Again, a subset of atoms can be selected with the subblock `Atoms`.

The value of the viscosity is written to the output, as well as to the KF file.

10.3.9 Diffusion Coefficient

The diffusion coefficient can be computed from a molecular dynamics trajectory in two ways.

1. As the integral over the velocity autocorrelation function.
2. As the slope of the mean square displacement of the atomic coordinates.

The latter is more commonly used, as the former requires trajectory information to be stored at very short time intervals. Note that the obtained values for the diffusion coefficients correspond to the temperature of the molecular dynamics simulation.

From Velocity Autocorrelation

The diffusion coefficient can be defined as an integral over the velocity autocorrelation function.

$$D = \frac{1}{d} \int_{t=0}^{t=t_{max}} \langle \mathbf{v}(0) \cdot \mathbf{v}(t) \rangle dt$$

The factor $\frac{1}{d}$ corrects for the dimension of the system, which we assume to equal the length of the provided vector \mathbf{v} . The dimension d equals 3, unless specified otherwise in the subblock `VecElements`. In a system that is periodic in less than 3 dimensions, it may make sense to provide only the vector elements along the periodic dimensions. By default, however, all vector elements provided are used.

The diffusion coefficient is computed if the task `AutoCorrelation` is selected, and if in the `AutoCorrelation` block `DiffusionCoefficient` is selected as the `Property`. The result is completely equivalent to selecting the task `AutoCorrelation` with `Velocities` as the `Property` keyword.

```
$AMSBIN/analysis <<eor
  Task AutoCorrelation
  AutoCorrelation
    Property DiffusionCoefficient
  End
eor
```

AutoCorrelation

Type Block

Recurring True

Description All input related to auto correlation functions.

Property

Type Multiple Choice

Default value DipoleDerivativeFromCharges

Options [Velocities, DipoleMomentFromCharges, InputValues, DiffusionCoefficient, DipoleDerivativeFromCharges, PressureTensor, Viscosity]

Description Compute the ACF either from velocities (from rkf), the dipole moment (from coordinates and atomic charges in rkf), the dipole moment derivative (from velocities and atomic charges in rkf), from the pressure tensor (from rkf), or from values specified in input. Selecting DiffusionCoefficient is equivalent to selecting Velocities. The default, DipoleDerivativeFromCharges, results in the computation of an IR spectrum.

From Mean Square Displacement

The mean square displacement becomes linear with time, after an initial time interval. We can therefore define the linear part of the function as follows.

$$MSD(t) = \langle \mathbf{r}(0) - \mathbf{r}(t) \rangle = at + b,$$

with a as the slope of the function. The diffusion coefficient is proportional to the slope a .

$$D = \frac{1}{2d}a$$

Here, d is the dimensionality of the system, or the length of the provided vector \mathbf{r} . The dimension d equals 3, unless specified otherwise in the subblock VecElements. In a system that is periodic in less than 3 dimensions, it may make sense to provide only the vector elements along the periodic dimensions. By default, however, all vector elements provided are used.

The diffusion coefficient is computed if the task MeanSquareDisplacement is selected, and if in the MeanSquareDisplacement block *DiffusionCoefficient* is selected as the Property. The result is completely equivalent to selecting the task MeanSquareDisplacement with *Coords* as the Property keyword.

```
$AMSBIN/analysis <<eor
  Task MeanSquareDisplacement
  MeanSquareDisplacement
    Property DiffusionCoefficient
  End
eor
```

MeanSquareDisplacement

Type Block

Recurring True

Description All input related to auto correlation functions.

Property

Type Multiple Choice

Default value Coords

Options [Coords, InputValues, DiffusionCoefficient]

Description Compute the MSD from the property selected here (from rkf). Selecting DiffusionCoefficient is equivalent to selecting the property Coords.

In both cases, a subset of atoms can be selected with the subblock Atoms, and a subset of vector elements (in this case elements 1=X, 2=Y, 3=Z for the Cartesian coordinates) can be selected with the subblock VecElements.

The value of the diffusion coefficient is written to the output, as well as to the KF file.

10.4 VCD Analysis: VCDtools

The auxiliary program *VCDtools* provides insight regarding the origin of the VCD intensity of a given normal mode. This is done by analyzing and visualizing the various contributions to the total Electric (E) and Magnetic (M) Dipole Transition Moments (DTM). *e.g.*, the contributions from atoms, electrons, nuclei and molecular fragments. The *VCDtools* program is accessible through the AMS-GUI and allows one to:

- 1) Scale the size of the atoms with the magnitude of their atomic EDTM or MDTM contributions.
- 2) Visualize the various contributions to the EDTMs and MDTMs by arrows.
- 3) Perform a General Coupled Oscillator (GCO) analysis to evaluate the interactions between the different parts of a molecule.
- 4) Decompose the total EDTM and MDTM into nuclear and electronic contributions to gain insight into effects induced in the VCD spectra by charge transfer.
- 5) Perform a VCD robustness analysis.

See also:

Tutorial: [Analysis of the VCD spectrum of Oxirane with VCDtools](#)

VCDtools requires only the standard result file *adf.rkf* from an VCD calculation using the *ADF* engine. Once this file is opened with *AMSSpectra* the *VCDtools* program will be accessible through the standard user interface of *AMSSpectra*.

VCDtools produces one ASCII file, *VCDtools.out* where all output from the program is printed. This file will be located in the *.results* folder in the directory of the opened *adf.rkf* result file. Additionally, *VCDtools* will run on the background every time a new normal mode is selected. It then computes the atomic EDTM and MDTM which can be displayed inside *AMSSpectra* in various ways.

The following references should be cited when publishing results obtained with *VCDtools* Refs.^{1,2,3}.

10.4.1 General Theory

The VCD intensity associated with the fundamental vibrational transition for a given normal mode j is given by the rotational strength (RS):

$$R_{01}(j) = -i\vec{E}_{01}^{tot}(j) \cdot \vec{M}_{10}^{tot}(j)$$

where $E_{01}^{tot}(j)$ and $M_{10}^{tot}(j)$ are the total EDTM and MDTM of normal mode j , i is the unit imaginary number.

Whiten the harmonic approximation the total EDTM and MDTM can be written as sums of atomic contributions:

$$\vec{E}_{01}^{tot}(j) = \sum_{\lambda=1}^N \vec{E}_{01}^{\lambda}(j)$$

$$\vec{M}_{10}^{tot}(j) = \sum_{\lambda=1}^N \vec{M}_{10}^{\lambda}(j)$$

where N is the total number of atoms in the molecule and λ runs over all atoms.

¹ V.P. Nicu, *Revisiting an old concept: the coupled oscillator model for VCD. Part 1: the generalised coupled oscillator mechanism and its intrinsic connection to the strength of VCD signals*, *Physical Chemistry Chemical Physics* 18, 21202 (2016) (<https://doi.org/10.1039/C6CP01282E>)

² V.P. Nicu, J. Neugebauer and E.J. Baerends, *Effects of Complex Formation on Vibrational Circular Dichroism Spectra*, *Journal of Physical Chemistry A* 112, 6978 (2008) (<https://doi.org/10.1021/jp710201q>)

³ M.A.J. Koenis, O. Visser, L. Visscher, W.J. Buma, V.P. Nicu, *GUI Implementation of VCDtools, A Program to Analyze Computed Vibrational Circular Dichroism Spectra*, *J. Chem. Inf. Model* 60, 259 (2020) (<https://pubs.acs.org/doi/abs/10.1021/acs.jcim.9b00956>)

10.4.2 General Coupled Oscillator Analysis

The GCO analysis computes the contribution to total rotational strength from the interaction of two molecular fragments. This information provides important insight regarding the source of the VCD intensity and the robustness of the computed VCD sign. In the following, a brief summary of the GCO theory originally published in Ref. ^{Page 325, 1} is given.

Following the original coupled oscillator VCD mechanism, the atoms of a molecule are grouped into three fragments: **A**, **B**, and **R**. The fragments **A** and **B** represent the important Coupling Oscillator (CO) fragments, while fragment **R** is the ancillary fragment containing the rest of the atoms. As a result, the total RS can be decomposed in three components:

$$R_{01}(j) = R_{01}^{\text{GCO}}(j) + R_{01}^{\text{IF}}(j) + R_{01}^{\text{R}}(j)$$

The first contribution $R_{01}^{\text{GCO}}(j)$, is the GCO contribution to the RS and is given by the interaction between the EDTM and MDTM of fragments **A** and **B**:

$$R_{01}^{\text{GCO}}(j) = -i \cdot \left[\vec{E}_{01}^{\text{A}}(j) \cdot \vec{M}_{10}^{\text{B}}(j) + \vec{E}_{01}^{\text{B}}(j) \cdot \vec{M}_{10}^{\text{A}}(j) \right]$$

The $R_{01}^{\text{IF}}(j)$ term represents the contribution from the individual fragments (IF) **A** and **B** without any interaction with other fragments:

$$R_{01}^{\text{IF}}(j) = -i \cdot \left[\vec{E}_{01}^{\text{A}}(j) \cdot \vec{M}_{10}^{\text{A}}(j) + \vec{E}_{01}^{\text{B}}(j) \cdot \vec{M}_{10}^{\text{B}}(j) \right]$$

and the $R_{01}^{\text{R}}(j)$ contribution contains all contributions from fragment **R**:

$$R_{01}^{\text{R}}(j) = -i \cdot \left[\vec{E}_{01}^{\text{A}}(j) \cdot \vec{M}_{10}^{\text{R}}(j) + \vec{E}_{01}^{\text{R}}(j) \cdot \vec{M}_{10}^{\text{A}}(j) \right] \\ - i \cdot \left[\vec{E}_{01}^{\text{B}}(j) \cdot \vec{M}_{10}^{\text{R}}(j) + \vec{E}_{01}^{\text{R}}(j) \cdot \vec{M}_{10}^{\text{B}}(j) + \vec{E}_{01}^{\text{R}}(j) \cdot \vec{M}_{10}^{\text{R}}(j) \right]$$

In the above equations $\vec{E}_{01}^{\text{X}}(j)$ and $\vec{M}_{10}^{\text{X}}(j)$, with $\text{X} = (\text{A}, \text{B}, \text{R})$, are the EDTM and MDTM associated with the three fragments.

Using the origin dependency of the MDTM, the GCO contribution can be rewritten in a form similar to the original CO term:

$$R_{01}^{\text{GCO}}(j) = \frac{\pi\nu_j}{c} \cdot \vec{Y}^{\text{GCO}}(j) \cdot \left[\vec{E}_{01}^{\text{A}}(j) \times \vec{E}_{01}^{\text{B}}(j) \right]$$

where $\vec{Y}^{\text{GCO}}(j)$ is the general coupled oscillator vector.

As shown in ref. ^{Page 325, 1} most normal modes of a molecule (i.e. not just the carbonyl stretching modes) can be interpreted in terms of the GCO mechanism. That is, for most normal modes one can define the GCO fragments **A** and **B** fragments in such a way that the $R_{01}^{\text{GCO}}(j)$ term represent the dominant contributions to the rotational strengths. This second expression for $R_{01}^{\text{GCO}}(j)$ does not depend on the MDTM (which is origin dependent). As such, it allows one to interpret the VCD intensity of a mode in terms of interacting EDTMs that are associated with the various moieties of a molecule and their relative orientation.

The identification of the GCO fragments (which are normal mode dependent) is not always trivial, especially, in molecules without symmetry. Consequently, *VCDtools* offers several options for dividing the molecule into fragments. In *AMSSpectra* these fragments are referred as 'Regions' in analogy to the regions in the *AMSSinput* program. Under the **Regions**-menu there are many options to set, alter and save the fragments. Additionally, *VCDtools* is able to make a guess for fragments **A** and **B** as will be discussed in more detail below.

10.4.3 Available options

Beside the standard calculation and visualization of the atomic contributions to the normal mode (NM) motion, EDTM and MDTM, *VCDtools* offers three more advanced tools that can be utilized when analyzing VCD spectra inside *AMSSpectra*:

- GCO Analysis
- Guess GCO Fragments
- NM Localization on Regions

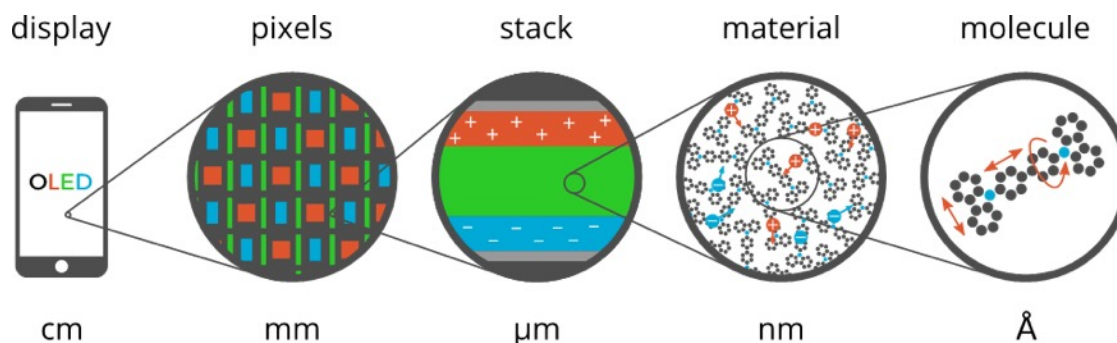
The first option, “*GCO Analysis*”, uses the above equations to decompose the RS in its different contributions. Printing both the values and important angles between the vectors. Before this option can be run two regions inside the molecule should be defined as fragments **A** and **B**. It is important that these regions do not contain the same atoms. Also since the decomposition is different for each NM, a specific NM should be selected.

The second option, “*Guess Fragments*”, guesses which atoms belong the fragments **A** and **B** for a selected normal mode. In doing so the $R_{01}^{\text{GCO}}(j)$ is maximized while keeping $R_{01}^{\text{R}}(j)$ low. Additionally, it ensures that the fragments are localized on a part of the molecule.

The third option, “*NM Localization on Regions*”, computes the percentage of the mass-weighted normal mode motion that is located on the atoms in the selected regions. One or multiple regions can be computed at the same time and the localizations are determined for all modes within a selected frequency window.

10.5 OLED workflows

Starting with the 2022 release of the Amsterdam Modeling Suite we include a set of *workflow scripts* for multiscale OLED modeling. These workflows are developed and validated in close [collaboration](https://www.scm.com/news/multiscale-oled-modeling-collaboration-with-simbeyond/) (<https://www.scm.com/news/multiscale-oled-modeling-collaboration-with-simbeyond/>) with [Simbeyond](https://simbeyond.com) (<https://simbeyond.com>) to bridge the gap between ab-initio atomistic modeling of OLED molecules with AMS, and device level kinetic Monte Carlo simulations using Simbeyond’s [Bumblebee code](https://simbeyond.com/bumblebee) (<https://simbeyond.com/bumblebee>). Together with Simbeyond, we attempt to provide a fully integrated multiscale simulation platform for the digital screening and prediction of successful OLED materials and devices.



The Amsterdam Modeling Suite implements the atomistic simulation part of this multiscale toolchain in the form of two workflow scripts:

- **Deposition (page 305)** The first step simulates the growth of a thin film in a *molecular dynamics* (page 90) and *force-bias Monte Carlo* (page 130) calculation mimicking physical vapor deposition.
- **Properties (page 314)** In the second step the morphology resulting from the deposition is used to obtain the distributions (and possibly spatial correlations) of molecular properties such as ionization potential, electron affinity and exciton energies at the DFT level. Each molecule’s environment is taken into account in a polarizable QM/MM scheme using the [DRF model](#).

The output of the *Properties* (page 314) workflow is an *HDF5 file* (page 316) containing a summary of the results for a material. This file can be opened in *AMSview* for a visualization of the results, but also directly imported into Simbeyond's *Bumblebee code* (<https://simbeyond.com/bumblebee>) to use it in simulations at the device level.

This manual page describes the technical details and options of the OLED workflow scripts. For a more hands-on introduction, you may want to start with the GUI tutorial, that will guide you through the entire workflow using the hole transport material β -NPB as an example.

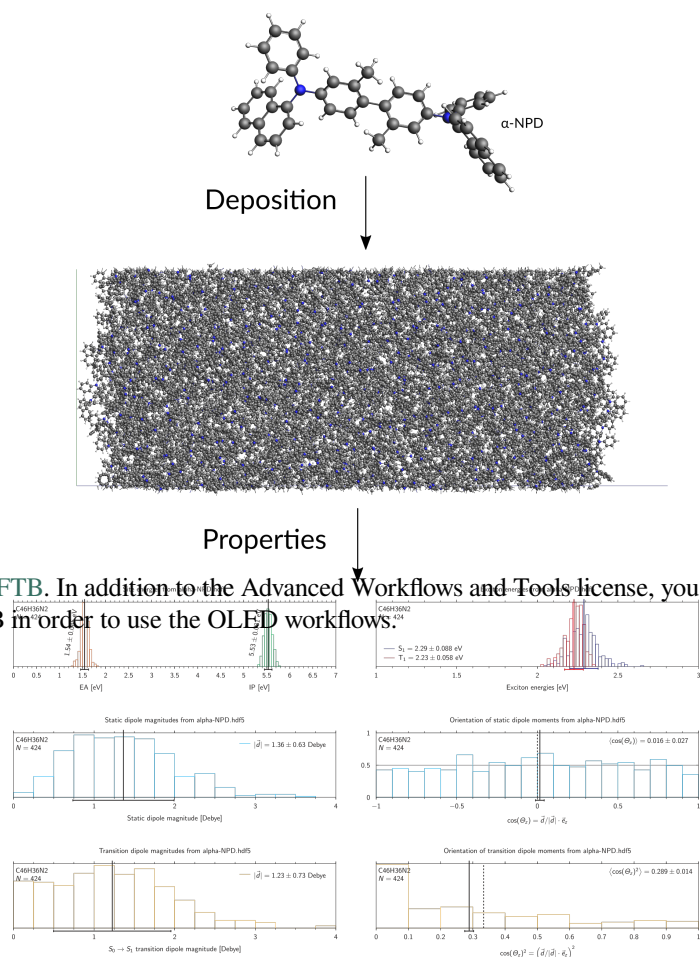
See also:

[Tutorial on multiscale modeling of OLED devices](#)

Note: The OLED workflow scripts use *ADF* and *DFTB*. In addition to the *Advanced Workflows and Tools license*, you will therefore also need a license for *ADF* and *DFTB* in order to use the OLED workflows.

10.5.1 New in AMS2023.1

- The exciton energies are now calculated using the PBE0 functional, and should be more accurate.
- The transfer integrals are now calculated with DFT and should be much more accurate than the GFN1-xTB calculated transfer integrals in AMS2022. (The GFN1-xTB transfer integrals were much too small.)
- The OLED material database has been updated and now contains the PBE0 exciton energies as well as the DFT transfer integrals. (The morphologies did not change with respect to the 2022 version.)
- Experimental: The deposition workflow can now *offload the calculation of forces to LAMMPS* (page 313), allowing much faster depositions if a GPU accelerated LAMMPS installation is available.
- **Various technical improvements to the properties workflow script:**
 - The HDF5 file is now created and populated with NaN values in the beginning of the workflow script. The NaN values are overwritten with the results as they come in, allowing the file to still be used in case the workflow is interrupted.
 - An interrupted workflow can now be restarted by specifying the output HDF5 file from the interrupted run with the `Restart` keyword. Any results on the HDF5 file will then not be recalculated.
 - The `SelectedMolecules` keyword allows to calculate properties for just a subset of the molecules.



- Result files of finished jobs will now be removed from disk after extracting the relevant properties. This massively reduces the disk space required to run the properties workflow script.
 - Should now consume less memory on the node executing the workflow script, and be more reliable.
 - Thanks to improvements in PLAMS, it is now much easier to run the workflow on multi-node allocations under SLURM.
- An issue with the automatic atom-typing in the deposition workflow has been fixed. (In AMS2022 nitrogen atoms would often get the N_3 type, when they should have been N_R.)

10.5.2 Deposition

The deposition workflow implements a series of mixed *molecular dynamics* (page 90) and *force-bias Monte Carlo* (page 130) calculations to simulate the growth of a thin film with physical vapor deposition.

The *molecule gun* (page 113) is used to shoot molecules at the substrate. Upon reaching the surface, the *force-bias Monte Carlo* (page 130) method is used to accelerate the search for favorable adsorption sites. This process is repeated until a thin film of a user-defined thickness has grown on the substrate.

To make this process computationally more efficient, the deposition happens in so called “cycles”. At the end of each deposition cycle, the bulk material at the bottom of the growing film is “trimmed off” and stored. Only the two top layers (each about 10 Å thick) are transferred to the next deposition cycle, where the lower of the two layers is frozen. This ensures that the trimmed off parts of the system fit perfectly together when the system is reassembled in the end of the simulation. By depositing in cycles we avoid simulating a lot of bulk material and are able to make the total computational cost linear in the thickness of the deposited film.

At the end of the simulation the layer deposited by the individual cycles are stacked and a short *molecular dynamics* (page 90) calculation on the entire film is used to anneal it from the deposition temperature down to 300K at ambient pressure.

An entire deposition with 6 deposition cycles (and the final equilibration to room temperature) is shown in the video on the right.

Basic input

The minimal input to the deposition workflow just specifies what to deposit:

```
#!/bin/sh
DEPOSITION_JOBNAME=myDeposition $AMSBIN/oled-deposition << EOF

Molecule
  SystemName myMol
End

System myMol
  ...
End

EOF
```

The `Molecule` block is only really used when depositing mixed molecule materials, e.g. host-guest systems. This will be explained in a *separate section* (page 310) below. For a single molecule deposition there should just be one `Molecule` block that references the only `System` block by name via the `SystemName` keyword, as shown in the example above.

The `System` block used by the OLED deposition script closely follows the `System` block in the input for the AMS driver, but supports only a subset of the keywords:

System

Type Block

Recurring True

Description Specification of the chemical system. For some applications more than one system may be present in the input. In this case, all systems except one must have a non-empty string ID specified after the `System` keyword. The system without an ID is considered the main one.

Atoms

Type Non-standard block

Description The atom types and coordinates. Unit can be specified in the header. Default unit is Angstrom.

GeometryFile

Type String

Description Read the geometry from a file (instead of from `Atoms` and `Lattice` blocks). Supported formats: `.xyz`

BondOrders

Type Non-standard block

Description Defined bond orders. Each line should contain two atom indices, followed by the bond order (1, 1.5, 2, 3 for single, aromatic, double and triple bonds) and (optionally) the cell shifts for periodic systems. May be used by MM engines and for defining constraints. If the system is periodic and none of the bonds have the cell shift defined then AMS will attempt to determine them following the minimum image convention.

Just like in the AMS driver, as an alternative to the `System` block, you can also use the `LoadSystem` block to *load a system* (page 40) directly from a `.rkf` file of a previous calculation.

The deposition workflow uses the `ForceField` engine for the *molecular dynamics* (page 90) simulation of the physical vapor deposition. In order to also support the deposition of metal containing compounds, we use the UFF force field with the `UFF4MOF-II` (<https://doi.org/10.1021/acs.jctc.6b00664>) parametrization for the deposition. As with any calculation with the `ForceField` engine you may manually provide (`UFF4MOF-II`) atom-types, atomic charges and bond orders in the input file:

```
System
  Atoms
    C [...] ForceField.Type=C_R ForceField.Charge=-0.1186
    N [...] ForceField.Type=N_R ForceField.Charge=-0.2563
    H [...] ForceField.Type=H_ ForceField.Charge=+0.1021
    [...]
  End
  BondOrders
    1 2 1.0
    1 5 1.5
    1 6 1.5
    [...]
  End
End
```

Whatever is not specified in the input will automatically be determined: the input system is optimized with ADF using the S12g exchange-correlation functional with a TZP basis set. At the optimized geometry, the `Charge Model 5` is used

to calculate the atomic charges, while the rounded [Nalewajski-Mrozek bond orders](#) determine the topology. See the [ADF manual](#) for details on the calculation of charges and bond orders. Finally, using the topology determined by the calculated bond orders, the [automatic UFF atom-typing](#) that is built into the [ForceField](#) engine is used to determine the atom-types.

If you want to make sure the correct atom-types and bonds are used in your calculation, we recommend building the system in AMSinput, where you can visually check the bond orders and atom-types to make sure they are correct. The result can then be exported into a file as a `System` block via **File** → **Export coordinates** → **.in**. For the atomic charges we recommend relying on the automatic calculation with ADF. (Just make sure the `ForceField.Charge` suffixes are not included in the atom block. Their absence will trigger the automatic charge calculation with ADF.)

By default a box of 60 x 60 x 120 Å is deposited. The first two dimensions give the surface area of the deposited layer, while the third dimension is the thickness of the layer. The size of the deposited box can be changed using the `Size` keyword in the `Box` block:

```
Box
  Size 60 60 120
End
```

Box

Type Block

Description Specifications of the box into which the material is deposited.

Size

Type Float List

Default value [60.0, 60.0, 120.0]

Unit Angstrom

GUI name Box size

Description Specify the desired size of the box. The final deposited box may have a different size.

The x- and y-axis are perpendicular to the direction of deposition, so these may be regarded as the width of the growing layer. The z-axis is the direction along which the deposition happens, so this determines the thickness of the deposited layer. Note that the x- and y-axis will be ignored if a custom substrate is used: the area of the box is then determined by the lattice of the substrate. The z-axis can still be freely chosen, but should be large enough that there is enough space for the substrate itself and to deposit more molecules on top of it.

With sizes typical for molecules used in OLED devices, the default box size results in a deposition of ~500 molecules. Note that the computational time of a deposition scales linearly with the thickness of the layer, but quadratically with the surface area. This is because a larger area requires both the deposition of more molecules to fill the box, but also makes each MD step more expensive as more molecules have to be simulated at the same time. When increasing the thickness of the layer, molecules at the bottom are first frozen, and later removed from the simulation altogether, giving an overall linear scaling.

The temperature at which the deposition is performed can be configured in the `Deposition` section.

```
Deposition
  Temperature float
End
```

Deposition

Type Block

Description Specifies the details of how molecules are deposited.

Temperature

Type Float

Default value 600.0

Description The temperature at which the deposition happens.

Finally, there are a couple more technical options in the `Deposition` section, that we suggest to leave at their default values.

```
Deposition
  Frequency integer
  TimeStep float
  ConstrainHXBonds Yes/No
  NumMolecules integer
End
```

Deposition

Type Block

Description Specifies the details of how molecules are deposited.

Frequency

Type Integer

Default value 10000

Description The frequency in MD steps at which new molecules will be added to the system.

TimeStep

Type Float

Default value 1.0

Unit Femtoseconds

Description The time difference per step.

ConstrainHXBonds

Type Bool

Default value Yes

GUI name Constrain H-* bonds

Description Constrain the bond length for all H-* bonds (i.e. any bond to a hydrogen atom). Doing this allows choosing a larger time step. If this option is disabled, the `TimeStep` needs to be reduced manually.

NumMolecules

Type Integer

Description The number of molecules that we will try to deposit. If not specified the number will be determined automatically such that the box becomes approximately full.

Output

Running the `oled-deposition` workflow script creates a single directory in which you can find all results of a deposition. By default this directory is named `oled-deposition.results`, but in order to avoid name clashes, that location can be changed with the `AMS_JOBNAME` environment variable. The example below will collect all results in the directory `myLayer.results`:

```
#!/bin/sh
AMS_JOBNAME=myLayer $AMSBIN/oled-deposition << EOF
...
EOF
```

Let us go through all files and folders in the working directory in the order in which they are created.

Firstly, the working directory contains a `oled-deposition.log` logfile. The contents of the logfile are identical to what you see on standard output when running the `oled-deposition` workflow.

The deposition workflow starts with a couple of calculations on single molecules in vacuum. Each of them runs in a separate folder, in which you can find the usual *AMS output files* (page 18) (such as `ams.rkf`):

```
myMol.dft_opt/
myMol.ff_opt/
myMol.equilibrate_ff_input_molecule/
```

Here `myMol` corresponds to the name of the molecule that was used in the input file. The `myMol.dft_opt` directory contains the results of the initial geometry optimization with ADF, which is used to determine the atomic charges and bond orders if these were not specified in the input. The `myMol.ff_opt` directory contains the results of a subsequent geometry optimization using the *ForceField* engine with the UFF4MOF-II forcefield. Finally in the `myMol.equilibrate_ff_input_molecule` directory a short MD simulation at the deposition temperature is performed to equilibrate the molecule to the desired temperature. We suggest visualizing the trajectory of this equilibration in *AMSmovie* to make sure the molecule does not undergo unexpected conformational changes that could be caused by wrong atom-types or bonds. If the molecule behaves strangely (or falls apart) at this point, one may need to go back and *assign atom-types and bonds manually* (page 306) in the input.

When *depositing mixtures* (page 310) you will see multiple instances of the three directories above: one for each deposited species.

Once all the preparatory work is done, the actual *deposition cycles* (page 305) each write a folder and (upon completion of the cycle) two files:

```
depo_cycle_1/
depo_box.1.in
depo_box.1.xyz
```

You can follow the progress of your deposition by opening the `ams.rkf` in the last `depo_cycle_*/` directory. The `depo_box.*.in` and `depo_box.*.xyz` files contain the entire morphology deposited so far: by visualizing them in order you can watch your material grow!

Important: The files with the `.in` extension contain the System geometry in form of a *System block* (page 31). This format contains bond orders, force field atom-types as well as atomic charges. It can be opened in *AMSinput* and *PLAMS* and should be the preferred format when working with the OLED workflow scripts in AMS. The `.xyz` file is in *extended XYZ format* (page 477) does *not* contain that extra information. Always use a `.in` file when transferring a system from one script to the next, e.g. when going from the OLED deposition to the OLED *properties workflow* (page 314).

Once all molecules have been deposited the entire box is annealed from the deposition temperature down to room temperature. This creates one directory and (upon completion) a `.in` and `.xyz` file containing the annealed morphologies:

```

equilibrate_box/
equil_box.in
equil_box.xyz

```

The last step is to take the room temperature morphology and perform a geometry optimization on it. This essentially removes all thermal vibrations and results in a geometry that is relaxed at the force field level. As you might expect, the last step also produces a folder and (upon completion) a `.in` and `.xyz` file:

```

optimize_box/
morphology.in
morphology.xyz

```

It is up to the user to decide whether to continue to the OLED *properties workflow* (page 314) with the morphology from `equil_box.in` (equilibrated to 300K) or `morphology.in` file (fully relaxed). We recommend using the fully relaxed morphology though. We also used fully relaxed morphologies for the generation of the *OLED material database* (page 323).

Deposition of host-guest materials

A deposition of host-guest materials can easily be done by specifying multiple `Molecule` and `System` blocks in the input. The following runscript generates a 95% to 5% mixture (by number of molecules) of two compounds:

```

#!/bin/sh
AMS_JOBNAME=host_guest $AMSBIN/oled-deposition << EOF

Molecule
  SystemName myHost
  MoleFraction 0.95
End
Molecule
  SystemName myGuest
  MoleFraction 0.05
End

System myHost
  ...
End
System myGuest
  ...
End

EOF

```

```

Molecule
  MoleFraction float
  SystemName string
End

```

Molecule

Type Block

Recurring True

GUI name Molecules

Description Specification of the molecule to be deposited.

MoleFraction

Type Float

Default value 1.0

GUI name Molar fraction

Description The relative occurrence of the molecule with regard to other deposited species. Only relevant for mixed molecule depositions.

SystemName

Type String

GUI name Molecule

Description String ID of a named [System] to be inserted. The lattice specified with this System, if any, is ignored and the main system's lattice is used instead.

You can have an arbitrary number of `Molecule` blocks in your input to deposit multi-component mixtures. Obviously, the box your are depositing must be large enough that it still contains at least a few molecules of the rarest component.

Note that multiple `Molecule` and `System` blocks can also be used to deposit different conformers of the same compound. While conformational changes can in principle happen over the course of the MD simulation, it may be a good idea to deposit a mixture of conformers directly if their geometries are very different.

Deposition of interfaces

By default the deposition will use a single graphene layer as a substrate. The graphene layer is removed after the first *deposition cycle* (page 305) and will not be included in the output morphologies, i.e. the `.in` files in the *working directory* (page 309). Note that the graphene layer is **not** present in the annealing of the entire morphology from deposition temperature to 300K, which is performed at the end of the workflow. The result of this is that both the bottom and top of the deposited thin-film by default represents an interface between the material and a vacuum.

Instead of depositing on a clean graphene sheet, the deposition workflow also supports custom substrates. This is intended to be used for depositing a thin film of one material on top of another material and allows users to study the interface between the two. A custom substrate is set up using the `Substrate` and `SubstrateSystem` keys in the `Box` block.

```
Box
  Substrate [Graphene | Custom]
  SubstrateSystem string
End
```

Box

Type Block

Description Specifications of the box into which the material is deposited.

Substrate

Type Multiple Choice

Default value Graphene

Options [Graphene, Custom]

Description The substrate on which to grow the layer.

SubstrateSystem

Type String

GUI name Custom substrate

Description String ID of a named [System] to be used as a substrate. (This is only used when the Substrate key is set to Custom.)

Here the value of the `SubstrateSystem` refers to a named `System` block in the input, representing the geometry of the substrate. The following example shows how to deposit a molecule B on top of a substrate of molecule A:

```
#!/bin/sh
AMS_JOBNAME=molB_on_molA $AMSBIN/oled-deposition << EOF

Molecule
  SystemName molB
End
System molB
  ...
End

Box
  Size 0 0 240
  Substrate Custom
  SubstrateSystem molA_substrate
End

System molA_substrate
  Atoms
    ...
  End
  BondOrders
    ...
  End
  Lattice
    ...
  End
End
EOF
```

The contents of the block `System molA_substrate` should be obtained by first running a deposition of molecule A: just use the `System` block found in e.g. the `equil_box.in` file of that deposition as the custom substrate for the next job. (Note that no attempt will be made to automatically determine atomic charges, bond orders, or force-field atom types for the molecules in the substrate. Taking the `System` block from the results of an earlier deposition is the easiest way ensure you are using exactly the same bonds, atom types and charges for the substrate molecules in the new calculation.)

Warning: The custom substrate option can currently not be used to deposit thin films on top of crystalline materials. The substrate must consist of individual molecules and be >20 Å thick, so that it can be split into a frozen (lower) and thermostatted (upper) layers.

Note that the `Box%Size` in the x- and y-direction is ignored when using a custom substrate: the size of the custom substrate is used instead. The thickness of the layer can be set manually when using a custom substrate, but it needs to accommodate both the already existing substrate as well as the newly grown film on top. Assume that the thickness of the substrate film is 120 Å in the example above. By setting the the z-value of the `Box%Size` to 240 Å, we will have space

to accommodate the substrate and then grow another layer of 120 Å thickness on top of it. Note that while the default graphene layer is *removed* from the morphology, a custom substrate will be *included* in the morphology.

Restarting

The OLED workflow scripts are based on the [PLAMS](#) scripting framework. As such it can rely on the [PLAMS rerun prevention](#) to implement restarting of interrupted depositions.

The easiest way to restart a deposition is to include the `--restart` (or short: `-r`) command line flag:

```
#!/bin/sh
AMS_JOBNAME=myDeposition $AMSBIN/oled-deposition --restart << EOF
...
EOF
```

This first (interrupted) run will have created the `myDeposition.results` directory. Running the above script again will move that directory to `myDeposition.results.bak` and reuse all successful jobs from the first run. (People already familiar with PLAMS will recognize that this works just like the `-r` flag on the [PLAMS launch script](#).) Note that this does not restart the previous deposition precisely at the point where it was interrupted. Instead it restarts from the beginning of the last *deposition cycle* (page 305).

When running a deposition workflow on a batch system such as SLURM, you may want to consider always including the `--restart` flag in your runscrip. It is not a problem if there are no previous results to restart from, but in case your job gets interrupted and automatically rescheduled, the `--restart` flag will make sure that it continues (approximately) where it stopped.

There is also the `--load` (or short: `-l`) command line flag:

```
#!/bin/sh
AMS_JOBNAME=newDepo $AMSBIN/oled-deposition -l oldDepo.results << EOF
...
EOF
```

While this can be used to accomplish the same thing the `--restart` flag would do, its best use is to specify a directory of a previous deposition of the same molecules. This can save you the initial step of doing the DFT calculations in order to determine the atomic charges and bonds. A perfect use it when you have already *deposited a mixture* (page 310), and later decide to change the ratio between the compounds: by specifying the results directory of the first deposition the initial DFT calculations can be skipped entirely. (Again, people already familiar with PLAMS will recognize that this works just like the `-l` flag on the [PLAMS launch script](#).)

LAMMPS offload

The OLED deposition workflow supports offloading the calculation of the force to a local LAMMPS installation. If a GPU accelerated LAMMPS is available, this can easily speed up the deposition by a factor of 5.

Note: Before enabling offloading, you will need to install LAMMPS and set up the environment as described in [Setting up LAMMPS](#).

If a local LAMMPS installation is available, it can easily be used through the following keywords in the OLED deposition input file.

```
LAMMPSoffload
  Enabled Yes/No
  UseGPU Yes/No
  UseOpenMP Yes/No
End
```

LAMMPSoffload**Type** Block**Description** Offload the calculation to LAMMPS via AMSPipe.**Enabled****Type** Bool**Default value** No**Description** Enable offloading the force field evaluation to LAMMPS instead of handling it internally in AMS.**UseGPU****Type** Bool**Default value** No**GUI name** Use GPU**Description** Accelerate LAMMPS calculations using a GPU. Requires a LAMMPS library built with the GPU package.**UseOpenMP****Type** Bool**Default value** No**GUI name** Use OpenMP**Description** Parallelize LAMMPS calculations using OpenMP threading. Requires a LAMMPS library built with the OMP package.

10.5.3 Properties

The properties workflow is used to obtain distributions (and possibly spatial correlations) of molecular properties such as ionization potential and electron affinity from the morphology. To accomplish this, it will perform DFT calculations on all individual molecules from the morphology, taking their environment into account in QM/MM calculation.

The exact workflow (with all default settings) is as follows:

1. For each molecule in the box, do a quick DFT calculation with LDA and a DZP basis and use the MDC-D charge model to determine atomic charges. These charges will be used for the electrostatic part of the embedding potential in the next step.
2. For each molecule in the box:
 - Determine which other molecules to consider as the environment. By default all molecules within 15 Å (atom-atom distance) are considered.
 - **Individually, for neutral molecule, cation, and anion:**
 - Optimize geometry of central QM molecule in frozen MM environment using GFN1-xTB and UFF4MOF-II with electrostatic embedding in the Hybrid engine.

- Do a DFT single point on the optimized geometry using **PBE** and an all-electron **TZ2P** basis. The environment is taken into account using a polarizable **DRF embedding**.
 - Calculate the (approximately) adiabatic ionization potential and electron affinity from the differences in total energy with respect to the neutral system.
 - Calculate **exciton energies** and transition dipole moments of the molecule with **TD-DFT** using the **PBE0** functional. This calculation is performed on the optimized geometry of the neutral molecule obtained earlier, and the environment is again taken into account using a polarizable **DRF embedding**.
3. For all pairs of neighboring molecules (within 4 Å atom-atom distance of each other) calculate the electron and hole **charge transfer integrals with DFT**.

What is described above is the workflow with all default settings. Various aspects of this (such as the ranges) can be tweaked from the input, see the *Settings section* (page 319) below.

Basic input

The simplest possible input for the `oled-properties` workflow script is just a single `System` block.

```
#!/bin/sh
$AMSBIN/oled-properties << EOF

System
  Atoms
  ...
  End
  Lattice
  ...
  End
  [BondOrders
  ...
  End]
End
EOF
```

Obviously, the `Atoms` and `Lattice` blocks are required, while the `BondOrders` block is optional. If the bond orders are present, they will be used to determine which parts of the system are connected, which ultimately determines which sets of atoms are considered distinct molecules. If the `BondOrders` block is not present, the bonds will be guessed. Since we only care about which atoms are bonded at all, and not on details such as the bond order, this should work quite reliably.

Nevertheless, if the morphology was obtained with the AMS *deposition workflow* (page 305), we can use the fact that it writes out the morphology as a `.in` file containing exactly the `System` block we need. Basically, we use the `morphology.in` output file of the deposition as the input for the properties script.

```
#!/bin/sh
$AMSBIN/oled-deposition << EOF
... see oled-deposition manual page ...
EOF

$AMSBIN/oled-properties < oled-deposition.results/morphology.in
```

This has the advantage that the bonds are guaranteed to be transferred without change between the two workflows.

By default the properties are calculated for all molecules in the morphology, but this can be limited with the `Select-edMolecules` keyword:

```
SelectedMolecules integer_list
```

SelectedMolecules

Type Integer List

Description Indices of the molecules to calculate properties for. If not present, all molecules will be used. Note that indexing starts at 0.

Output

Results directory

Running the `oled-properties` workflow script creates a single directory in which you can find all results of the calculation. By default this directory is named `oled-properties.results`, but in order to avoid name clashes, that location can be changed with the `AMS_JOBNAME` environment variable. The example below will collect all results in the directory `myMaterial.results`:

```
#!/bin/sh
AMS_JOBNAME=myMaterial $AMSBIN/oled-properties << EOF
...
EOF
```

This will create the `myMaterial.results` directory with the following files:

```
myMaterial.results/
├─ oled-properties.log
├─ oled-properties.rkf
└─ properties.hdf5
```

The primary output file is the `properties.hdf5` file, which we will discuss in the next section.

While the workflow is still running, you will also find subdirectories with the output of the individual DFT calculations in the results directory. By default these subdirectories are deleted as soon as the relevant properties have been extracted. Only the output of failed calculations is kept to aid in debugging any issues. What is kept or deleted can be configured with the following keyword:

StoreResultFiles

Type Multiple Choice

Default value Failed

Options [None, Failed, All]

Description Whether to keep the full result files from all the individual jobs. By default the result files from all jobs for a particular molecule will be deleted after all relevant results have been extracted and stored on the HDF5 file. Note that keeping the full results for all molecules can easily require hundreds of gigabytes of storage space.

Data on the HDF5 file

The main output file of an OLED properties calculation is a small [HDF5 file](https://en.wikipedia.org/wiki/Hierarchical_Data_Format) (https://en.wikipedia.org/wiki/Hierarchical_Data_Format) called `properties.hdf5`. It contains the results that are usually interesting for the design of OLED materials, such as site energies, exciton energies, (transition) dipole moments, etc. This file can be imported into Simbeyond's [Bumblebee code](https://simbeyond.com/bumblebee) (<https://simbeyond.com/bumblebee>) to use your calculated material in a device level kinetic Monte Carlo simulation. The following groups and datasets can be found on the HDF5 file. Note that all arrays on the HDF5 file are indexes starting from zero.

The `species` group contains information about the different molecular species making up the morphology. There are two arrays in the `species` group whose size is equal to the number of different species (`numSpecies`):

species.name An array of human readable names identifying the molecular species making up the morphology. Currently this is just the molecular formula in [Hill notation](https://en.wikipedia.org/wiki/Chemical_formula#Hill_system) (https://en.wikipedia.org/wiki/Chemical_formula#Hill_system).

species.smiles An array of [SMILES](https://en.wikipedia.org/wiki/Simplified_molecular-input_line-entry_system) (https://en.wikipedia.org/wiki/Simplified_molecular-input_line-entry_system) strings for the different molecular species. May contain a dummy value in case the determination of the SMILES string from the 3D structure fails for a species.

The `molecules` group contains the complete geometrical description of the morphology. It contains a number of arrays, (almost) all of which have the total number of molecules (`numMolecules`) as their size:

molecules.species An array of integers containing the species a molecule in for of an index into the arrays in the `species` group.

molecules.lattice (3 x 3) array containing the lattice vectors in Ångstrom.

molecules.position (`numMolecules` x 3) array containing the center of mass positions of all molecules in Ångstrom. Note that all center of mass positions are within the parallelepiped spanned by the lattice vectors, i.e. all fractional coordinates are in the [0,1] range.

molecules.atoms This is an `numMolecules` sized 1D array, where each element itself is an array of `string`, `float`, `float`, `float` tuples representing `symbol`, `x`, `y`, `z`. The `x`, `y` and `z` coordinates are given in Ångstrom.

molecules.bonds This is an `numMolecules` sized 1D array, where each element itself is an array of `int`, `int`, `float` tuples representing `atom1`, `atom2`, `bondOrder`. Here `atom1` and `atom2` are indices into the corresponding element of the `molecules.atoms` array. The `bondOrder` is a floating point number, where the value of 1.5 is used to represent an aromatic bond.

The site energies are contained in the `energies` group on the HDF5 file:

energies.IP A `numMolecules` sized array containing the first ionization potential for each molecule in eV.

energies.EA A `numMolecules` sized array containing the first electron affinity for each molecule in eV.

energies.HOMO A `numMolecules` sized array containing the Kohn-Sham orbital energy of the highest occupied orbital in eV. If requested via the `NumAdditionalOrbitalEnergies` keyword in the *input* (page 319) of the properties workflow, more arrays of this type (`HOMO-1`, `HOMO-2`, ...) may exist and contain the orbital energies of lower lying occupied orbitals.

energies.LUMO A `numMolecules` sized array containing the Kohn-Sham orbital energy of the lowest unoccupied orbital in eV. If requested via the `NumAdditionalOrbitalEnergies` keyword in the *input* (page 319) of the properties workflow, more arrays of this type (`LUMO+1`, `LUMO+2`, ...) may exist and contain the orbital energies of higher lying virtual orbitals.

Similarly the exciton energies (in eV) can be found in the `exciton_energies` group. If the calculation of exciton energies was disabled by setting `NumExcitations` to 0 in the *input* (page 319), this information is not present.

exciton_energies.S1 Energies of the first excited singlet state (S1) with respect to the ground state. Higher singlet excitation energies may be found in more arrays of this type (`S2`, `S3`, ...) if their calculation was requested by setting `NumExcitations` to a value larger 1.

exciton_energies.T1 Energies of the first excited triplet state (T1) with respect to the ground state. Higher triplet excitation energies may be found in more arrays of this type (T2, T3, ...) if their calculation was requested by setting `NumExcitations` to a value larger 1.

Static dipole moments and transition dipole moments (in Debye) can be found in their respective groups:

static_multipole_moments.dipole_moment (`numMolecules x 3`) array containing the dipole moment vectors for each molecule.

transition_dipole_moments.S1_S0 (`numMolecules x 3`) array containing the transition dipole moment vectors for the S0 → S1 transition for each molecule. Transition dipole moments for higher singlet excitations may be found in more arrays of this type (S2_S0, S3_S0, ...) if their calculation was requested by setting `NumExcitations` to a value larger 1.

If the calculation of transfer integrals is requested with the `TransferIntegrals%Type` key in the *input* (page 319), the `pairs` and `transfer_integrals` groups will also be available on the HDF5 file, containing the following datasets:

pairs.indices A (`numPairs x 2`) array of integers containing the molecule indices for all pairs of molecules that were considered close enough to trigger the calculation of transfer integrals between them.

transfer_integrals.electron A `numPairs` sized array containing the transfer integral (in eV) for electrons between each pair.

transfer_integrals.hole A `numPairs` sized array containing the transfer integral (in eV) for holes between each pair.

Accessing the HDF5 file

The easiest way to view the data from the HDF5 file is to open it in the GUI using the [AMSview](#) module. There you can easily plot histograms of all the calculated properties, but also visualize the spacial distribution of the properties.

For more custom built analysis, the HDF5 file can easily be opened from Python using the [h5py](https://www.h5py.org/) (<https://www.h5py.org/>) library, which is included in the [AMS Python Stack](#). The following code snippet shows how to calculate the mean and standard deviation of the ionization potential:

```
import h5py

with h5py.File("properties.hdf5", "r") as f:
    IPs = f['energies']['IP'][:]
    print("IP = ", IPs.mean(), "±" , IPs.std())
```

The above snippet is only suitable for calculations of pure compounds, as we are calculating the mean and standard deviation over *all* molecules, not taking their species into account. For *mixtures* (page 310) calculating these properties *per species* would be much more useful. This can easily be accomplished by using an appropriate mask on the `IPs` array for the calculation of mean and standard deviation:

```
import h5py
import numpy as np

with h5py.File("properties.hdf5", "r") as f:
    IPs = f['energies']['IP'][:]
    speciesIDs = f['molecules']['species'][:]

    for specID, specName in enumerate(f['species']['name']):
        mask = (speciesIDs==specID) & (~np.isnan(IPs))
        print(specName)
        print("IP = ", IPs[mask].mean(), "±" , IPs[mask].std())
```


Note how we also use the mask to exclude all NaN elements in the array from the calculation of the mean and standard deviation. Occasional NaN values in the arrays on the HDF5 file indicate that a property could not be calculated for a molecule because the job for it crashed or failed in some other way. This is not a problem as long as it happens only rarely, but the NaN values need to be excluded from the analysis.

Additional settings

The OLED properties workflow script has a few options that determine what properties will be calculated and/or written to the *HDF5 file* (page 317) file:

```
NumAdditionalOrbitalEnergies integer
NumExcitations integer
TransferIntegrals
  Include
    Cutoff float
    Metric [CoM | Atoms | Atoms_noH]
  End
  Exclude
    Cutoff float
    Metric [CoM | Atoms | Atoms_noH]
  End
  Type [None | Fast | Full]
End
```

NumAdditionalOrbitalEnergies

Type Integer

Default value 1

Description The number of additional orbital energies to write to the HDF5 file. A value of N means to write everything up to HOMO-N and LUMO+N.

NumExcitations

Type Integer

Default value 1

Description The number of excited states to calculate. By default the S₁ and T₁ states will be calculated. The calculation of excited states is currently only supported for systems with a closed-shell ground state.

TransferIntegrals

Type Block

Description Configures the details of the calculation of electron and hole transfer integrals.

Exclude

Type Block

Description Configures which dimers NOT to calculate transfer integrals for.

Cutoff

Type Float

Default value 4.0

Unit Angstrom

GUI name Exclude beyond

Description Exclude dimers for which the distance is larger than this threshold. Acts as a quick pre-screening to reduce the number of dimers to calculate transfer integrals for.

Metric

Type Multiple Choice

Default value Atoms

Options [CoM, Atoms, Atoms_noH]

Description The metric used to calculate the distance between two molecules.

- CoM: use the distance between the centers of mass of the two molecules.
- Atoms: Use the distance between the two closest atoms of two molecules.
- Atoms_noH: Use the distance between the closest non-hydrogen atoms of the two molecules.

Include

Type Block

Description Configures which dimers transfer integrals are calculated for.

Cutoff

Type Float

Default value 4.0

Unit Angstrom

GUI name Include within

Description Transfer integrals will be calculated for all molecule pairs within a cutoff distance from each other. This distance can be measured using different metrics, see the corresponding `Metric` keyword.

Metric

Type Multiple Choice

Default value Atoms

Options [CoM, Atoms, Atoms_noH]

Description The metric used to calculate the distance between two molecules.

- CoM: use the distance between the centers of mass of the two molecules.
- Atoms: Use the distance between the two closest atoms of two molecules.
- Atoms_noH: Use the distance between the closest non-hydrogen atoms of the two molecules.

Type

Type Multiple Choice

Default value Fast

Options [None, Fast, Full]

Description The method used for the calculation of the transfer integrals.

There are also a few options to tweak some aspects of the workflow. We have not properly tested their effect on the results. When changing these options, verify your results against calculations using all default settings.

```

Embedding
  Charges [DFTB | DFT]
  Cutoff float
  Metric [CoM | Atoms | Atoms_noH]
  Type [None | DRF]
End
Relax [None | Neutral | All]
OccupationSmearing [None | Ions | All]

```

Embedding**Type** Block**Description** Configures details of how the environment is taken into account.**Charges****Type** Multiple Choice**Default value** DFT**Options** [DFTB, DFT]**Description** Which atomic charges to use for the DRF embedding.

- DFTB: Use the self-consistent Mulliken charges from a quick DFTB calculation with the GFN1-xTB model.
- DFT: Use the MDC-D charges from a relatively quick DFT calculation using LDA and a DZP basis set.

Cutoff**Type** Float**Default value** 15.0**Unit** Angstrom**Description** The cutoff distance determining which molecules will be considered the environment of the central molecule. The maximum possible cutoff distance is half the length of the smallest lattice vector. The distance can be measured using different metrics, see the `Metric` keyword.**Metric****Type** Multiple Choice**Default value** Atoms**Options** [CoM, Atoms, Atoms_noH]**Description** The metric used to calculate the distance between two molecules.

- CoM: use the distance between the centers of mass of the two molecules.
- Atoms: Use the distance between the two closest atoms of two molecules.
- Atoms_noH: Use the distance between the closest non-hydrogen atoms of the two molecules.

Type**Type** Multiple Choice**Default value** DRF**Options** [None, DRF]

Description The type of embedding used to simulate the molecular environment.

Relax

Type Multiple Choice

Default value All

Options [None, Neutral, All]

Description Which geometries to relax prior to taking the energy differences for the calculation of ionization potential and electron affinity. The relaxation is done at the DFTB level using the GFN1-xTB model Hamiltonian with electrostatic embedding in a UFF environment.

- None: Use the geometries directly from the input.
- Neutral: Relax the uncharged molecule and use its optimized geometry for the neutral as well as the ionic systems. This gives (approximately) the vertical ionization potential and electron affinity.
- All: Individually relax the neutral systems and the ions before calculating the total energies. This gives (approximately) the adiabatic ionization potential and electron affinity.

OccupationSmearing

Type Multiple Choice

Default value Ions

Options [None, Ions, All]

Description Determines for which systems the electron smearing feature in ADF will be used. If enabled, the molecular orbital occupations will be smeared out with a 300K Fermi-Dirac distribution. This makes SCF convergence easier, as the occupation of energetically close orbitals does not jump when their energetic order flips. See the ADF manual for details. It is recommended to keep this option enabled for the ionic systems, which are more likely to suffer from difficult SCF convergence.

Parallelization

The OLED properties workflow consists of independent chains of calculations for the individual molecules, and therefore scales very well when running on parallel machines. The OLED properties workflow is computationally very expensive. While could theoretically run it on your local machine, you will need HPC facilities to do these calculations within any reasonable time frame.

Luckily, running the OLED workflow via a batch system has become much easier in the 2023 version, thanks to improvements in the underlying PLAMS library. Basically the `.run` script for the `oled-properties` workflow script can just be submitted to the batch system like any other AMS job.

Note: Multi-node OLED properties jobs are currently only supported for SLURM based clusters. For other batch systems, you will be limited to running the jobs on a single node.

The workflow script will then internally take care of scheduling the individual jobs within the allocation that was made for it. All available CPUs are divided into groups, and each group of codes works together on one molecule before moving on to the next. By default 8 CPUs work together, so the `oled-properties` script submitted to a 128 core cluster allocation, would internally do calculations for 16 molecules at the same time, each one using 8 cores. The size of the groups can be configured with the `CoresPerJob` keyword:

```
CoresPerJob integer
```

CoresPerJob**Type** Integer**Default value** 8

Description The number of CPU cores used for each job in the workflow. Combined with the total number of cores used (set by the `NSCM` environment variable or the `-n` command line argument), this indirectly determines the number of simultaneously running jobs. The default value should usually be a good choice. When changing this value, make sure you are using all allocated cores by setting a value that divides the total number of cores, as well as the number of cores on each node.

Restarting

Results are continuously written to the HDF5 file as they are calculated. If a job is interrupted, it will therefore leave an incomplete HDF5 file on disk, which can be used to restart the workflow by passing it to the `Restart` keyword:

```
Restart string
```

Restart**Type** String

Description The HDF5 file from a previous calculation on the same morphology. Data already calculated on the restart file will just be copied over and not be recalculated.

Calculations are then only done for molecules (and dimers) for which not all results have been found on the restart HDF5 file.

This can be combined with the `--load` (or short: `-l`) flag, which uses the [PLAMS rerun prevention](#) and may prevent rerunning jobs for which the full result files are still available in the results directory of the failed job.

```
$AMSBIN/oled-properties -l "failed.results" << EOF
Restart failed.results/properties.hdf5

System
...
End

EOF
```

10.5.4 Material database

The OLED workflows come with a set of precalculated results for standard materials. These are just the results you would get if you ran both the deposition and properties workflow with all default settings on these materials. This data can be used as a reference to judge the performance of the workflows before running them on your own compounds.

Due to its size, the OLED material database is not included with AMS, but can easily be installed via [AMSpackages](#). Once the material database is installed, you can click either the folder icon next to it in [AMSpackages](#), or the **Open** button on the input panel for the deposition workflow in [AMSinput](#) to open it in your file browser. Data for each material is stored in a separate directory, e.g.:

```
beta-NPB/  
├─ beta-NPB.in  
├─ morphology.in  
├─ properties.hdf5  
└─ properties.pdf
```

Here `beta-NPB.in` contains the 3D structure of the deposited molecule. (It is basically the input to the deposition workflow, as all other settings were left at their default values.) Note that all molecules from the OLED material database can also be found in AMSinput through the search box at the top right. The result of the deposition is stored as the `morphology.in` file, which can be opened in AMSinput and directly be used as input for the properties workflow. The resulting properties are stored in the `properties.hdf5` file, see [HDF5 file](#) (page 317) above for details. A quick overview of the properties (e.g. the histograms) can be viewed by opening the `properties.pdf` file in a document viewer.

As of the 2023.1 release, the OLED material database contains data for the following pure materials, as well as a number of host-guest systems:

Pure materials

Compound	PubChem CID	calc. IP $\pm \sigma$ [eV] ^{Page 325, 1}	calc. EA $\pm \sigma$ [eV]
BCP	65149 (https://pubchem.ncbi.nlm.nih.gov/compound/65149)	6.62 \pm 0.20	1.37 \pm 0.18
CBP	11248716 (https://pubchem.ncbi.nlm.nih.gov/compound/11248716)	6.06 \pm 0.11	1.43 \pm 0.12
mCBP	23386664 (https://pubchem.ncbi.nlm.nih.gov/compound/23386664)	4.16 \pm 0.10	1.35 \pm 0.13
mCP	22020377 (https://pubchem.ncbi.nlm.nih.gov/compound/22020377)	7.24 \pm 0.089	1.14 \pm 0.089
mer-Alq3	16683111 (https://pubchem.ncbi.nlm.nih.gov/compound/16683111)	5.81 \pm 0.29	1.87 \pm 0.29
fac-Alq3	16683111 (https://pubchem.ncbi.nlm.nih.gov/compound/16683111)	5.87 \pm 0.33	1.84 \pm 0.32
fac-Irppy3	59117881 (https://pubchem.ncbi.nlm.nih.gov/compound/59117881)	5.76 \pm 0.25	1.54 \pm 0.26
mer-Irppy3	59117881 (https://pubchem.ncbi.nlm.nih.gov/compound/59117881)	5.47 \pm 0.17	1.55 \pm 0.18
α -MADN	53403806 (https://pubchem.ncbi.nlm.nih.gov/compound/53403806)	6.06 \pm 0.081	1.65 \pm 0.081
β -MADN (isomer)	53403806 (https://pubchem.ncbi.nlm.nih.gov/compound/53403806)	6.00 \pm 0.082	1.69 \pm 0.085
α -NPB	5069127 (https://pubchem.ncbi.nlm.nih.gov/compound/5069127)	5.44 \pm 0.089	1.56 \pm 0.083
α -NPB-2Me (+ 2 methyl groups)	5069127 (https://pubchem.ncbi.nlm.nih.gov/compound/5069127)	5.53 \pm 0.081	1.54 \pm 0.085
β -NPB	21881245 (https://pubchem.ncbi.nlm.nih.gov/compound/21881245)	5.43 \pm 0.075	1.51 \pm 0.074
β -NPB-2Me (+ 2 methyl groups)	21881245 (https://pubchem.ncbi.nlm.nih.gov/compound/21881245)	5.51 \pm 0.075	1.48 \pm 0.074
2-TNATA	16184079 (https://pubchem.ncbi.nlm.nih.gov/compound/16184079)	5.04 \pm 0.088	1.63 \pm 0.067
MT-DATA	11061735 (https://pubchem.ncbi.nlm.nih.gov/compound/11061735)	4.98 \pm 0.089	1.11 \pm 0.072
NBPhen	53403424 (https://pubchem.ncbi.nlm.nih.gov/compound/53403424)	4.07 \pm 0.17	1.85 \pm 0.16
Spiro-TAD	16134428 (https://pubchem.ncbi.nlm.nih.gov/compound/16134428)	5.24 \pm 0.062	1.38 \pm 0.078
T2T / TMBT ²	59336459 (https://pubchem.ncbi.nlm.nih.gov/compound/59336459)	6.63 \pm 0.079	1.80 \pm 0.075
T2T / TMBT	59336459 (https://pubchem.ncbi.nlm.nih.gov/compound/59336459)	6.62 \pm 0.080	1.81 \pm 0.077
TAPC	94071 (https://pubchem.ncbi.nlm.nih.gov/compound/94071)	5.26 \pm 0.058	0.791 \pm 0.070
TBRb	23576810 (https://pubchem.ncbi.nlm.nih.gov/compound/23576810)	5.33 \pm 0.063	1.98 \pm 0.060
TCTA	9962045 (https://pubchem.ncbi.nlm.nih.gov/compound/9962045)	5.68 \pm 0.095	1.50 \pm 0.092
TPBi	21932919 (https://pubchem.ncbi.nlm.nih.gov/compound/21932919)	6.41 \pm 0.19	1.58 \pm 0.20

¹ For the calculation of the mean and standard deviation of IP and EA, data points with a modified Z score > 16 were discarded as outliers. This only affects a few systems that had isolated outliers, e.g. due to SCF convergence problems.

² T2T and TMBT are actually just two different names for the same compound. We did not realize this until after running the calculations. Both sets of results are included in the database.

Host-guest systems

Component	PubChem CID	calc. IP $\pm \sigma$ [eV]	calc. EA $\pm \sigma$ [eV]
95% CBP	11248716 (https://pubchem.ncbi.nlm.nih.gov/compound/11248716)	7.06 \pm 0.12	1.45 \pm 0.14
5% fac-Irppy3	59117881 (https://pubchem.ncbi.nlm.nih.gov/compound/59117881)	8.89 \pm 0.12	1.60 \pm 0.12

Component	PubChem CID	calc. IP $\pm \sigma$ [eV]	calc. EA $\pm \sigma$ [eV]
95% CBP	11248716 (https://pubchem.ncbi.nlm.nih.gov/compound/11248716)	6.05 \pm 0.094	1.43 \pm 0.11
5% PtOEP	636283 (https://pubchem.ncbi.nlm.nih.gov/compound/636283)	6.08 \pm 0.094	1.85 \pm 0.11

Component	PubChem CID	calc. IP $\pm \sigma$ [eV]	calc. EA $\pm \sigma$ [eV]
93.05% mCBP	23386664 (https://pubchem.ncbi.nlm.nih.gov/compound/23386664)	6.14 \pm 0.11	1.34 \pm 0.13
6.3% 4CzIPN-Me	102198498 (https://pubchem.ncbi.nlm.nih.gov/compound/102198498) (+ 8 methyl groups)	5.96 \pm 0.13	2.47 \pm 0.13
0.65% TBRb	23576810 (https://pubchem.ncbi.nlm.nih.gov/compound/23576810)	5.39 \pm 0.096	2.04 \pm 0.098

10.6 Conformers

Conformers is a flexible tool for conformer generation. It implements the RDKit¹, CREST² and Simulated Annealing conformer generation methods and can be combined with any *AMS engine* (page 250).

Tip: You can use **Conformers** from the Graphical User Interface or from `python with PLAMS`.

See also:

Tutorial on Conformer generation and Boltzmann-weighted spectra

10.6.1 Overview

This is a simple example showing how to generate conformers of ethanol:

```
#!/bin/sh
$AMSBIN/conformers << EOF

Task Generate

System
```

(continues on next page)

¹ G. Landrum, *Rdkit documentation* Release 2013 (<https://buildmedia.readthedocs.org/media/pdf/rdkit/latest/rdkit.pdf>)

² P. Pracht, F. Bohle, S. Grimme, *Automated exploration of the low-energy chemical space with fast quantum chemical methods* Physical Chemistry Chemical Physics: PCCP, 19 Feb 2020, 22(14):7169-7192 (<https://doi.org/10.1039/c9cp06869d>)

(continued from previous page)

```

Atoms
  C -4.537101 -0.602542 -0.008859
  C -3.601843 -1.804345  0.037274
  O -2.267293 -1.387375 -0.058902
  H -4.301877  0.096761  0.821305
  H -5.588912 -0.942676  0.095614
  H -4.425039 -0.071643 -0.977931
  H -3.829607 -2.474689 -0.818032
  H -3.766077 -2.377916  0.977441
  H -2.012143 -1.043722  0.837186
End
End

Engine ForceField
EndEngine
EOF

```

The most important input options are:

- **Task:** the task for the Conformers tool. Here we simply **Generate** a set of conformers starting from an initial structure. See the *Tasks* (page 327) section for more information.
- **System:** in the *System block* (page 31) we specify the initial structure of the molecule for which you want to generate conformers, in this case an ethanol molecule.
- **Engine:** during the conformers generation, atomistic calculations will be executed under the hood to compute energy and forces. With the *engine* (page 329) block you can specify which atomistic engine to use and the options for the engine.

Tip: By default, the computationally fast (but not very accurate) *ForceField engine* is used to compute energy and forces. If you need more accurate geometries and energies for your conformers, you can specify a more accurate (but slow) engine in the generation step. Alternatively, you can use the *Optimize, Filter and Score tasks* (page 327) to efficiently get accurate geometries and energies while keeping the computational cost to a minimum. See *Workflow* (page 331) for an example.

When running the script above, a folder called `conformers.results` will be created and the generated conformers will be saved in there (in `.xyz` and `.rkf` formats). See the general *Input, execution and output* (page 9) section for more information.

10.6.2 Main Input Options

Tasks

You can specify the task for the Conformers tool via the `Task` input option:

```
Task [Generate | Optimize | Filter | Score | Expand]
```

The main (and default) **Task** is **Generate**: given an initial structure, the Conformers tool will generate a set of conformers.

The other tasks, described below, can be used to refine or combine previously generated conformer sets. The *Workflow* (page 331) example shows how the various tasks can be combined in a simple workflow to efficiently obtain accurate conformers.

Task

Type Multiple Choice

Default value Generate

Options [Generate, Optimize, Filter, Score, Expand]

Description The task to be performed by the Conformers tool.

‘Generate’: given a molecule, generate a set of conformers. Note: this task will automatically optimize, filter and score the conformers.

‘Optimize’: given a previously generated set of conformers, optimize, filter and score the structures using the specified engine.

‘Filter’: given one or more previously generated set of conformers, merge them into a single conformer set and filter out duplicate conformers. Note: this will not optimize or re-score the conformers.

‘Score’ given one or more previously generated set of conformers, re-score them by computing the energy using the specified engine. Note: this will only do a single point calculation, and will not optimize the structures.

In case of ‘Optimize’, ‘Filter’ and ‘Score’ you can specify the input conformer set(s) using the ‘InputConformersSet’ keyword.

Input molecule(s)

For the `Generate` task you can use the `System` or `LoadSystem` blocks to specify the input molecule. See the *System block* (page 31) documentation for a detailed description.

For the `Optimize`, `Filter` and `Score` tasks, you should instead provide the results of a previously run Conformers calculation as input via the `InputConformersSet` keyword. See also the *Examples* (page 331) section.

```
InputConformersSet string
```

InputConformersSet

Type String

Recurring True

Description The path to a file containing a set of conformers.

The file should be either an ‘conformers.rkf’ file (i.e. the results file of conformers) or a concatenated .xyz file.

You can specify multiple input conformers sets by including the `InputConformersSet` keyword multiple times.

When loading conformers using the `InputConformersSet` key, you can optionally specify the `InputMaxEnergy` option:

```
InputMaxEnergy float
```

InputMaxEnergy

Type Float

Unit kcal/mol

Description Threshold for filtering out high-energy conformers when loading conformers sets using the `InputConformerSet` keyword. Conformers with an larger relative energy will not be loaded.

A similar option is the `InputMaxConfs` key, which will use only the k lowest energy conformers for an integer input k :

```
InputMaxConfs integer
```

InputMaxConfs

Type Integer

Description The maximum number of conformers to carry forward when loading conformer sets. If this input is not specified, this limit will not be imposed.

Engine

With the **Engine** block you can specify which atomistic engine to use and the options for the engine. See the [AMS engine](#) (page 250) documentation for more info.

If no engine block is specified, the [ForceField engine](#) (with the UFF force field) will be used as default.

Generators

Three different methods of conformer generation are implemented: [RDKit](#)^{Page 325, 1}, [CREST](#)[?] and [ANNEALING](#). The **default** generation method is **RDKit**.

You can select which method to use in the `Generator` block:

```
Generator
  Method [RDKit | CREST | ANNEALING]
End
```

Generator

Type Block

Description Options for the conformer generator.

Method

Type Multiple Choice

Default value RDKit

Options [RDKit, CREST, ANNEALING]

GUI name Generator method

Description Method used to generate the conformers.

The RDKit generator is based on random distance matrix method. This is the recommended (and default) method.

The CREST Generator uses a multi-step workflow with meta-dynamics simulations to explore the conformers space of a molecule. This can be a powerful conformer search method, but it is generally computationally expensive compared to the RDKit generator.

The ANNEALING generator performs a simulated annealing simulation to explore conformer space.

Input options for the various methods can be specified in their respective input blocks. See the section [Other input options](#) (page 333) for the complete set of input options.

Conformers Equivalence

An important aspect of conformers generation is the reduction of a set of geometries into a set of unique conformers. As the Conformer tool generates new potential conformers, it needs to be able to determine whether a structure is a new conformer (in which case it is added to the list of unique conformers) or whether is simply a slightly different geometry of an already observed conformer (in which case, the structure is discarded).

The conformer tool therefore needs a procedure that, given two geometries, is able to discriminate between the following situations:

- the two geometries correspond to the same conformer
- the two geometries correspond to distinct conformers

In the `Equivalence` block various options related to this equivalence procedure can be specified.

```
Equivalence
  Method [AMS | TFD | RMSD | CREST]
End
```

Equivalence

Type Block

Description Options for the procedure determining whether two structures are equivalent or distinct conformers.

Method

Type Multiple Choice

Default value CREST

Options [AMS, TFD, RMSD, CREST]

GUI name Equivalence method

Description Method used to determine (and filter out) equivalent conformers.

The CREST equivalence method relies on rotational constants comparisons. For this reason, conformers with the same rotational constants (such as mirror images) will be considered equivalent conformers.

The AMS equivalence method uses a distance matrix and dihedrals to compare conformers. This equivalence method can be computationally expensive for large molecules.

The TFD equivalence method uses the Torsion Fingerprint Difference as implemented in RDKit.

The RMSD equivalence method uses the RDKit GetBestRMS implementation.

Input options for the various methods can be specified in their respective input blocks. See the section *Other input options* (page 333) for the complete set of input options.

Filtering

The Conformers tool can automatically filter out conformers based on some criteria, e.g. it will discard high energy conformers.

The filtering options can be specified in the `Filter` block:

```
Filter
  MaxEnergy float
  RemoveNonMinima Yes/No
End
```

Filter

Type Block

Description Options for the conformer filtering.

MaxEnergy

Type Float

Unit kcal/mol

Description Threshold for filtering out high-energy conformers. If the relative energy of a conformer with respect to the lowest conformer is larger than this value, the conformer will be discarded.

RemoveNonMinima

Type Bool

Default value No

Description For the final set of conformers, explicitly check that the geometry corresponds to a local minimum, and remove it if it does not. Note: this will run a PES point characterization, which can be computationally expensive!

10.6.3 Examples

Workflow

During the conformers generation (i.e. the “generate” *task* (page 327)), a large number of atomistic calculations will be executed under the hood. This can get computationally very expensive if an accurate *engine* (page 329) (such as ADF) is used. This is why the default engine is the computationally fast (but not very accurate) *ForceField* engine.

By combining the *Generate*, *Optimize* and *Score* tasks you can build a simple workflow to get accurate geometries and energies while keeping the computational cost to a minimum.

A typical workflow might look like this:

1. Generate a set of conformers using `Task Generate` with the fast but approximate *ForceField* engine
2. Re-optimize the geometries generated in the previous step using `Task Optimize` with a more accurate engine (e.g. DFTB)
3. Re-score the conformers using the using `Task Score` with an accurate engine (e.g. ADF)

```
#!/bin/sh

# Simple workflow:
# - generate an initial set of 1-bromo-3-chloropropane conformers with UFF_
→ (ForceField engine)
# - re-optimize the conformers with GFN1-xTB (DFTB engine)
# - re-score the GFN1-xTB-optimized conformers using DFT energies (ADF engine)

AMS_JOBNAME=generate_uff $AMSBIN/conformers << EOF

Task Generate

System
  Atoms
    Br    -4.16969843    2.48953245    -0.00000000
    C     -2.69926018    3.75062981    -0.00000000
    C     -1.36372383    3.00977020    -0.00000000
    C     -0.19648214    3.99512105     0.00000000
    Cl    1.35297276     3.11657146     0.00000000
    H     -2.78129583    4.39009878     0.90457474
    H     -2.78129583    4.39009878    -0.90457474
    H     -1.30112035    2.36381643    -0.90271681
    H     -1.30112035    2.36381643     0.90271681
    H     -0.24025734    4.63864134     0.90438917
    H     -0.24025734    4.63864134    -0.90438917
  End
End

Engine ForceField
  Type UFF
EndEngine
EOF

AMS_JOBNAME=optimize_gfn1xtb $AMSBIN/conformers << EOF

Task Optimize

InputConformersSet generate_uff.results/conformers.rkf

Engine DFTB
  Model GFN1-xTB
EndEngine
EOF

AMS_JOBNAME=score_dft $AMSBIN/conformers << EOF

Task Score

InputConformersSet optimize_gfn1xtb.results/conformers.rkf

# Here we use the default ADF settings. For real calculations, you
# should use a larger basis set (e.g. TZP) and a better XC functional

Engine ADF
EndEngine
```

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```
EOF

echo "Final conformers:"
cat score_dft.results/conformers.xyz
```

10.6.4 References

10.6.5 Other input options

Here we document more advanced input options for the Conformer tool. **See the section [Main Input Options](#) (page 327) for the most important input option.**

Output

Type Block

Description Options regarding the output and result files.

KeepWorkDir

Type Bool

Default value No

Description Do not remove the working directories after the conformer generation is finished.

rkf

Type Bool

Default value Yes

Description Save the final conformers in .rkf format. The file 'conformers.rkf' will be located in the results directory. You can visualize this file using the AMSMovie GUI module.

sdf

Type Bool

Default value Yes

Description Save the final conformers in .sdf format. The file 'conformers.sdf' will be located in the results directory.

xyz

Type Bool

Default value Yes

Description Save the final conformers in .xyz format. The file 'conformers.xyz' will be located in the results directory.

RNGSeed

Type Integer

Description Initial seed for the (pseudo)random number generator. If this is unset, the generator will be seeded randomly from external sources of entropy and the generated conformers will be non-deterministic.

Generator

Type Block

Description Options for the conformer generator.

ANNEALING

Type Block

Description Options for the annealing generator. This generator creates conformers by performing a simulated annealing simulation.

MolecularDynamics

Type Block

Description Configures molecular dynamics (with the velocity-Verlet algorithm) with and without thermostats. This block allows to specify the details of the molecular dynamics calculation.

Checkpoint

Type Block

Description Sets the frequency for storing the entire MD state necessary for restarting the calculation.

Frequency

Type Integer

Default value 1000

GUI name Checkpoint frequency

Description Write the MD state and engine-specific data to the respective .rkf files once every N steps.

WriteProperties

Type Bool

Default value No

Description Write the properties from the properties section to the Checkpoint file once every N steps.

InitialVelocities

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

File

Type String

Description AMS RKF file containing the initial velocities.

RandomVelocitiesMethod

Type Multiple Choice

Default value Exact

Options [Exact, Boltzmann, Gromacs]

GUI name Velocity randomization method

Description Specifies how are random velocities generated. Three methods are available.

Exact: Velocities are scaled to exactly match set random velocities temperature.

Boltzmann: Velocities are not scaled and sample Maxwell-Boltzmann distribution. However, the distribution is not corrected for constraints.

Gromacs: Velocities are scaled to match set random velocities temperature, but removal of net momentum is performed only after the scaling. Resulting kinetic energy is lower based on how much net momentum the system had.

Temperature

Type Float

Unit Kelvin

GUI name Initial temperature

Description Sets the temperature for the Maxwell-Boltzmann distribution when the type of the initial velocities is set to random, in which case specifying this key is mandatory.

AMSinput will use the first temperature of the first thermostat as default.

Type

Type Multiple Choice

Default value Random

Options [Zero, Random, FromFile, Input]

GUI name Initial velocities

Description Specifies the initial velocities to assign to the atoms. Three methods to assign velocities are available.

Zero: All atom are at rest at the beginning of the calculation.

Random: Initial atom velocities follow a Maxwell-Boltzmann distribution for the temperature given by the [MolecularDynamics%InitialVelocities%Temperature] keyword.

FromFile: Load the velocities from a previous ams result file.

Input: Atom's velocities are set to the values specified in the [MolecularDynamics%InitialVelocities%Values] block, which can be accessed via the Expert AMS panel in AMSinput.

Values

Type Non-standard block

Description This block specifies the velocity of each atom, in Angstrom/fs, when [MolecularDynamics%InitialVelocities%Type] is set to Input. Each row must contain three floating point values (corresponding to the x,y,z component of the velocity vector) and a number of rows equal to the number of atoms must be present, given in the same order as the [System%Atoms] block.

NSteps

Type Integer

Default value 1000

GUI name Number of steps

Description The number of steps to be taken in the MD simulation.

Preserve**Type** Block**Description** Periodically remove numerical drift accumulated during the simulation to preserve different whole-system parameters.**AngularMomentum****Type** Bool**Default value** Yes**GUI name** : Angular momentum**Description** Remove overall angular momentum of the system. This option is ignored for 2D and 3D-periodic systems.**CenterOfMass****Type** Bool**Default value** No**GUI name** : Center of mass**Description** Translate the system to keep its center of mass at the coordinate origin. This option is not very useful for 3D-periodic systems.**Momentum****Type** Bool**Default value** Yes**GUI name** Preserve: Total momentum**Description** Remove overall (linear) momentum of the system.**Print****Type** Block**Description** This block controls the printing of additional information to stdout.**System****Type** Bool**Default value** No**Description** Print the chemical system before and after the simulation.**Velocities****Type** Bool**Default value** No**Description** Print the atomic velocities before and after the simulation.**Restart****Type** String**GUI name** Restart from**Description** The path to the ams.rkf file from which to restart the simulation.**Shake**

Type Block

Description Parameters of the Shake/Rattle algorithm.

A11

Type String

Recurring True

GUI name Constrain all

Description Constraint description in one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 and the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then all bonds between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk '*' denoting any atom. The distance, if present, must be in Angstrom. If it is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at certain points of the simulation (at the start or right after adding/removing atoms) can be constrained, which means that the bonds may need to be specified in the System block.

Warning: the triangles constraint should be used with care because each constrained bond or angle means removing one degree of freedom from the dynamics. When there are too many constraints (for example, "All triangles H C H" in methane) some of them may be linearly dependent, which will lead to an error in the temperature computation.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

ConvergeR2

Type Float

Default value 1e-08

Description Convergence criterion on the max squared difference, in atomic units.

ConvergeRV

Type Float

Default value 1e-08

Description Convergence criterion on the orthogonality of the constraint and the relative atomic velocity, in atomic units.

Iterations

Type Integer

Default value 100

Description Number of iterations.

ShakeInitialCoordinates

Type Bool

Default value Yes

Description Apply constraints before computing the first energy and gradients.

Thermostat

Type Block

Recurring True

Description This block allows to specify the use of a thermostat during the simulation. Depending on the selected thermostat type, different additional options may be needed to characterize the specific thermostat' behavior.

BerendsenApply

Type Multiple Choice

Default value Global

Options [Local, Global]

GUI name Apply Berendsen

Description Select how to apply the scaling correction for the Berendsen thermostat:
- per-atom-velocity (Local) - on the molecular system as a whole (Global).

ChainLength

Type Integer

Default value 10

GUI name NHC chain length

Description Number of individual thermostats forming the NHC thermostat

Duration

Type Integer List

GUI name Duration(s)

Description Specifies how many steps should a transition from a particular temperature to the next one in sequence take.

Region

Type String

Default value *

Description The identifier of the region to thermostat. The default '*' applies the thermostat to the entire system. The value can be a plain region name, or a region expression, e.g. '*-myregion' to thermostat all atoms that are not in myregion, or 'regionA+regionB' to thermostat the union of the 'regionA' and 'regionB'. Note that if multiple thermostats are used, their regions may not overlap.

Tau

Type Float

Unit Femtoseconds

GUI name Damping constant

Description The time constant of the thermostat.

Temperature

Type Float List

Unit Kelvin

GUI name Temperature(s)

Description The target temperature of the thermostat.

You can specify multiple temperatures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one T to the next T (using a linear ramp). For NHC thermostat, the temperature may not be zero.

Type

Type Multiple Choice

Default value None

Options [None, Berendsen, NHC]

GUI name Thermostat

Description Selects the type of the thermostat.

TimeStep

Type Float

Default value 0.25

Unit Femtoseconds

Description The time difference per step.

Trajectory

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

PrintFreq

Type Integer

GUI name Printing frequency

Description Print current thermodynamic properties to the output every N steps. By default this is done every SamplingFreq steps.

SamplingFreq

Type Integer

Default value 100

GUI name Sample frequency

Description Write the the molecular geometry (and possibly other properties) to the .rkf file once every N steps.

TProfileGridPoints

Type Integer

Default value 0

Description Number of points in the temperature profile. If TProfileGridPoints > 0, a temperature profile along each of the three lattice axes will be written to the .rkf file. The temperature at a given profile point is calculated as the total temperature of all atoms inside the corresponding slice of the simulation box, time-averaged over all MD steps since the previous snapshot. By default, no profile is generated.

WriteBonds

Type Bool

Default value Yes

Description Write detected bonds to the .rkf file.

WriteCharges

Type Bool

Default value Yes

Description Write current atomic point charges (if available) to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze charges.

WriteCoordinates

Type Bool

Default value Yes

Description Write atomic coordinates to the .rkf file.

WriteEngineGradients

Type Bool

Default value No

Description Write atomic gradients (negative of the atomic forces, as calculated by the engine) to the History section of ams.rkf.

WriteMolecules

Type Bool

Default value Yes

Description Write the results of molecule analysis to the .rkf file.

WriteVelocities

Type Bool

Default value Yes

Description Write velocities to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze the velocities.

Temperatures

Type Float List

Default value [298.0, 798.0]

Unit Kelvin

Description The minimum and maximum temperature of the annealing simulation. The simulation will start at the highest temperature, and cool down to the lowest.

UseShake

Type Bool

Default value No

Description Constrain all -H bonds with shake. If turned on, the MD timestep is automatically increased.

CREST

Type Block

Description Options for the CREST generator. The CREST generator performs a set of metadynamics simulations (using the METADYNAMICS generator), then a set of MD simulations (using the MD expander), and finally it does a combinatorial expansion of the generated conformers using the GC expander. This sequence is repeated in an iterative fashion until the lowest energy conformer no longer changes.

ConvergenceQualityCrude

Type Multiple Choice

Default value None

Options [Normal, Good, VeryGood, Excellent, None]

Description The tightness of the convergence of the crude geometry pre-optimizations. If set to none it will be selected two levels below ConvergenceQuality.

ConvergenceQualityTight

Type Multiple Choice

Default value None

Options [Normal, Good, VeryGood, Excellent, None]

Description The tightness of the convergence of the final geometry optimizations. If set to none it will be selected the same as ConvergenceQuality.

GCStep

Type Bool

Default value Yes

Description Whether or not to include the combinatorial expansion of the conformers using the GC Generator. For big systems this step can be very time consuming. By default it is set to True.

UseShake

Type Bool

Default value Yes

Description Whether or not SHAKE should be turned on in the MD and Metadynamics simulations. If this is turned on, the MD timestep is automatically increased (from 2 to 5 fs).

METADYNAMICS

Type Block

Description Produces conformers by running a set of CREST-RMSD metadynamics simulations with different biases, extracting snapshots, and optimizing those.

ConvergenceQualityCrude

Type Multiple Choice

Default value none

Options [normal, good, verygood, excellent, none]

Description The tightness of the convergence of the crude geometry pre-optimizations. If set to none it will be selected two levels below ConvergenceQuality.

MolecularDynamics

Type Block

Description Configures molecular dynamics (with the velocity-Verlet algorithm) with and without thermostats. This block allows to specify the details of the molecular dynamics calculation.

Checkpoint

Type Block

Description Sets the frequency for storing the entire MD state necessary for restarting the calculation.

Frequency

Type Integer

Default value 1000

GUI name Checkpoint frequency

Description Write the MD state and engine-specific data to the respective .rkf files once every N steps.

WriteProperties

Type Bool

Default value No

Description Write the properties from the properties section to the ChecoPoint file once every N steps.

InitialVelocities

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

File

Type String

Description AMS RKF file containing the initial velocities.

RandomVelocitiesMethod

Type Multiple Choice

Default value Exact

Options [Exact, Boltzmann, Gromacs]

GUI name Velocity randomization method

Description Specifies how are random velocities generated. Three methods are available.

Exact: Velocities are scaled to exactly match set random velocities temperature.

Boltzmann: Velocities are not scaled and sample Maxwell-Boltzmann distribution. However, the distribution is not corrected for constraints.

Gromacs: Velocities are scaled to match set random velocities temperature, but removal of net momentum is performed only after the scaling. Resulting kinetic energy is lower based on how much net momentum the system had.

Temperature

Type Float

Unit Kelvin

GUI name Initial temperature

Description Sets the temperature for the Maxwell-Boltzmann distribution when the type of the initial velocities is set to random, in which case specifying this key is mandatory.

AMSinput will use the first temperature of the first thermostat as default.

Type

Type Multiple Choice

Default value Random

Options [Zero, Random, FromFile, Input]

GUI name Initial velocities

Description Specifies the initial velocities to assign to the atoms. Three methods to assign velocities are available.

Zero: All atom are at rest at the beginning of the calculation.

Random: Initial atom velocities follow a Maxwell-Boltzmann distribution for the temperature given by the [MolecularDynamics%InitialVelocities%Temperature] keyword.

FromFile: Load the velocities from a previous ams result file.

Input: Atom's velocities are set to the values specified in the [MolecularDynamics%InitialVelocities%Values] block, which can be accessed via the Expert AMS panel in AMSinput.

Values

Type Non-standard block

Description This block specifies the velocity of each atom, in Angstrom/fs, when [MolecularDynamics%InitialVelocities%Type] is set to Input. Each row must contain three floating point values (corresponding to the x,y,z component of the velocity vector) and a number of rows equal to the number of atoms must be present, given in the same order as the [System%Atoms] block.

NSteps

Type Integer

Default value 1000

GUI name Number of steps

Description The number of steps to be taken in the MD simulation.

Preserve

Type Block

Description Periodically remove numerical drift accumulated during the simulation to preserve different whole-system parameters.

AngularMomentum

Type Bool

Default value Yes

GUI name : Angular momentum

Description Remove overall angular momentum of the system. This option is ignored for 2D and 3D-periodic systems.

CenterOfMass

Type Bool

Default value No

GUI name : Center of mass

Description Translate the system to keep its center of mass at the coordinate origin. This option is not very useful for 3D-periodic systems.

Momentum

Type Bool

Default value Yes

GUI name Preserve: Total momentum

Description Remove overall (linear) momentum of the system.

Print

Type Block

Description This block controls the printing of additional information to stdout.

System

Type Bool

Default value No

Description Print the chemical system before and after the simulation.

Velocities

Type Bool

Default value No

Description Print the atomic velocities before and after the simulation.

Restart

Type String

GUI name Restart from

Description The path to the ams.rkf file from which to restart the simulation.

Shake

Type Block

Description Parameters of the Shake/Rattle algorithm.

A11**Type** String**Recurring** True**GUI name** Constrain all**Description** Constraint description in one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 and the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then all bonds between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk '*' denoting any atom. The distance, if present, must be in Angstrom. If it is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at certain points of the simulation (at the start or right after adding/removing atoms) can be constrained, which means that the bonds may need to be specified in the System block.

Warning: the triangles constraint should be used with care because each constrained bond or angle means removing one degree of freedom from the dynamics. When there are too many constraints (for example, "All triangles H C H" in methane) some of them may be linearly dependent, which will lead to an error in the temperature computation.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

ConvergeR2**Type** Float**Default value** 1e-08**Description** Convergence criterion on the max squared difference, in atomic units.**ConvergeRV****Type** Float**Default value** 1e-08**Description** Convergence criterion on the orthogonality of the constraint and the relative atomic velocity, in atomic units.**Iterations****Type** Integer**Default value** 100**Description** Number of iterations.**ShakeInitialCoordinates****Type** Bool**Default value** Yes**Description** Apply constraints before computing the first energy and gradients.**Thermostat**

Type Block

Recurring True

Description This block allows to specify the use of a thermostat during the simulation. Depending on the selected thermostat type, different additional options may be needed to characterize the specific thermostat' behavior.

BerendsenApply

Type Multiple Choice

Default value Global

Options [Local, Global]

GUI name Apply Berendsen

Description Select how to apply the scaling correction for the Berendsen thermostat:

- per-atom-velocity (Local) - on the molecular system as a whole (Global).

ChainLength

Type Integer

Default value 10

GUI name NHC chain length

Description Number of individual thermostats forming the NHC thermostat

Duration

Type Integer List

GUI name Duration(s)

Description Specifies how many steps should a transition from a particular temperature to the next one in sequence take.

Region

Type String

Default value *

Description The identifier of the region to thermostat. The default '*' applies the thermostat to the entire system. The value can be a plain region name, or a region expression, e.g. '*-myregion' to thermostat all atoms that are not in myregion, or 'regionA+regionB' to thermostat the union of the 'regionA' and 'regionB'. Note that if multiple thermostats are used, their regions may not overlap.

Tau

Type Float

Unit Femtoseconds

GUI name Damping constant

Description The time constant of the thermostat.

Temperature

Type Float List

Unit Kelvin

GUI name Temperature(s)

Description The target temperature of the thermostat.

You can specify multiple temperatures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one T to the next T (using a linear ramp). For NHC thermostat, the temperature may not be zero.

Type

Type Multiple Choice

Default value None

Options [None, Berendsen, NHC]

GUI name Thermostat

Description Selects the type of the thermostat.

TimeStep

Type Float

Default value 0.25

Unit Femtoseconds

Description The time difference per step.

Trajectory

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

PrintFreq

Type Integer

GUI name Printing frequency

Description Print current thermodynamic properties to the output every N steps. By default this is done every SamplingFreq steps.

SamplingFreq

Type Integer

Default value 100

GUI name Sample frequency

Description Write the the molecular geometry (and possibly other properties) to the .rkf file once every N steps.

TProfileGridPoints

Type Integer

Default value 0

Description Number of points in the temperature profile. If TProfileGridPoints > 0, a temperature profile along each of the three lattice axes will be written to the .rkf file. The temperature at a given profile point is calculated as the total temperature of all atoms inside the corresponding slice of the simulation box, time-averaged over all MD steps since the previous snapshot. By default, no profile is generated.

WriteBonds

Type Bool

Default value Yes

Description Write detected bonds to the .rkf file.

WriteCharges

Type Bool

Default value Yes

Description Write current atomic point charges (if available) to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze charges.

WriteCoordinates

Type Bool

Default value Yes

Description Write atomic coordinates to the .rkf file.

WriteEngineGradients

Type Bool

Default value No

Description Write atomic gradients (negative of the atomic forces, as calculated by the engine) to the History section of ams.rkf.

WriteMolecules

Type Bool

Default value Yes

Description Write the results of molecule analysis to the .rkf file.

WriteVelocities

Type Bool

Default value Yes

Description Write velocities to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze the velocities.

NWidthsHeights

Type Integer List

Default value [4, 3]

Description The number of different Gaussian widths and heights respectively used in the metadynamics simulations. By default 4 different widths are used and 3 different heights, resulting in 12 different metadynamics simulations.

SimulationSuccessFraction

Type Float

Default value 0.4

Description The fraction of planned metadynamics steps that has to have succeeded in order for the metadynamics iteration to be considered a success.

UseShake**Type** Bool**Default value** No**Description** Constrain all -H bonds with shake. If turned on, the MD timestep is automatically increased.**MaxEnergy****Type** Float**Unit** kcal/mol**Description** Threshold for filtering out high-energy conformers. If the relative energy of a conformer with respect to the lowest conformer is larger than this value, the conformer will be discarded.**Method****Type** Multiple Choice**Default value** RDKit**Options** [RDKit, CREST, ANNEALING]**GUI name** Generator method**Description** Method used to generate the conformers.

The RDKit generator is based on random distance matrix method. This is the recommended (and default) method.

The CREST Generator uses a multi-step workflow with meta-dynamics simulations to explore the conformers space of a molecule. This can be a powerful conformer search method, but it is generally computationally expensive compared to the RDKit generator.

The ANNEALING generator performs a simulated annealing simulation to explore conformer space.

Preoptimization**Type** Block**Description** If this block is enabled geometries will be preoptimized. After preoptimization the high energy conformers will be discarded, and then from the remaining set the unoptimized geometries will be optimized at higher level. This is to prevent the preoptimizer from collapsing different conformers into a single false minimum. As a result, preoptimization is only useful if MaxEnergy is chosen low.**Enable****Type** Bool**Default value** No**Description** Perform preoptimization at a low level of accuracy.**Engine****Type** Block**Description** The engine specifics to be used for preoptimization.**PreoptFactor****Type** Integer

Default value 2

Description This factor is multiplied with MaxEnergy, to determine which high energy conformers can be discarded after preoptimization.

RDKit

Type Block

Description Options for the RDKit generator. This generator produces initial guesses for conformers using the RDKit ETKDG method, followed by AMS geometry optimizations.

InitialNConformers

Type Integer

GUI name Initial no. of conformers

Description Number of geometries initially created by RDKit, before AMS geometry optimization and filtering. If not set, the number will be automatically set, based on the number of rotational bonds.

MaxConfs

Type Integer

Default value 5000

Description If InitialNConformers is not set, then the number of conformers will be automatically set, with a maximum of MaxConfs.

MinConfs

Type Integer

Default value 10

Description If InitialNConformers is not set, then the number of conformers will be automatically set, with a minimum of MinConfs.

NconfsEstimationFactor

Type Integer

Default value 100

Description If InitialNConformers is not set, then the number of conformers will be automatically set based on the number of rotational bonds. The resulting number is then multiplied by this factor (default: 100), to ensure that enough conformers will be created.

RDKitETKDG

Type Block

Description Settings for the call to RDKits ETKDG conformer generator tool.

BestRMSDThreshold

Type Float

Default value -1.0

Description After ETKDG conformer generation by RDKit, RDKit can be used to remove duplicates via the BestRMS algorithm. This filter does exactly the same as the RMSD equivalence detector in the Equivalence block.

ConstrainedAtoms

Type Integer List

Description The indices of the atoms to constrain during ETKDG conformer generation.

Forcefield

Type Multiple Choice

Default value None

Options [None, UFF, MMFF]

Description The name of the RDKit forcefield to use for geometry optimization at the end of ETKDG conformer generation (by default no geometry optimization is performed). Using the RDKit internal optimization may make the subsequent geometry optimizations with AMS faster.

Parallel

Type Bool

Default value No

Description Experimental: Parallelize the RDKit generation step by calling the RDKit conformer generation method in parallel from multiple processes.

RMSDThreshold

Type Float

Default value -1.0

Description Root Mean Square deviation threshold for removing similar/equivalent conformations during the RDKit ETKDG procedure. By default there is no pruning (value: -1).

UseExpTorsionAnglePrefs

Type String

Default value default

Description Impose experimental torsion angle preferences in RDKit ETKDG conformer generation. By default the RDKit version determines whether or not to switch this on.

RNGSeed

Type Integer

Description Initial guesses for conformers can be randomly generated by RDKit, using the ETKDG algorithm. For reproducibility, a random number seed can be provided here.

TORSION

Type Block

Description Options for the TorsionGenerator, which generates geometries by enumerative rotation around rotatable bonds. This is the slowest of all generator, and quickly becomes infeasible for large systems. Currently does not work for systems with interconnected rings.

Dtheta

Type Float

Default value 60.0

Description The angle over which the bonds are rotated, in order to create a new conformer.

Expander

Type Block

Description Options for the conformer expander. The Expander expands an existing conformer set, by adding new conformers to it. The new conformers are generated from the original conformers in the set. Unlike the generators, the outcome of an expander is therefore very dependent on the input conformations.

The GC generator uses a genetic algorithm to create a combinatorial expansion by combining local substructures. The MD expander start MD simulations from the conformers in the set, and extracts snapshots to create new conformers. Both these expanders are part of the CREST generator.

GC

Type Block

Description Options for the genetic algorithm for combinatorial expansion of conformer geometries. This generator only works if a non-zero set of conformers is already provided.

Parallel

Type Bool

Default value Yes

Description Determines if the combinatorial expansion of conformers should be performed in parallel or not (default: True).

RMSDThreshold

Type Float

Default value 0.25

Description Newly generated geometries are only considered unique if their RMSD from all other newly generated geometries is larger than this threshold.

MD

Type Block

Description Produces conformers by running a set of MD simulations at different elevated temperatures, extracting snapshots, and optimizing those.

MolecularDynamics

Type Block

Description Configures molecular dynamics (with the velocity-Verlet algorithm) with and without thermostats. This block allows to specify the details of the molecular dynamics calculation.

Checkpoint

Type Block

Description Sets the frequency for storing the entire MD state necessary for restarting the calculation.

Frequency

Type Integer

Default value 1000

GUI name Checkpoint frequency

Description Write the MD state and engine-specific data to the respective .rkf files once every N steps.

WriteProperties

Type Bool

Default value No

Description Write the properties from the properties section to the ChecoPoint file once every N steps.

InitialVelocities

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

File

Type String

Description AMS RKF file containing the initial velocities.

RandomVelocitiesMethod

Type Multiple Choice

Default value Exact

Options [Exact, Boltzmann, Gromacs]

GUI name Velocity randomization method

Description Specifies how are random velocities generated. Three methods are available.

Exact: Velocities are scaled to exactly match set random velocities temperature.

Boltzmann: Velocities are not scaled and sample Maxwell-Boltzmann distribution. However, the distribution is not corrected for constraints.

Gromacs: Velocities are scaled to match set random velocities temperature, but removal of net momentum is performed only after the scaling. Resulting kinetic energy is lower based on how much net momentum the system had.

Temperature

Type Float

Unit Kelvin

GUI name Initial temperature

Description Sets the temperature for the Maxwell-Boltzmann distribution when the type of the initial velocities is set to random, in which case specifying this key is mandatory.

AMSinput will use the first temperature of the first thermostat as default.

Type

Type Multiple Choice

Default value Random

Options [Zero, Random, FromFile, Input]

GUI name Initial velocities

Description Specifies the initial velocities to assign to the atoms. Three methods to assign velocities are available.

Zero: All atom are at rest at the beginning of the calculation.

Random: Initial atom velocities follow a Maxwell-Boltzmann distribution for the temperature given by the [MolecularDynamics%InitialVelocities%Temperature] keyword.

FromFile: Load the velocities from a previous ams result file.

Input: Atom's velocities are set to the values specified in the [MolecularDynamics%InitialVelocities%Values] block, which can be accessed via the Expert AMS panel in AMSinput.

Values

Type Non-standard block

Description This block specifies the velocity of each atom, in Angstrom/fs, when [MolecularDynamics%InitialVelocities%Type] is set to Input. Each row must contain three floating point values (corresponding to the x,y,z component of the velocity vector) and a number of rows equal to the number of atoms must be present, given in the same order as the [System%Atoms] block.

NSteps

Type Integer

Default value 1000

GUI name Number of steps

Description The number of steps to be taken in the MD simulation.

Preserve

Type Block

Description Periodically remove numerical drift accumulated during the simulation to preserve different whole-system parameters.

AngularMomentum

Type Bool

Default value Yes

GUI name : Angular momentum

Description Remove overall angular momentum of the system. This option is ignored for 2D and 3D-periodic systems.

CenterOfMass

Type Bool

Default value No

GUI name : Center of mass

Description Translate the system to keep its center of mass at the coordinate origin. This option is not very useful for 3D-periodic systems.

Momentum

Type Bool

Default value Yes

GUI name Preserve: Total momentum

Description Remove overall (linear) momentum of the system.

Print

Type Block

Description This block controls the printing of additional information to stdout.

System

Type Bool

Default value No

Description Print the chemical system before and after the simulation.

Velocities

Type Bool

Default value No

Description Print the atomic velocities before and after the simulation.

Restart

Type String

GUI name Restart from

Description The path to the ams.rkf file from which to restart the simulation.

Shake

Type Block

Description Parameters of the Shake/Rattle algorithm.

A11

Type String

Recurring True

GUI name Constrain all

Description Constraint description in one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 and the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then all bonds between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk '*' denoting any atom. The distance, if present, must be in Angstrom. If it is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at certain points of the simulation (at the start or right after adding/removing atoms) can be constrained, which means that the bonds may need to be specified in the System block.

Warning: the triangles constraint should be used with care because each constrained bond or angle means removing one degree of freedom from the dynamics. When there are too many constraints (for example, "All triangles H C H" in methane) some of them may be linearly dependent, which will lead to an error in the temperature computation.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

ConvergeR2

Type Float

Default value 1e-08

Description Convergence criterion on the max squared difference, in atomic units.

ConvergeRV

Type Float

Default value 1e-08

Description Convergence criterion on the orthogonality of the constraint and the relative atomic velocity, in atomic units.

Iterations

Type Integer

Default value 100

Description Number of iterations.

ShakeInitialCoordinates

Type Bool

Default value Yes

Description Apply constraints before computing the first energy and gradients.

Thermostat

Type Block

Recurring True

Description This block allows to specify the use of a thermostat during the simulation. Depending on the selected thermostat type, different additional options may be needed to characterize the specific thermostat' behavior.

BerendsenApply

Type Multiple Choice

Default value Global

Options [Local, Global]

GUI name Apply Berendsen

Description Select how to apply the scaling correction for the Berendsen thermostat:

- per-atom-velocity (Local) - on the molecular system as a whole (Global).

ChainLength

Type Integer

Default value 10

GUI name NHC chain length

Description Number of individual thermostats forming the NHC thermostat

Duration**Type** Integer List**GUI name** Duration(s)**Description** Specifies how many steps should a transition from a particular temperature to the next one in sequence take.**Region****Type** String**Default value** ***Description** The identifier of the region to thermostat. The default '*' applies the thermostat to the entire system. The value can be a plain region name, or a region expression, e.g. '*-myregion' to thermostat all atoms that are not in myregion, or 'regionA+regionB' to thermostat the union of the 'regionA' and 'regionB'. Note that if multiple thermostats are used, their regions may not overlap.**Tau****Type** Float**Unit** Femtoseconds**GUI name** Damping constant**Description** The time constant of the thermostat.**Temperature****Type** Float List**Unit** Kelvin**GUI name** Temperature(s)**Description** The target temperature of the thermostat.

You can specify multiple temperatures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one T to the next T (using a linear ramp). For NHC thermostat, the temperature may not be zero.

Type**Type** Multiple Choice**Default value** None**Options** [None, Berendsen, NHC]**GUI name** Thermostat**Description** Selects the type of the thermostat.**TimeStep****Type** Float**Default value** 0.25**Unit** Femtoseconds**Description** The time difference per step.**Trajectory**

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

PrintFreq

Type Integer

GUI name Printing frequency

Description Print current thermodynamic properties to the output every N steps. By default this is done every SamplingFreq steps.

SamplingFreq

Type Integer

Default value 100

GUI name Sample frequency

Description Write the the molecular geometry (and possibly other properties) to the .rkf file once every N steps.

TProfileGridPoints

Type Integer

Default value 0

Description Number of points in the temperature profile. If TProfileGridPoints > 0, a temperature profile along each of the three lattice axes will be written to the .rkf file. The temperature at a given profile point is calculated as the total temperature of all atoms inside the corresponding slice of the simulation box, time-averaged over all MD steps since the previous snapshot. By default, no profile is generated.

WriteBonds

Type Bool

Default value Yes

Description Write detected bonds to the .rkf file.

WriteCharges

Type Bool

Default value Yes

Description Write current atomic point charges (if available) to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze charges.

WriteCoordinates

Type Bool

Default value Yes

Description Write atomic coordinates to the .rkf file.

WriteEngineGradients

Type Bool

Default value No

Description Write atomic gradients (negative of the atomic forces, as calculated by the engine) to the History section of ams.rkf.

WriteMolecules

Type Bool

Default value Yes

Description Write the results of molecule analysis to the .rkf file.

WriteVelocities

Type Bool

Default value Yes

Description Write velocities to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze the velocities.

Ngeoms

Type Integer

Default value 4

Description At each temperature, MD simulations are started from Ngeoms different starting geometries. The starting geometries are extracted from the provided conformer set. If the conformer set is empty, then no more than a single geometry per temperature can be provided, limiting the total number of MD simulations.

Temperatures

Type Float List

Default value [400.0, 500.0]

Unit Kelvin

Description The list of different temperatures at which MD simulations are run.

UseShake

Type Bool

Default value No

Description Constrain all -H bonds with shake. If turned on, the MD timestep is automatically increased.

MaxEnergy

Type Float

Unit kcal/mol

Description Threshold for filtering out high-energy conformers. If the relative energy of a conformer with respect to the lowest conformer is larger than this value, the conformer will be discarded.

Method

Type Multiple Choice

Default value GC

Options [MD, GC]

GUI name Generator method

Description Method used to generate the conformers.

Preoptimization

Type Block

Description If this block is enabled geometries will be preoptimized. After preoptimization the high energy conformers will be discarded, and then from the remaining set the unoptimized geometries will be optimized at higher level. This is to prevent the preoptimizer from collapsing different conformers into a single false minimum. As a result, preoptimization is only useful if MaxEnergy is chosen low.

Enable

Type Bool

Default value No

Description Perform preoptimization at a low level of accuracy.

Engine

Type Block

Description The engine specifics to be used for preoptimization.

PreoptFactor

Type Integer

Default value 2

Description This factor is multiplied with MaxEnergy, to determine which high energy conformers can be discarded after preoptimization.

RDKitETKDG

Type Block

Description Settings for the call to RDKit's ETKDG conformer generator tool.

BestRMSDThreshold

Type Float

Default value -1.0

Description After ETKDG conformer generation by RDKit, RDKit can be used to remove duplicates via the BestRMS algorithm. This filter does exactly the same as the RMSD equivalence detector in the Equivalence block.

Forcefield

Type Multiple Choice

Default value None

Options [None, UFF, MMFF]

Description The name of the RDKit forcefield to use for geometry optimization at the end of ETKDG conformer generation (by default no geometry optimization is performed). Using the RDKit internal optimization may make the subsequent geometry optimizations with AMS faster.

Parallel

Type Bool

Default value No

Description Experimental: Parallelize the RDKit generation step by calling the RDKit conformer generation method in parallel from multiple processes.

RMSDThreshold

Type Float

Default value -1.0

Description Root Mean Square deviation threshold for removing similar/equivalent conformations during the RDKit ETKDG procedure. By default there is no pruning (value: -1).

UseExpTorsionAnglePrefs

Type String

Default value default

Description Impose experimental torsion angle preferences in RDKit ETKDG conformer generation. By default the RDKit version determines whether or not to switch this on.

RNGSeed

Type Integer

Description Initial guesses for conformers can be randomly generated by RDKit, using the ETKDG algorithm. For reproducibility, a random number seed can be provided here.

Equivalence

Type Block

Description Options for the procedure determining whether two structures are equivalent or distinct conformers.

AMS

Type Block

Description Options for the AMS method of checking equivalence. This method uses the atomic distance matrices and the torsion angles between heavy atoms to determine if conformer candidates are duplicates.

DihedralThreshold

Type Float

Default value 30.0

Description Maximum difference a dihedral can have for a conformer to be considered a duplicate.

DistanceThreshold

Type Float

Default value 0.1

Description Maximum difference a distance between two atoms can have for a conformer to be considered a duplicate.

EnergyThreshold

Type Float

Default value 0.2

Unit kcal/mol

Description The energy difference beyond which two conformers are always considered distinct.

IrrelevantAtoms

Type Integer List

Description To detect equivalence, only a subset of atoms is used. The atoms that are excluded from equivalence comparison should be specified here. By default only non-hydrogen atoms will be used for the comparison. Numbering starts at 0.

AcceptAll

Type Bool

Default value No

Description If set to True, add any candidate to the set without checks of connectivity changes, stereo- or cis/trans isomerization, or duplication.

AcceptIsomers

Type Bool

Default value No

Description If set to True, perform all checks of a new conformer candidate, except for the stereo- or cis/trans isomerization check.

CREST

Type Block

Description Options for the CREST method of checking equivalence. This method uses the rotational constants of conformer candidates to determine if they are duplicates.

EnergyThreshold

Type Float

Default value 0.05

Unit kcal/mol

Description The energy difference beyond which two conformers are always considered distinct.

RMSDThreshold

Type Float

Default value 0.125

Description Threshold for the RMSD between two conformers that determines if they are duplicates or rotamers (according to the CREST rotamer definition.)

ScaledRotationalConstantSettings

Type Block

Description By default, the equivalence of two geometries is determined mainly by comparing the rotational constants, and weighing the difference based on the average anisotropy of the two systems. This procedure has several settings that can be user defined.

RotationalConstantThreshold

Type Float

Default value 0.003

Description Threshold for the difference in rotational constants that determines if two geometries are duplicates. The threshold is weighed by the anisotropy of the systems. Note: in the grimme code they use 0.01 as `bconst_threshold`, but this leads to a lot of misclassifications (i.e. different conformers are classified as equivalent rotamers) So, here we use a smaller default value.

CheckForDuplicates

Type Bool

Default value Yes

Description If set to True, check any new conformer candidate for duplication, and only accept unique conformers. If set to False, accept duplicates into the set.

Method

Type Multiple Choice

Default value CREST

Options [AMS, TFD, RMSD, CREST]

GUI name Equivalence method

Description Method used to determine (and filter out) equivalent conformers.

The CREST equivalence method relies on rotational constants comparisons. For this reason, conformers with the same rotational constants (such as mirror images) will be considered equivalent conformers.

The AMS equivalence method uses a distance matrix and dihedrals to compare conformers. This equivalence method can be computationally expensive for large molecules.

The TFD equivalence method uses the Torsion Fingerprint Difference as implemented in RDKit.

The RMSD equivalence method uses the RDKit `GetBestRMS` implementation.

RMSD

Type Block

Description Options for the RMSD method of checking equivalence. This method uses the RDKit implementation of `GetBestRMS`, which enumerates over atomic permutations for pairs of geometries to detect duplicates based on the RMSD value.

EnergyThreshold

Type Float

Default value 0.05

Unit kcal/mol

Description The energy difference beyond which two conformers are always considered distinct.

RMSDThreshold

Type Float

Default value 0.125

Description Threshold on the RMSD difference to determine if two geometries represent the same conformer. This value is in Angstrom.

TFD

Type Block

Description Options for the TFD method of checking equivalence. This method uses the Torsion Finger Print method to determine if two conformer candidates are duplicates.

EnergyThreshold

Type Float

Default value 0.05

Unit kcal/mol

Description The energy difference beyond which two conformers are always considered distinct.

TFDThreshold

Type Float

Default value 0.05

Description Threshold on the torsion fingerprint difference to determine if two geometries represent the same conformer. This value is unit-less.

GeometryOptimization

Type Block

Description Some options / details regarding the optimization procedure.

ConvergenceQuality

Type Multiple Choice

Default value VeryGood

Options [Normal, Good, VeryGood, Excellent]

GUI name Convergence

Description The tightness of the convergence of the geometry optimizations. Lower quality levels may lead to badly converged geometries being classified as distinct conformers.

Keep

Type Multiple Choice

Default value None

Options [None, all]

Description Keep all the output files of the geometry optimizations. If set to 'all', must be used in combination with Output%KeepWorkDir.

MaxOptimizations

Type Integer

Default value 1000

Description Set a maximum to the number of geometries accepted for optimization at once, per AMSWorker (so should be multiplied by the number of cores used). If not set, the disc size requirements can become too large.

UseAMSWorker**Type** Bool**Default value** Yes**Description** Whether the set of optimizations should be run via the AMSWorkerPool or via regular AMSJobs.**WriteGeometries****Type** Block**Description** Determines if and where optimized geometries will be written to file during optimization. When the AMSWorker is used, then the write interval depends on MaxOptimizations. If enabled, must be used in combination with Output%KeepWorkDir.**Dirname****Type** String**Default value** conf_tmpdir**Description** The name of the folder that should contain the optimized geometries.**Enabled****Type** Bool**Default value** No**Description** Enables or disables the periodic writing of optimized geometries to file

10.7 AtomTyping

AtomTyping is a simple tool for assigning atom types to molecular systems. Currently only the GAFF force field is implemented. It uses AMBER's Antechamber under the hood.

10.7.1 Command Line Tool

This is a simple example showing how to generate force field parameters for ethanol:

```
#!/bin/sh
$AMSBIN/atomtyping << EOF

Type GAFF

System
  Atoms
    C -4.537101 -0.602542 -0.008859
    C -3.601843 -1.804345  0.037274
    O -2.267293 -1.387375 -0.058902
    H -4.301877  0.096761  0.821305
    H -5.588912 -0.942676  0.095614
    H -4.425039 -0.071643 -0.977931
    H -3.829607 -2.474689 -0.818032
    H -3.766077 -2.377916  0.977441
    H -2.012143 -1.043722  0.837186
```

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```
End
End
EOF
```

The most important input options are:

- **Type:** The force field type for which atom types and charges should be generated. Currently only GAFF is implemented, and this is also default.
- **System:** in the *System block* (page 31) we specify the initial structure of the molecule for which you want to generate force field information.

The utility creates a new AMS input file for a ForceField engine job using the new forcefield parameters. The new input is written to the logfile, and it is also stored in the .rkf file. The user can change the file as needed, or import it into amsinput and change settings from there.

Tip: GAFF atomtyping by Antechamber involves an AM1 geometry optimization of all molecules, in order to determine the atomic charges. For very big systems this can be very time consuming. There is an option to only compute AM1 single point atomic charges, with the option *AntechamberTask SinglePoint*. Do keep in mind that this will make the resulting force field parameters less reliable.

10.7.2 Python scripting

It is also possible to run atomtyping via Python scripting.

```
from scm.plams import Settings, Molecule
from scm.plams import init, finish
from scm.atomtyping import AtomTypingJob, AtomTypingResults

init()

# Run the atomtyping job
mol = Molecule('mol.in')
settings = Settings()
job = AtomTypingJob(molecule=mol, settings=settings)
results = job.run()

# Create the forcefield job (change the settings if needed)
newjob = results.get_plamsjob()
newjob.settings.input.ams.Task = GeometryOptimization

finish()
```


10.8 AMSbatch

It is often necessary to repeat an identical job for many different systems. The 2023 release of the Amsterdam Modeling Suite adds the AMSbatch utility program to do this.

Tip: AMSbatch only covers the very simple case of repeating the exact same jobs for multiple systems. More complicated workflows with processing of results can easily be implemented by using our *scripting tools* (page 25) (e.g. PLAMS).

10.8.1 Overview

The input of AMSbatch is basically identical to the input of an AMS job. The only difference is with the *System blocks* (page 31). For AMSbatch every System block needs to have a unique name (supplied in the header of the block), which will be used as the identifier of the system. Consider the following example input, which independently does a geometry optimization followed by a normal modes calculation for two systems (CO and water):

```
#!/bin/sh

AMS_JOBNAME=go_freq $AMSBIN/amsbatch << EOF

Task GeometryOptimization
Properties NormalModes=True

Engine DFTB
[...]
EndEngine

System Water
  Atoms
    O 0 0 0
    H 0 1 0
    H 1 0 0
  End
End

System CO
  Atoms
    C 0 0 0
    O 0 0 1
  End
End

EOF
```

Just like the AMS driver, running AMSbatch will create a *results directory* (page 18) on disk. Inside of the results directory, you will find subdirectories for the individual jobs (identified by their System name), containing the usual AMS output files. Running the script above would produce the following output:

```
go_freq.results/
├── amsbatch.log
├── amsbatch.rkf
├── CO
│   ├── ams.log
│   └── ams.rkf
```

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```

|   |— CO.dill
|   |— CO.err
|   |— CO.in
|   |— CO.out
|   |— CO.run
|   |— dftb.rkf
|   |— output.xyz
|— Water
|   |— ams.log
|   |— ams.rkf
|   |— dftb.rkf
|   |— output.xyz
|   |— Water.dill
|   |— Water.err
|   |— Water.in
|   |— Water.out
|   |— Water.run

```

10.8.2 Loading systems from file

Instead of supplying all systems individually in the input, AMSbatch also supports to a few ways to load multiple systems from files at once.

The `SystemsFromSMILES` keyword allows to run jobs directly on collections of SMILES strings, using RDKit to generate the initial 3D structure of the system:

```

SystemsFromSMILES
Methane, C
Ethane, CC
Propane, CCC
Butane, CCCC
Pentane, CCCCC
Hexane, CCCCCC
End

```

SystemsFromSMILES

Type Non-standard block

Description Generates systems from SMILES strings using the `plams.from_smiles()` functions. Each line should contain first the system identifier separated by a comma from its SMILES string, e.g.:
'propanol, CCCO'

The `SystemsFromConformers` keyword can be used to load a set of conformers as found by our *Conformers tool* (page 326). This is especially useful as the last step of a conformer workflow, e.g. to do a single point for the calculation of spectra on each conformer within an energy window:

```

SystemsFromConformers
File string
MaxEnergy float
End

```

SystemsFromConformers

Type Block

Description Constructs a series of systems (with identifiers ‘conformer1’, ‘conformer2’, etc.) from a RKF or XYZ file from a Conformers run.

File

Type String

Description A path to an RKF or concatenated XYZ file.

MaxEnergy

Type Float

Unit Hartree

Description Energy cut-off relative to lowest energy conformer.

See also:

[Tutorial on Conformer generation and Boltzmann-weighted spectra](#)

Finally, the `SystemsFromTrajectory` keyword allows reading frames from a trajectory in RKF or XYZ format:

```
SystemsFromTrajectory
  File string
  Frames integer_list
End
```

SystemsFromTrajectory

Type Block

Description Constructs a series of systems (with identifiers ‘frame1’, ‘frame2’, etc.) from a trajectory file.

File

Type String

Description A path to an RKF or concatenated XYZ file.

Frames

Type Integer List

Description List of frames to load from the file. If not specified, all frames will be loaded.

10.8.3 Restart

AMSbatch based on the [PLAMS](#) scripting framework. As such it can rely on the [PLAMS rerun prevention](#) to implement restarting of interrupted depositions. The easiest way to restart an AMSbatch job is to include the `--restart` (or short: `-r`) command line flag:

```
#!/bin/sh
AMS_JOBNAME=myjob $AMSBIN/amsbatch --restart << EOF
...
EOF
```

This first (interrupted) run will have created the `myjob.results` directory. Running the above script again will move that directory to `myjob.results.bak` and reuse all successful jobs from the first run. (People already familiar with PLAMS will recognize that this works just like the `-r` flag on the [PLAMS launch script](#).)

EXAMPLES

11.1 Geometry optimization

11.1.1 Example: Simple geometry optimization

Download GO_formaldehyde_noSCC.run

```
#!/bin/sh

$AMSBIN/ams << EOF

  Task GeometryOptimization

  System
    Atoms [Bohr]
      C  0.0  0.0  -1.0
      O  0.0  0.0  1.247
      H  0.0 -1.738 -2.097
      H  0.0  1.738 -2.097
    End
  End

  Engine DFTB
    ResourcesDir Dresden
    Model DFTB0
    DispersionCorrection Auto
  EndEngine

EOF
```

11.1.2 Example: Two-stage geometry optimization with initial Hessian

Download 2StepGO.run

```
#!/bin/sh

# Preoptimization with DFTB and calculation of the Hessian
# =====
#
# We will reuse the geometry optimized at the DFTB level as a starting point for
# the DFT geometry optimization. We will also calculate the real Hessian with
```

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```
# DFTB and use that as the initial Hessian for the Quasi-Newton based
# optimization at the DFT level. DFTB is so fast compared to DFT, that all of
# this is basically instantaneous. Our goal here is really just to reduce the
# number of steps in the DFT geometry optimization. If we save just a single
# step there, the initial DFTB calculation will already have paid for itself ...
```

```
AMS_JOBNAME=dftb_preopt $AMSBIN/ams << EOF
```

```
# Specify the system geometry: Aspirin
```

```
System
```

```
  Atoms
```

```
  C      0.000000  0.000000  0.000000
  C      1.402231  0.000000  0.000000
  C      2.091015  1.220378  0.000000
  C      1.373539  2.425321  0.004387
  C     -0.034554  2.451759  0.016301
  C     -0.711248  1.213529  0.005497
  O     -0.709522  3.637718  0.019949
  C     -2.141910  1.166077 -0.004384
  O     -2.727881  2.161939 -0.690916
  C     -0.730162  4.530447  1.037168
  C     -0.066705  4.031914  2.307663
  H     -0.531323 -0.967191 -0.007490
  H      1.959047 -0.952181 -0.004252
  H      3.194073  1.231720 -0.005862
  H      1.933090  3.376356 -0.002746
  O     -2.795018  0.309504  0.548870
  H     -2.174822  2.832497 -1.125018
  O     -1.263773  5.613383  0.944221
  H     -0.337334  4.693941  3.161150
  H      1.041646  4.053111  2.214199
  H     -0.405932  3.005321  2.572927
```

```
End
```

```
End
```

```
# Do a geometry optimization.
```

```
Task GeometryOptimization
```

```
# Also compute the Hessian at the optimized geometry.
```

```
Properties
```

```
  Hessian True
```

```
End
```

```
# Settings for the DFTB engine:
```

```
Engine DFTB
```

```
  Model DFTB3
```

```
  ResourcesDir DFTB.org/3ob-3-1
```

```
EndEngine
```

```
EOF
```

```
# Geometry optimization with DFT
```

```
# =====
```

```
AMS_JOBNAME=dft_opt $AMSBIN/ams << EOF
```

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```

# Start from the geometry that is already optimized at the DFTB level.
LoadSystem
  File dftb_preopt.results/dftb.rkf
End
# (equivalent to loading the system from dftb_preopt.results/ams.rkf)

Task GeometryOptimization

GeometryOptimization
  InitialHessian
    # Load the DFTB Hessian as the initial Hessian for the
    # Quasi-Newton based optimizer.
    Type FromFile
    File dftb_preopt.results
  End
End

# Settings for the BAND engine:
Engine BAND
  Basis Type=TZP
  XC GGA=PBE
EndEngine

EOF

```

11.1.3 Example: Periodic lattice optimization under pressure

Download `Diamond_under_pressure.run`

```

#!/bin/sh

# Calculate the phonon dispersion curves for diamond under pressure.

# Loop over pressure values (in GPa):
for P in -40 0 40 160 ; do
AMS_JOBNAME=pressure_$P $AMSBIN/ams << EOF

  Task GeometryOptimization

  System
    Atoms
      C -0.44625 -0.44625 -0.44625
      C 0.44625 0.44625 0.44625
    End
    Lattice
      0.0 1.785 1.785
      1.785 0.0 1.785
      1.785 1.785 0.0
    End
  End

  GeometryOptimization
    OptimizeLattice Yes
    Convergence Gradients=1e-5 StressEnergyPerAtom=1E-5
    Method Quasi-Newton
  End
End

```

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```

End

EngineAddons
  Pressure $P
End

Properties
  # Request the calculation of phonons at the optimized geometry.
  Phonons Yes
End

NumericalPhonons
  SuperCell
    2 0 0
    0 2 0
    0 0 2
  End
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/mio-1-1
  KSpace
    Type Symmetric
    Symmetric KInteg=5
  End
  Technical AnalyticalStressTensor=False
EndEngine

EOF
done

```

11.1.4 Example: Phase Transition Due To External Nonuniform Stress

Download `Diamond_from_pressure.run`

```

#!/bin/sh

# Starting from hexagonal graphite we optimize the crystal
# under the influence of a non-uniform stress tensor.
# The system will undergo a phase transition to a diamond structure
AMS_JOBNAME=Graphite2Diamond $AMSBIN/ams << eor

Task GeometryOptimization
EngineAddons
  ExternalStress
    StressTensorVoigt 0 0 0.01 0 -0.0003 0
  End
End
System
  Atoms
    C 0.0000 0.0000 1.6507
    C 0.0000 0.0000 -1.6507
    C 0.0000 -1.4225 1.6507
    C 0.0000 1.4225 -1.6507

```

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```

End
  Lattice
    1.2319 -2.1338 0.0000
    1.2319 2.1338 0.0000
    0.0000 0.0000 6.6029
  End
End
GeometryOptimization
  MaxIterations 300
  OptimizeLattice Yes
  Convergence
    Energy 1.0e-6
    Gradients 1.0e-5
    Step 1.0e-4
  End
End
UseSymmetry No
Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/3ob-3-1
  DispersionCorrection D3-BJ
  KSpace
    Quality Basic
  End
EndEngine

eor

# The diamond structure is still compressed under the influence of the external_
↪stress.
# We now disable this term and relax the unit cell with the same DFTB model
AMS_JOBNAME=DiamondRelaxation $AMSBIN/ams << eor

Task GeometryOptimization
LoadSystem
  File Graphite2Diamond.results/ams.rkf
End
GeometryOptimization
  MaxIterations 300
  OptimizeLattice Yes
  Convergence
    Energy 1.0e-6
    Gradients 1.0e-5
    Step 1.0e-4
  End
End
UseSymmetry No
LoadEngine Graphite2Diamond.results/dftb.rkf

eor

```

11.1.5 Example: Boron nitride optimization under external stress

Download ExternalStress_BN.run

```
#!/bin/sh

# Some (fairly arbitrary) external stress in atomic units:
external_stress='0.001 0.0003 -0.0007 0.0005 0.0004 0.001'

# The external stress applied here will result in pretty large deformations.
# Since the external stress energy term becomes more and more approximate the
# larger the deformation from the initial cell is, after the first optimization,
# one should run a second geometry optimization starting from the converged
# results of the first one.

# It is always good practice to validate the optimization under external stress
# by computing the stress tensor of the final optimized geometry: the stress
# tensor at the optimized geometry should match the external stress applied during
# the optimization, but with reversed signs.

AMS_JOBNAME=first_go $AMSBIN/ams << eor

Task GeometryOptimization

System
  Atoms
    B 0.0 0.0 0.0
    N 0.905 0.905 0.905
  End
  Lattice
    0.0 1.81 1.81
    1.81 0.0 1.81
    1.81 1.81 0.0
  End
  SuperCell 2 2 2
End

GeometryOptimization
  OptimizeLattice Yes
  # The convergence threshold should be smaller than the applied external stress:
  Convergence Gradients=1.0E-4
End

# We want the external stress to break the symmetry:
UseSymmetry No

EngineAddons
  ExternalStress
    StressTensorVoigt $external_stress
  End
End

Engine ForceField
EndEngine
eor

# The second geometry optimization starting from the results of the first one:
```

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```
AMS_JOBNAME=second_go $AMSBIN/ams << eor

Task GeometryOptimization

LoadSystem
  File first_go.results/ams.rkf
End

GeometryOptimization
  OptimizeLattice Yes
  Convergence Gradients=1.0E-5
End

UseSymmetry No

EngineAddons
  ExternalStress
    StressTensorVoigt $external_stress
  End
End

LoadEngine first_go.results/forcefield.rkf
eor

# In the final calculation we simply compute the stress tensor of the final
# geometry, which should be the opposite of the external stress tensor applied
# during the optimization.

AMS_JOBNAME=sp $AMSBIN/ams << eor

Task SinglePoint

LoadSystem
  File second_go.results/ams.rkf
End

UseSymmetry No

Properties StressTensor=Yes

LoadEngine first_go.results/forcefield.rkf
eor

echo "Applied external stress tensor (order: xx,yy,zz,yz,xz,xy):"
echo $external_stress
echo "Resulting final stress tensor:"
$AMSBIN/amsreport sp.results/forcefield.rkf -r "AMSResults%StressTensor#12.6f##3"
```

11.1.6 Example: Graphene optimization under external stress

Download ExternalStress_graphene.run

```
#!/bin/sh

# Here we perform an optimization under external stress using the
# UpdateReferenceCell option. When using this option the energy during
# the geometry optimization will not necessarily go down, but the final
# stress will match the ExternalStress with much higher accuracy.

AMS_JOBNAME=go $AMSBIN/ams << eor

Task GeometryOptimization

System
  Atoms
    C 0.0          0.0          0.0
    C 1.23647204352 0.7138774661 0.0
  End
  Lattice
    1.23647204352 -2.1416324015 0.0
    1.23647204352  2.1416324015 0.0
  End
End

UseSymmetry no

EngineAddons
  ExternalStress
    StressTensorVoigt 0.01 0.02 0.003
    UpdateReferenceCell Yes
  End
End

GeometryOptimization
  Method SCMGO
  OptimizeLattice Yes
  Convergence Gradients=1.0E-4
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/psc-0-3
  KSpace Quality=Normal
EndEngine
eor

# Here we compute the stress tensor at the optimized geometry to validate
# the optimization under stress

AMS_JOBNAME=sp $AMSBIN/ams << eor

Task SinglePoint

LoadSystem
  File go.results/ams.rkf
```

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```

End

UseSymmetry no

Properties
  StressTensor Yes
End

LoadEngine go.results/dftb.rkf
eor

echo "Resulting final stress tensor:"
$AMSBIN/amsreport sp.results/dftb.rkf -r "AMSResults%StressTensor#12.6f##2"

```

11.1.7 Example: Constrained optimizations

Download constraints.run

```

#!/bin/sh

# This example demonstrates the setup of all different types of constraints.
# Note that all constraints types can be combined with each other, as long as
# the resulting set of constraints actually makes sense. (It must of course be
# possible to satisfy all of them at the same time. AMS is not able to check
# that and you might get really surprising results if that is not the case ...)

# 1. Angle constraints
# =====

AMS_JOBNAME=angle "$AMSBIN/ams" << EOF

Task GeometryOptimization

GeometryOptimization
  Convergence Step=1.0e-3
End

System
  Atoms
    O   0.001356   0.000999   0.000000
    H   0.994442  -0.037855   0.000000
    H  -0.298554   0.948531   0.000000
  End
End

Constraints
  # Fix the H--O--H angle to 125 degrees.
  Angle  3 1 2 125.0
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir Dresden
  DispersionCorrection Auto

```

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```
EndEngine
EOF

# 2. Distance constraints
# =====

AMS_JOBNAME=dist "$AMSBIN/ams" << EOF

Task GeometryOptimization

GeometryOptimization
  Convergence Step=1.0e-3
End

System
  Atoms
    O   0.001356   0.000999   0.000000
    H   0.994442  -0.037855   0.000000
    H  -0.298554   0.948531   0.000000
  End
  BondOrders
    1 2 1.0
    1 3 1.0
  End
End
Constraints
  # Fix the OH bond distances to 1.03 Angstrom, for which bonds need to be
  →defined in the System block
  All bonds O H to 1.03
  # Alternatively you can list the distances one by one as follows
  # Distance 1 2 1.03
  # Distance 1 3 1.03
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir Dresden
  DispersionCorrection Auto
EndEngine
EOF

# 3. Dihedral angle constraint
# =====

AMS_JOBNAME=dihed "$AMSBIN/ams" << EOF

Task GeometryOptimization

GeometryOptimization
  Convergence Step=1.0e-3
End

System
```

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```

      Atoms
      C   -0.004115   -0.000021   0.000023
      C   1.535711    0.000022    0.000008
      H   -0.399693    1.027812   -0.000082
      H   -0.399745   -0.513934    0.890139
      H   -0.399612   -0.513952   -0.890156
      H   1.931188    0.514066    0.890140
      H   1.931432    0.513819   -0.890121
      H   1.931281   -1.027824    0.000244
      End
End

Constraints
  # Fix the dihedral angle H(6)--C(2)--C(1)--H(3) to 20 degrees.
  Dihedral  6 2 1 3 20.00
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir Dresden
  DispersionCorrection Auto
EndEngine

EOF

# 4a. Fixed atom constraint (Atoms keyword)
# =====

AMS_JOBNAME=atom "$AMSBIN/ams" << EOF

Task GeometryOptimization

GeometryOptimization
  Convergence Energy=1.0e-6 Gradients=1.0e-4 Step=1.0e-3
  CoordinateType Cartesian
End

System
  Atoms
    C   -0.2460249052   -1.70363153    0.0005128649944
    O   1.152833576     -1.81594932   -0.0004409224206
    C   1.489235475     0.61782051    10.0004771689226
    O   0.5700116914    0.627761615   10.0005491194077
  End
End

Constraints
  # Fix atom 1 and 2 at their initial positions.
  Atom 1
  Atom 2
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/mio-1-1
EndEngine

```

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```

EOF

# 4b. Fixed atom constraint (AtomList keyword)
# =====

AMS_JOBNAME=atomlist "$AMSBIN/ams" << EOF

  Task GeometryOptimization

  GeometryOptimization
    Convergence Energy=1.0e-6 Gradients=1.0e-4 Step=1.0e-3
    CoordinateType Cartesian
  End

  System
    Atoms
      C   -0.2460249052   -1.70363153    0.0005128649944
      O   1.152833576     -1.81594932   -0.0004409224206
      C   1.489235475     0.61782051    10.0004771689226
      O   0.5700116914    0.627761615   10.0005491194077
    End
  End

  Constraints
    # Fix atom 1 and 2 at their initial positions.
    AtomList 1:2
  End

  Engine DFTB
    Model SCC-DFTB
    ResourcesDir DFTB.org/mio-1-1
  EndEngine

```

```

EOF

# 4c. Fixed atom constraint (FixedRegion keyword)
# =====

AMS_JOBNAME=region "$AMSBIN/ams" << EOF

  Task GeometryOptimization

  GeometryOptimization
    Convergence Energy=1.0e-6 Gradients=1.0e-4 Step=1.0e-3
    CoordinateType Cartesian
  End

  System
    Atoms
      C   -0.2460249052   -1.70363153    0.0005128649944   region=fixed
      O   1.152833576     -1.81594932   -0.0004409224206   region=fixed
      C   1.489235475     0.61782051    10.0004771689226
      O   0.5700116914    0.627761615   10.0005491194077
    End
  End

```

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```

End

Constraints
  # Fix all atoms in region "fixed"
  FixedRegion fixed
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/mio-1-1
EndEngine

EOF

# 4d. Fixed atom constraint (overlapping combination)
# =====

AMS_JOBNAME=combination "$AMSBIN/ams" << EOF

  Task GeometryOptimization

  GeometryOptimization
    Convergence Energy=1.0e-6 Gradients=1.0e-4 Step=1.0e-3
    CoordinateType Cartesian
  End

  System
    Atoms
      C   -0.2460249052   -1.70363153    0.0005128649944   region=fixed
      O    1.152833576    -1.81594932   -0.0004409224206   region=fixed
      C    1.489235475     0.61782051    10.0004771689226
      O    0.5700116914    0.627761615   10.0005491194077
    End
  End

  Constraints
    Atom 1
    AtomList 1 2
    FixedRegion fixed
  End

  Engine DFTB
    Model SCC-DFTB
    ResourcesDir DFTB.org/mio-1-1
  EndEngine

EOF

# 5. Fixed coordinate constraint
# =====

AMS_JOBNAME=coord "$AMSBIN/ams" << EOF

  Task GeometryOptimization

```

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```

GeometryOptimization
  Convergence Energy=1.0e-6 Gradients=1.0e-4 Step=1.0e-3
  CoordinateType Cartesian
End

System
  Atoms
    C -0.2460249052 -1.70363153 0.0005128649944
    O 1.152833576 -1.81594932 -0.0004409224206
    C 1.489235475 0.61782051 10.0004771689226
    O 0.5700116914 0.627761615 10.0005491194077
  End
End

Constraints
  # Fix the x-coordinate of all atoms.
  Coordinate 1 x
  Coordinate 2 x
  Coordinate 3 x
  Coordinate 4 x
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/mio-1-1
EndEngine

EOF

# 6. Fixed atom constraint (in periodic system)
# =====

AMS_JOBNAME=pbcatom "$AMSBIN/ams" << EOF

Task GeometryOptimization

GeometryOptimization
  Convergence Step=1.0e-3
End

System
  Atoms
    C -1.23 -0.710140830 0.0
    C -1.23 -0.710140830 3.8
    C 0.0 0.0 0.4
    C 0.0 -1.42028166 3.355
  End

  Lattice
    1.23 -2.130422493309719 0.0
    1.23 2.130422493309719 0.0
  End
End

Constraints
  # Fix atom 1 and 3 at their initial positions.

```

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```

Atom 1
Atom 3
End

Engine DFTB
Model SCC-DFTB
ResourcesDir DFTB.org/mio-1-1
KSpace Quality=GammaOnly
EndEngine

EOF

# 7. Block constraints (with listing the atoms in a block)
# =====

AMS_JOBNAME=block_list "$AMSBIN/ams" << EOF

Task GeometryOptimization

System
Atoms
C 0.5584839616765542 0.5023705181144142 -0.4625483159356394
C 1.07173137896726 0.2125484528111251 -1.892767990599312
C 1.699248504588085 -1.006061067555322 -2.191856791501442
C 2.242484629452111 -1.236470028363516 -3.455616615521399
C 2.18874580207099 -0.2444337131062739 -4.435483595049287
C 1.604409798904145 0.9866950282217637 -4.135465239465763
C 1.061086793296828 1.217355116664161 -2.871773146851866
H 1.763625603740592 -1.780903563899969 -1.431707209662057
H 2.716038261390732 -2.190869049673275 -3.672115451399807
H 2.611833078693977 -0.4241619800888815 -5.420308290235123
H 1.578029796368043 1.774138556616255 -4.884624561698751
H 0.6247213391616491 2.187200330357715 -2.64521108544713
C 1.303528070245188 -0.1416812092038768 0.7303699949711653
C 0.8164830922475474 -1.314631142230651 1.326337082260565
C 1.531799364672407 -1.947399963062604 2.342825210379356
C 2.757684862125068 -1.432061688813837 2.765634667957531
C 3.271640455523863 -0.2897364031184506 2.150731553729188
C 2.556535912403799 0.3432056352653093 1.134221563049466
H -0.128925843064934 -1.7366201913903 0.9939642396630857
H 1.133600273086767 -2.849990046242235 2.799740694330775
H 3.31486005979636 -1.925049398411132 3.557912279830031
H 4.236604921323707 0.1064455961800578 2.457138367063388
H 2.976510069814392 1.222131876866508 0.6510413538003352
C -0.930165749820548 0.9153412637395284 -0.5420710991631585
C -1.791729737216814 0.6892660986048864 0.5418285200469819
C -3.111373625199894 1.139542032267652 0.5090625363459357
C -3.586568528476239 1.843983986018719 -0.5977864609101087
C -2.726152821786783 2.111108432452229 -1.663369105880468
C -1.406454626777386 1.660929752085611 -1.63085383469072
H -1.428888457076976 0.1571120160719108 1.417905619994904
H -3.76723983501283 0.9462006794587581 1.35432032282366
H -4.614972346570283 2.194578435055282 -0.6233521468909432
H -3.080200905921361 2.678981846821393 -2.520207901691867
H -0.7413545301831963 1.891248563160919 -2.459672151335554
C 1.235557647765805 1.735720249011045 0.1803884343948648

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```

C 1.377191890012647 1.826646222422494 1.573181692925026
C 1.905898822116255 2.975086608901246 2.16214311213053
C 2.280792642899383 4.061906342938987 1.371311861877147
C 2.105006642447361 3.998471351380415 -0.0115253875199488
C 1.576317094651283 2.850163227898022 -0.6007264381779673
H 1.072424817958776 0.9937816064904853 2.202306496283991
H 2.017471491684088 3.023369029562452 3.242524256706377
H 2.693031233132915 4.956641734238467 1.830324484771476
H 2.372569859099136 4.8485771293401 -0.6342066225733602
H 1.427765851939196 2.820397327218896 -1.677480576376967

End
End

GeometryOptimization
  Convergence
    Energy 1.0e-6
    Gradients 1.0e-4
    Step 1.0e-4
  End
End

Constraints
  # Create blocks from the 4 phenyl groups by specifying the atom indices
  # explicitly. (The indices follow the order in the System%Atoms block,
  # where we happen to have the atoms belonging to the different phenyl
  # groups consecutive.)
  BlockAtoms 2 3 4 5 6 7 8 9 10 11 12
  BlockAtoms 13 14 15 16 17 18 19 20 21 22 23
  BlockAtoms 24 25 26 27 28 29 30 31 32 33 34
  BlockAtoms 35 36 37 38 39 40 41 42 43 44 45
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-3-1
  DispersionCorrection D3-BJ
EndEngine

EOF

# 8. Block constraints (with named blocks)
# =====

AMS_JOBNAME=block_names "$AMSBIN/ams" << EOF

Task GeometryOptimization

System
  Atoms
    C 0.5584839616765542 0.5023705181144142 -0.4625483159356394
    C 1.07173137896726 0.2125484528111251 -1.892767990599312
↪region=phenyl1
    C 1.699248504588085 -1.006061067555322 -2.191856791501442
↪region=phenyl1
    C 2.242484629452111 -1.236470028363516 -3.455616615521399
↪region=phenyl1

```

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C	2.18874580207099	-0.2444337131062739	-4.435483595049287	└
↔region=phenyl1				
C	1.604409798904145	0.9866950282217637	-4.135465239465763	└
↔region=phenyl1				
C	1.061086793296828	1.217355116664161	-2.871773146851866	└
↔region=phenyl1				
H	1.763625603740592	-1.780903563899969	-1.431707209662057	└
↔region=phenyl1				
H	2.716038261390732	-2.190869049673275	-3.672115451399807	└
↔region=phenyl1				
H	2.611833078693977	-0.4241619800888815	-5.420308290235123	└
↔region=phenyl1				
H	1.578029796368043	1.774138556616255	-4.884624561698751	└
↔region=phenyl1				
H	0.6247213391616491	2.187200330357715	-2.64521108544713	└
↔region=phenyl1				
C	1.303528070245188	-0.1416812092038768	0.7303699949711653	└
↔region=phenyl2				
C	0.8164830922475474	-1.314631142230651	1.326337082260565	└
↔region=phenyl2				
C	1.531799364672407	-1.947399963062604	2.342825210379356	└
↔region=phenyl2				
C	2.757684862125068	-1.432061688813837	2.765634667957531	└
↔region=phenyl2				
C	3.271640455523863	-0.2897364031184506	2.150731553729188	└
↔region=phenyl2				
C	2.556535912403799	0.3432056352653093	1.134221563049466	└
↔region=phenyl2				
H	-0.128925843064934	-1.7366201913903	0.9939642396630857	└
↔region=phenyl2				
H	1.133600273086767	-2.849990046242235	2.799740694330775	└
↔region=phenyl2				
H	3.31486005979636	-1.925049398411132	3.557912279830031	└
↔region=phenyl2				
H	4.236604921323707	0.1064455961800578	2.457138367063388	└
↔region=phenyl2				
H	2.976510069814392	1.222131876866508	0.6510413538003352	└
↔region=phenyl2				
C	-0.930165749820548	0.9153412637395284	-0.5420710991631585	└
↔region=phenyl3				
C	-1.791729737216814	0.6892660986048864	0.5418285200469819	└
↔region=phenyl3				
C	-3.111373625199894	1.139542032267652	0.5090625363459357	└
↔region=phenyl3				
C	-3.586568528476239	1.843983986018719	-0.5977864609101087	└
↔region=phenyl3				
C	-2.726152821786783	2.111108432452229	-1.663369105880468	└
↔region=phenyl3				
C	-1.406454626777386	1.660929752085611	-1.63085383469072	└
↔region=phenyl3				
H	-1.428888457076976	0.1571120160719108	1.417905619994904	└
↔region=phenyl3				
H	-3.76723983501283	0.9462006794587581	1.35432032282366	└
↔region=phenyl3				
H	-4.614972346570283	2.194578435055282	-0.6233521468909432	└
↔region=phenyl3				
H	-3.080200905921361	2.678981846821393	-2.520207901691867	└
↔region=phenyl3				

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      H  -0.7413545301831963  1.891248563160919  -2.459672151335554  _
↔region=phenyl3
      C  1.235557647765805  1.735720249011045  0.1803884343948648  _
↔region=phenyl4
      C  1.377191890012647  1.826646222422494  1.573181692925026  _
↔region=phenyl4
      C  1.905898822116255  2.975086608901246  2.16214311213053  _
↔region=phenyl4
      C  2.280792642899383  4.061906342938987  1.371311861877147  _
↔region=phenyl4
      C  2.105006642447361  3.998471351380415  -0.0115253875199488  _
↔region=phenyl4
      C  1.576317094651283  2.850163227898022  -0.6007264381779673  _
↔region=phenyl4
      H  1.072424817958776  0.9937816064904853  2.202306496283991  _
↔region=phenyl4
      H  2.017471491684088  3.023369029562452  3.242524256706377  _
↔region=phenyl4
      H  2.693031233132915  4.956641734238467  1.830324484771476  _
↔region=phenyl4
      H  2.372569859099136  4.8485771293401  -0.6342066225733602  _
↔region=phenyl4
      H  1.427765851939196  2.820397327218896  -1.677480576376967  _
↔region=phenyl4
      End
    End

    GeometryOptimization
      Convergence
        Energy 1.0e-6
        Gradients 1.0e-4
        Step 1.0e-4
      End
    End

    Constraints
      # Use the region from System%Atoms to set up the block constraints.
      Block phenyl1
      Block phenyl2
      Block phenyl3
      Block phenyl4
    End

    Engine DFTB
      Model DFTB3
      ResourcesDir DFTB.org/3ob-3-1
      DispersionCorrection D3-BJ
    EndEngine

EOF

# 9. Frozen strain components
# =====

AMS_JOBNAME=freezestrain "$AMSBIN/ams" << EOF

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```
Task GeometryOptimization

GeometryOptimization
  OptimizeLattice Yes
  Convergence Step=1.0e-3
End

Constraints
  # Keeps first two lattice vectors orthogonal to the third. Also fixes the
  # length of the third vector, keeping the graphene layer compressed.
  FreezeStrain xz yz zz
End

System
  Atoms
    C 1.332002504889882e-05 -0.0005830055256093706 -8.209389319526933e-06
    C -1.22799350000696 -0.7102112812520209 2.281155685325205e-06
    C -0.0006872840163290542 -0.0003386565731411325 -1.981477647175959
    C 1.2274512359848 0.7092866246929653 -1.981478017299119
    C 2.455989750017203 -0.000767672446473915 -5.638209535859324e-06
    C 1.227983749989149 -0.7105220051279582 3.556077144406634e-06
    C 2.45553905980411 -0.0003697961984884611 -1.981476578954899
    C 3.68349483597652 0.7093774139714127 -1.981475303736415
    C 4.912014119974971 -0.0004697689000645081 8.202057640607653e-06
    C 3.68401303002027 -0.7103327188132248 -6.644074866545941e-06
    C 4.911561265976663 -0.0002732185613776612 -1.98147535090646
    C -3.685503114025999 0.7094747213946447 -1.98147447813657
    C -2.457004890026731 -0.0008782302621621878 8.760751751649826e-06
    C -3.684994169978904 -0.7103491590560944 -6.913500704937906e-06
    C -2.45740142402999 -0.0002120088132086839 -1.981473170030486
    C -1.229200584026242 0.709517932531879 -1.98147439816519
    C 1.227980230018157 2.127401471357515 -5.950364005944094e-06
    C 9.469984377119545e-06 1.417970232416515 5.120417805695729e-06
    C 1.227229005981529 2.127790824745807 -1.981476944534885
    C 2.45544009594217 2.837313001498961 -1.981464045820237
    C 3.683977240012926 2.127396400995821 -4.237131224100653e-06
    C 2.456019429974761 1.41770041892015 8.271514976735398e-06
    C 3.683520895940616 2.127826615636785 -1.981463536474189
    C 4.911484545967099 2.837408990674362 -1.981472216079415
    C 6.140019459971655 2.127636216669431 9.289406940173374e-06
    C 4.912011129977858 1.417969521782559 7.256699431696856e-06
    C 6.139527915931508 2.12792209328836 -1.981460550680031
    C -2.457504644023984 2.837506078460876 -1.981475136785154
    C -1.229001220032881 2.127025640069692 1.077705178964691e-05
    C -2.457025360024441 1.417788944250494 8.010947395781608e-06
    C -1.229428944072945 2.128012192586653 -1.981459091806229
    C -0.001217694074323372 2.837543459113209 -1.981458639351295
    C 2.455982410005773 4.255441598373883 -1.892083560740779e-06
    C 1.228003499971814 3.545886142064043 9.237737681677788e-06
    C 2.455221785970465 4.255792992279458 -1.981473318340598
    C -1.228386974045185 -3.547700260767117 -1.981468190394571
    C 4.911976899993052 4.255411828501257 2.27723146438149e-06
    C 3.684014579960917 3.545723396055813 1.280915829951697e-05
    C 4.911520375955087 4.255828023455356 -1.981468278811
    C 1.227655395958869 -3.547614761418386 -1.98146951906497
    C -2.457018900008975 4.255512695928259 2.943041159330732e-06
    C 6.140026009993287 3.545891232143294 2.20060806891485e-06
```

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```
C 7.367526315913146 4.255927240986645 -1.981454533470139
C -6.141340994042006 -3.547511474074143 -1.981469232026619
C -0.001002500050462096 4.255387679251578 1.654017565004685e-05
C -1.228981830007242 3.545851372434187 2.37503105142233e-06
C -0.00142595404759982 4.256013860539822 -1.981467396982039
C -3.685044664049419 -3.547477052980626 -1.981466802486946
C -1.227808819999351 -2.12938224692705 -2.127801149456805e-07
C -2.455832350038186 -2.838708610558109 1.251523005803983e-05
C -1.228620264037983 -2.129205540950233 -1.981470550283798
C -0.0004192140835714842 -1.419477849521901 -1.981455609514733
C 1.228193719957573 -2.129406616582517 1.390527520593389e-05
C 0.0001477699611014405 -2.839255138681037 1.274825905530347e-05
C 1.227684425953123 -2.129163359695275 -1.981467635427455
C 2.455626385910209 -1.419413169537493 -1.981453570671329
C -6.140842350045955 -2.129322170430451 1.506226938282425e-05
C 2.456153479955113 -2.839200210115958 1.47101339575357e-05
C 3.683689305925244 -2.129064842197087 -1.981458500475127
C -4.913374384079035 -1.419316522220884 -1.981457095053834
C -3.684843340052955 -2.129350560151249 1.735547419229382e-05
C -4.912808430047692 -2.839071261955975 1.563048016823986e-05
C -3.685268534086676 -2.128978772839927 -1.98145459141338
C -2.45712732409351 -1.419353221465499 -1.981452351546793
C -2.996192032925579e-05 -0.000699242152149526 3.962939886687566
C -1.228003971875175 -0.7103778453492622 3.962925088122617
C -0.000700355908038296 -0.0003332148789394825 1.981452859744668
C 1.227439704045832 0.7092909964964251 1.981467977918086
C 2.455972288079895 -0.000591484995550912 3.962939812711258
C 1.228003298120663 -0.7104549535647978 3.962926452096982
C 2.455542044092204 -0.0003647244468015716 1.981452779807835
C 3.683482354040657 0.7093820057289575 1.981469673526022
C 4.912000348117807 -0.0004686671456845799 3.96292738718769
C 3.683997778083127 -0.7103249572456309 3.962938753391991
C 4.911548884078128 -0.0002680168299863262 1.981457393146928
C -3.685515265933381 0.7094801331342701 1.981461165904004
C -2.457014661901717 -0.0008761383582568633 3.962933787286889
C -3.685007531928472 -0.7103425373777408 3.962942555784025
C -2.457412705931413 -0.0002065770405354501 1.981460520958165
C -1.229211335932976 0.7095228343414065 1.98146103281522
C 1.227967348110556 2.127386193561453 3.962929764672974
C -4.281883530521391e-06 1.417919455416095 3.96292782690195
C 1.227218624090811 2.127796526544795 1.981453236878594
C 2.455427384033809 2.83731889320433 1.981471917810995
C 3.683966438104317 2.127406352683383 3.962931809362267
C 2.456006178071116 1.417740879775001 3.962942690498066
C 3.683508864080636 2.127831077384122 1.981456571921596
C 4.911472874041424 2.837414422441095 1.981469423240322
C 6.140006188100173 2.127640908364754 3.96293316778528
C 4.912000948062944 1.417975193600739 3.962945368689221
C 6.139515384034993 2.127928054994523 1.981471530520008
C -2.457516635928298 2.837511270211092 1.981459501137365
C -1.229012451945974 2.127104470095207 3.962948291371187
C -2.457033631907664 1.417792836176979 3.962935736248542
C -1.229441855971066 2.128017364296635 1.981473516125039
C -0.001231065982844282 2.83754798082405 1.981477377543141
C 2.455970918062962 4.255446730162459 3.962945363741043
C 1.227990978068837 3.545888883850297 3.962943437699987
C 2.455207564067417 4.255798083939164 1.981460905296909
```

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C -1.228397585936881 -3.54769452897796 1.981462310609218
C 4.911964488060532 4.255420650159205 3.962946159605713
C 3.684002968100828 3.545727757822979 3.962932953064215
C 4.911507194030889 4.25583213519047 1.981472875202606
C 1.22764468406568 -3.547609799614339 1.981461473160161
C -2.457027591902453 4.255510887977889 3.962934029953071
C 6.140011718057854 3.545898453762834 3.962947035832434
C 7.367513404018803 4.25593209270268 1.981476837527609
C -6.141352815949912 -3.547506482310592 1.981466583645511
C -0.001013701916043441 4.255385511194097 3.962938483249906
C -1.228995721948309 3.545866003895579 3.962949056786192
C -0.001438315946372004 4.256019262267359 1.98146542401001
C -3.68505504595736 -3.547472521146422 1.981469025022036
C -1.227817711946263 -2.129397354545356 3.962948386486201
C -2.45584760189824 -2.838693919188594 3.962932647309199
C -1.22863031596877 -2.129200899095368 1.981472763926178
C -0.0004312259786934947 -1.419471387806733 1.981476015973903
C 1.228183428085925 -2.129384525179524 3.962937836939656
C 0.0001342880538246494 -2.839225227582055 3.962948356816577
C 1.227671624025677 -2.129158527960262 1.981474583888431
C 2.455614294015247 -1.419407657803005 1.981478001551132
C -6.140855951953014 -2.129314868796188 3.962950599781267
C 2.456139408049645 -2.839212628030558 3.962949726809414
C 3.683677514018658 -2.12905939044384 1.98147688315868
C -4.913386125957436 -1.419311390469788 1.981469050050141
C -3.68485488196171 -2.129348928295441 3.96295344930467
C -4.91282016191732 -2.839063750265042 3.962938899273355
C -3.685281025994509 -2.12897353111013 1.981481200585353
C -2.457141595966529 -1.419347949824808 1.981472029890663

End
Lattice
  9.825000579999999 0.0 0.0
  4.91182904 8.51302256 0.0
  0.0 0.0 8.0

End
End

Engine DFTB
  Model DFTB
  ResourcesDir DFTB.org/mio-1-1
  KSpace
  Quality GammaOnly
End
EndEngine

EOF

# 10. Equalized strain components
# =====

AMS_JOBNAME=equalstrain "$AMSBIN/ams" << EOF

Task GeometryOptimization

GeometryOptimization
  OptimizeLattice Yes

```

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```
Convergence Step=1.0e-3
End

Constraints
  # Keep the cell cubic, but allow the size of the cube to vary.
  FreezeStrain xy xz yz
  EqualStrain  xx yy zz
End

System
  Atoms
    C -0.132285 3.230196 3.399625
    H 0.67231 2.571995 3.747816
    H -0.546925 3.782407 4.25108
    H -0.921872 2.627955 2.935193
    H 0.267346 3.938428 2.664409
    C 2.647972 3.79511 0.161215
    H 2.745753 2.707187 0.254494
    H 2.108302 4.189352 1.030219
    H 2.093026 4.03506 -0.753279
    H 3.644808 4.248843 0.113424
    C -3.290954 -3.607704 -3.419879
    H -4.099867 -4.000479 -4.046956
    H -2.386445 -3.482146 -4.026458
    H -3.088346 -4.309774 -2.602634
    H -3.589157 -2.638419 -3.003466
    C -3.900392 1.971446 -2.092972
    H -2.821972 1.97396 -1.895882
    H -4.303924 2.977719 -1.930439
    H -4.394183 1.265761 -1.414725
    H -4.081488 1.668344 -3.130841
    C -3.143958 -3.520015 3.393796
    H -3.128547 -4.088022 2.456262
    H -3.994325 -3.845525 4.004334
    H -3.24151 -2.450891 3.171766
    H -2.211449 -3.695621 3.94282
    C -0.31406 -0.626145 3.522914
    H -0.044022 0.228271 4.154493
    H -1.353702 -0.912447 3.720437
    H 0.346904 -1.471041 3.749005
    H -0.205421 -0.349364 2.467723
    C 3.411151 -3.454122 0.161835
    H 2.877462 -2.569463 0.528433
    H 4.211866 -3.141886 -0.518755
    H 2.711585 -4.107617 -0.372385
    H 3.843691 -3.997522 1.010048
    H -3.283653 -0.451758 -4.172013
    H -1.922139 0.6502520000000001 -3.802207
    H -2.586463 -0.412172 -2.523601
    C -2.360175 -0.332772 -3.593334
    H -1.648446 -1.117408 -3.875514
    C 3.046249 -3.33059 3.76859
    H 2.414628 -3.18136 2.88506
    H 2.465863 -3.831302 4.55235
    H 3.39517 -2.358701 4.136729
    H 3.909333 -3.950995 3.500222
    C -3.086408 3.73574 0.4638
```

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```
H -2.559805 3.990117 -0.463465
H -2.394025 3.813016 1.310247
H -3.469203 2.710618 0.397221
H -3.922599 4.429208 0.611196
C 3.736451 0.338903 -0.234383
H 4.139844 -0.659226 -0.441391
H 4.286082 0.789262 0.6004350000000001
H 2.675343 0.256879 0.028602
H 3.844535 0.968696 -1.125179
C -0.953217 3.761489 -3.029722
H -0.738671 2.687271 -2.986546
H -2.017033 3.913231 -3.24677
H -0.349572 4.223228 -3.819817
H -0.707592 4.222226 -2.065757
C 3.438238 3.368005 3.536049
H 3.718968 3.030104 2.531632
H 4.305113 3.831685 4.021198
H 3.102844 2.509703 4.129906
H 2.62603 4.10053 3.461459
C -0.093351 2.447961 0.147782
H 0.412783 2.191741 -0.790311
H -1.100739 2.015519 0.149423
H -0.163522 3.53817 0.239205
H 0.478074 2.046413 0.99281
C -0.067378999999999999 -1.067744 -0.644773
H 0.831493 -1.69444 -0.611303
H -0.920384 -1.630791 -0.248288
H -0.271712 -0.77696 -1.681851
H 0.091087 -0.168785 -0.037648
C -3.13266 0.095347 1.684164
H -2.468956 -0.758832 1.506078
H -3.797646 -0.127993 2.526632
H -3.731911 0.285949 0.786162
H -2.532126 0.982263 1.917783
C -3.650862 -2.700373 -0.074687
H -4.155919 -2.467829 0.87013
H -2.740814 -3.276506 0.129574
H -3.385824 -1.767849 -0.58654
H -4.32089 -3.289309 -0.711913
C 3.803884 3.754796 -3.348637
H 3.946713 2.667857 -3.350306
H 2.769436 3.987861 -3.626912
H 4.48894 4.214494 -4.07059
H 4.010448 4.148971 -2.34674
C 2.868209 0.11231 2.894284
H 2.317604 0.914041 2.388417
H 2.406222 -0.09055000000000001 3.867554
H 3.909847 0.420825 3.041412
H 2.839161 -0.7950739999999999 2.279753
C -0.320765 -3.560008 1.887422
H -0.965068 -2.68183 2.011986
H 0.02585 -3.901247 2.869895
H 0.543227 -3.294315 1.26713
H -0.88707 -4.36264 1.400678
C 2.415398 -1.437717 -2.776235
H 1.964383 -1.676188 -3.746573
H 2.445411 -2.340763 -2.155392
```

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```
H 1.816728 -0.668767 -2.274091
H 3.43507 -1.065149 -2.928883
C -3.625996 2.934989 3.78523
H -4.070333 2.734452 2.803299
H -3.043299 2.064066 4.107404
H -4.421782 3.131813 4.513121
H -2.968572 3.809626 3.717096
C 1.422335 1.538945 -3.931672
H 0.608488 0.8054 -3.894205
H 2.3282 1.060135 -4.321529
H 1.616409 1.921293 -2.92272
H 1.136242 2.368954 -4.588236
C 0.028875 -3.521123 -2.677443
H 0.240436 -2.624091 -3.271089
H -0.857142 -3.347281 -2.055678
H 0.888225 -3.744967 -2.034598
H -0.156019 -4.368152 -3.348409

End
Lattice
  10.0 0.0 0.0
  0.0 10.0 0.0
  0.0 0.0 10.0
End
End
Engine DFTB
  Model DFTB
  ResourcesDir DFTB.org/mio-1-1
  KSpace
  Quality GammaOnly
  End
EndEngine
EOF
```

11.2 Transition state search

11.2.1 Example: TS search starting from initial Hessian

Download COChainFreqTS.run

```
#!/bin/sh

# This example demonstrates in the first step how to calculate the Hessian.
# The second run uses the pre-calculated Hessian and performs a transition
# state search along the frequency mode with the smallest frequency.

# First run: Calculate Hessian
# =====

AMS_JOBNAME=hessian $AMSBIN/ams << EOF
```

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```
Task SinglePoint

Properties
  Hessian True
End

System
  Atoms
    C 0.0 0.0 0.0
    O 1.5 0.5 0.0
  End
  Lattice
    3.2 0.0 0.0
  End
End

Engine Band
  Basis Type=DZP
  KSpace Quality=Good
EndEngine

EOF

# Second run: TS search with initial Hessian
# =====

AMS_JOBNAME=TS $AMSBIN/ams << EOF

Task TransitionStateSearch

System
  Atoms
    C 0.0 0.0 0.0
    O 1.5 0.5 0.0
  End
  Lattice
    3.2 0.0 0.0
  End
End

GeometryOptimization
  Convergence Gradients=1.0e-4
  InitialHessian
    # Load the pre-calculated Hessian as the initial Hessian for the
    # transition state search using the Quasi-Newton based optimizer.
    Type FromFile
    File hessian.results/band.rkf
  End
End

Properties
  # Also calculate normal modes in the end, so we can see if we actually
  # found a transition state.
  NormalModes True
End
```

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```

Engine Band
  Basis Type=DZP
  KSpace Quality=Good
EndEngine

EOF

```

11.2.2 Example: PES scan and TS search for H2 on graphene

Download PESScan_and_TS_H2_on_Graphene.run

```

#!/bin/sh

# First we do a 2D PES scan varying the z-coordinate of the two hydrogen atoms
# In this example we will keep the graphene slab fixed. From a physical/chemical
# standpoint this is not a good approximation. The graphene slab is
# intentionally not perfectly symmetric.

AMS_JOBNAME=PESScan $AMSBIN/ams << EOF

Task PESScan

System
  Atoms
    H 0.0 1.53633037 1.1
    H 0.0 -0.11341359 1.1
    C 0.001 1.42028166 0.0
    C 1.230 2.13042249 0.0
    C 1.230 -0.71014083 0.0
    C 2.460 0.00000000 0.0
    C 2.460 1.42028167 0.0
    C 0.000 0.00000000 0.0
  End
  Lattice
    3.69 -2.13042249 0.0
    0.00 4.26084499 0.0
  End
End

PESScan
  ScanCoordinate
    nPoints 10
    Coordinate 1 Z 1.1 2.0
  End
  ScanCoordinate
    nPoints 10
    Coordinate 2 Z 1.1 2.0
  End
End

GeometryOptimization
  Convergence Step=1.0e-3
End

Constraints

```

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```

# Fix the entire graphene slab.
Atom 3
Atom 4
Atom 5
Atom 6
Atom 7
Atom 8
End

Engine DFTB
Model DFTB
ResourcesDir DFTB.org/3ob-3-1
DispersionCorrection D3-BJ
KSpace
Type Symmetric
Symmetric KInteg=3
End
EndEngine

EOF

# A human looks at the PES scan and picks a reasonable starting point for the
# TS search. (Normally you would do that in AMSMovie by looking at the PES and
# then exporting the geometry into an xyz file.)

#
#      _      _
#      ___))      [ / | \
#      ) //o      | | ]
#      _ ( _ >      | | ]
#      (O) \__<      | | ]
#      [/] / \ \      [__|/_
#      [ \ ] | ( \      _/_ \_
#      [ / ] | \ \ \_ \_ /
#      [ \ ] | \ \_E/%%/|_
#      [ / ] |===== ( )

cat << EOF > initial_geometry_for_TS.xyz
8
H      0.4145668856457391      1.72927656037925      1.100000023839768      region=H2
H      -0.05533871972549955      -0.06805093626643093      1.500000013242627      region=H2
C      0.001      1.42028166      0.0
C      1.230      2.13042249      0.0
C      1.230      -0.71014083      0.0
C      2.460      0.00000000      0.0
C      2.460      1.42028167      0.0
C      0.000      0.00000000      0.0
VEC1 3.69 -2.13042249 0.0
VEC2 0.0 4.26084499 0.0
EOF

# Compute the partial initial Hessian to be used in the transition state
# search. (The Hessian will be computed only for the hydrogen atoms.)

AMS_JOBNAME=Hessian $AMSBIN/ams << EOF

```

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```
Task SinglePoint

System
  # Load the geometry we just saved.
  GeometryFile initial_geometry_for_TS.xyz
End

Properties
  # Calculate the Hessian (implied when calculating normal modes) ...
  NormalModes True
  # ... but only the part related to the hydrogen atoms.
  SelectedRegionForHessian H2
End

Engine DFTB
  Model DFTB
  ResourcesDir DFTB.org/3ob-3-1
  DispersionCorrection D3-BJ
  KSpace
  Type Symmetric
  Symmetric KInteg=3
  End
EndEngine

EOF

echo "Extract the frequencies from the kf file using amsreport:"
$AMSBIN/amsreport Hessian.results/dftb.rkf -r "Vibrations%Frequencies[cm-1]##1"

# Do a transition state search using the initial Hessian just computed (the
# Graphene slab is constrained). Also compute the final Hessian for the
# hydrogen atoms to validate the TS.

AMS_JOBNAME=TS $AMSBIN/ams << EOF

Task TransitionStateSearch

System
  # Load the geometry we just saved.
  GeometryFile initial_geometry_for_TS.xyz
End

GeometryOptimization
  Quasi-Newton
  Step TrustRadius=0.05
  End
  Convergence Gradients=1.0e-4
  InitialHessian
  # Load previously calculated Hessian as initial Hessian for a
  # transition state search with the Quasi-Newton optimizer.
  Type FromFile
  File Hessian.results/dftb.rkf
  End
End
```

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```
TransitionStateSearch
  # Follow the mode with the smallest frequency.
  ModeToFollow 1
  # (This is also the default, we wouldn't need to specify this.)
End

Constraints
  # Fix the entire graphene slab.
  Atom 3
  Atom 4
  Atom 5
  Atom 6
  Atom 7
  Atom 8
End

Properties
  NormalModes Yes
  SelectedRegionForHessian H2
End

Engine DFTB
  Model DFTB
  ResourcesDir DFTB.org/3ob-3-1
  DispersionCorrection D3-BJ
  KSpace
  Type Symmetric
  Symmetric KInteg=3
  End
EndEngine

EOF

echo "Extract energy from the rkf file using amsreport:"
$AMSBIN/amsreport TS.results/dftb.rkf -r "AMSResults%Energy"
```

11.3 Nudged Elastic Band (NEB)

11.3.1 Nudged Elastic Band (NEB) Examples

Here are a few examples showing how the NEB method can be used to obtain the the path and transition state of a reaction.

See also:

Nudged Elastic Band (NEB) Documentation (page 75)

HCN isomerization reaction with NEB

Download NEB_HCN.run

H2 dissociation on graphene

Download NEB_H2_on_graphene.run

Running multiple NEB calculations using PLAMS

Download NEB.plms

This example should be executed using PLAMS.

See also:

PLAMS documentation and tutorial

11.4 Intrinsic reaction coordinate (IRC)

11.4.1 Example: IRC for HCN

Download IRC_HCN.run

```
#!/bin/sh

# == IRC scan of the reaction path ==

# The IRC calculation is split in two steps to illustrate the Restart feature.

# In the first calculation only a few points are computed along the so-called
# 'forward' path. The definition of which is 'forward' and which is
# 'backward' depends on the sign of the largest component of the normal mode
# corresponding to the reaction coordinate.

# The RKF file from this partial IRC scan serves as restart file
# for the next calculations that will continue the IRC scan.

# The 'MaxPoints' key in the IRC block is used to limit the number of IRC
# points to compute.

AMS_JOBNAME=irc1 $AMSBIN/ams << eor

Task IRC
System
  Atoms
    C      0.000000000000      0.000000000000      0.000000000000
    N      0.000000000000      0.000000000000     -1.182644220000
    H     -1.103250760411      0.000000000000     -0.322462130000
  End
End
```

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```

IRC
  MaxPoints 5
  Direction Forward
  CoordinateType Cartesian
  InitialHessian
    Type Calculate
  End
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-3-1
EndEngine

eor

# In the second IRC run, the IRC scan is finished. We start with the RKF file
# from the previous run and omit the MaxPoints from the settings, which means
# that the default 100 will be used. Note that the 100 also includes any points
# computed in the previous calculation. The program starts on
# the forward path, continuing where the first calculation had stopped,
# and completes it. Since we set the Direction to Both
# then AMS proceeds to the backward path. After both paths are finished a summary
# of the path characteristics is printed at the end of the output file.

AMS_JOBNAME=irc2 $AMSBIN/ams << eor

Task IRC
System
  Atoms
    C      0.000000000000      0.000000000000      0.000000000000
    N      0.000000000000      0.000000000000     -1.182644220000
    H     -1.103250760411      0.000000000000     -0.322462130000
  End
End

IRC
  Restart
    File irc1.results/ams.rkf
  End
  ! Change options from the ones found in the restart file
  ! (MaxIRCPoints and MaxPoints will be reset to defaults automatically)
  Direction Both
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-3-1
EndEngine

eor

```

11.4.2 Example: TS and IRC for Claisen reaction

Download TS_and_IRC_Claisen.run

```

#!/bin/sh

# Transition State Search (TS search) followed by Intrinsic Reaction
# Coordinates (IRC) for two similar Claisen rearrangement reactions.

# =====
# Claisen rearrangement from C=CCC1C=CC=CC1=O to C=CCOc1ccccc1
# =====

AMS_JOBNAME=TS_molecule $AMSBIN/ams << eor

Task TransitionStateSearch

System
  Atoms
    C -1.6622561642524 -1.4933421191817 0.6484353677288
    C -2.6070283916282 -1.7718977641902 -0.3933564306530
    C -2.7546368861548 -3.0534770331072 -0.8757259422474
    C -1.9443405437492 -4.1131780924428 -0.3870796280948
    C -1.0139402388630 -3.8827189276564 0.5979937257975
    C -0.7543606665660 -2.5518266272325 1.0788971265869
    H -3.2590342954832 -0.9734836183880 -0.7410179986476
    H -3.5074724102535 -3.2690301027846 -1.6324229738243
    H -2.1044351565280 -5.1220091436618 -0.7615296311573
    H -0.4323033724363 -4.7107876462166 1.0021729248699
    H -0.3533176373037 -2.4841001370767 2.0927436180830
    O -1.5058234397159 -0.2844936546832 1.1029538316409
    C 0.1375150486634 0.3928947854321 0.4626789880484
    C 1.0578648498087 -0.6180364119671 0.7737587143345
    C 0.8861173890663 -1.8991002496105 0.2125497351161
    H 0.5725481135101 -1.9591100578644 -0.8292382400922
    H -0.2171264706145 0.4859594211539 -0.5641152540806
    H 0.1902646842718 1.3359879065177 1.0025369222419
    H 1.5779002347488 -0.5540482019233 1.7307360489935
    H 1.6031168776346 -2.6724262749099 0.4842127285858
  End
End

Properties NormalModes=Yes

GeometryOptimization
  InitialHessian Type=Calculate
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/3ob-3-1
EndEngine
eor

AMS_JOBNAME=IRC_molecule $AMSBIN/ams << eor

```

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```

Task IRC

IRC
  MaxIterations 1000
  InitialHessian
    Type FromFile
    File TS_molecule.results
  End
end

LoadSystem
  File TS_molecule.results/ams.rkf
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/3ob-3-1
EndEngine
eor

# =====
# Claisen rearrangement for a (periodic) polymer containing the same aromatic
# ring of the previous calculation (from C=CC1C=CC=CC1=O to C=CCOc1cccc1)
# =====

AMS_JOBNAME=TS_polymer $AMSBIN/ams << eor

Task TransitionStateSearch

System
  Atoms
    C  9.4367476128766   1.6156795441351   0.8542644025030
    C  8.6813349262903   0.7302865575002   0.0170374963868
    C  9.3238583586638  -0.1438417574104  -0.8314773024306
    C 10.741095802442   -0.1538813927018  -0.9297572682512
    C 11.499909556383   0.6929842950328  -0.1576524435776
    C 10.884234857485   1.6861365363275   0.6817028097694
    C  7.1928255650616   0.6847044785103   0.0090333093191
    H  8.7472521390038  -0.8479982636647  -1.4293934603813
    H 11.224348014063  -0.8771406786637  -1.5831686891584
    C 12.930798908912   0.8113031163622  -0.1971191730819
    H 11.474366091679   2.0120169601893   1.5412690799783
    O  8.8401614254340   2.4539245100299   1.6503819438045
    C  9.0152184164720   4.1939147755043   0.9354292967913
    C 10.386800460742   4.3070474573655   0.6675488559614
    C 10.983233806221   3.4166811386158  -0.2473786535066
    H 10.425317882010   3.1661173633779  -1.1491528320010
    H  8.3301833043316   4.0024301166114   0.1091130317749
    H  8.5863952766270   4.7863410214548   1.7409077918798
    H 11.023307058306   4.7274400682699   1.4475913648158
    H 12.053474297431   3.5124067242738  -0.4244212846926
    C 13.897191373368  -0.0308805104165  -0.7206407708622
    C 15.267346128343   0.2274543686942  -0.4348415320624
    C 16.387786908031  -0.4341710477973  -0.8962646879782
    C  6.2048264493065  -0.0924013581064  -0.6266734325417
    C  4.8694123304551   0.1638639419185  -0.3442585289372

```

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```
C 3.7074226634814 -0.4584344973285 -0.8689206409329
C 2.4653410147781 0.0102007864139 -0.4848760767909
H 16.298210512111 -1.2787892169088 -1.5797017846452
H 3.7984002771976 -1.2806821291979 -1.5787594353897
H 6.8240750625775 1.4435007199212 0.7047818340481
H 13.314194383001 1.6434188966421 0.3984353613768
H 13.626424975736 -0.8770823766787 -1.3528414377622
H 15.451469431625 1.0743039058568 0.2322503424471
H 2.4641684561885 0.8477050600186 0.2182734314177
H 6.4819803798672 -0.8741436365939 -1.3339335062636
H 4.6807561767470 0.9698264886906 0.3703766590249
End
Lattice
 15.210 0.0 0.0
End
End
Properties
  NormalModes Yes
End
GeometryOptimization
  Method Quasi-Newton
  InitialHessian Type=Calculate
End
Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/3ob-3-1
EndEngine
eor

AMS_JOBNAME=IRC_polymer $AMSBIN/ams << eor

Task IRC

IRC
  MaxIterations 1000
  InitialHessian
    Type FromFile
    File TS_polymer.results
  End
  Direction Forward
end

LoadSystem
  File TS_polymer.results/ams.rkf
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/3ob-3-1
EndEngine
eor
```

11.5 PES scan

11.5.1 Example: Linear transit

Download LinearTransit.run

```
#!/bin/sh

echo "====="
echo "HCN isomerization"
echo "====="
echo

AMS_JOBNAME=HCN_isomerization $AMSBIN/ams << EOF

  Task PESScan
  # (Linear transit is just a PES scan with 1 scan coordinate.)

  System
  Atoms
    C      0.00000000    0.00000000    1.04219000
    H      0.00000000    0.00000000   -0.03324000
    N      0.00000000    0.00000000    2.20064000
  End
End

  PESScan
  ScanCoordinate
  nPoints 25
  Angle 2 1 3 180.0 0.0
  End
End

  Engine DFTB
  Model DFTB0
  ResourcesDir DFTB.org/mio-1-1
EndEngine

EOF

echo
echo "====="
echo "Water angle transit"
echo "====="
echo

AMS_JOBNAME=water_angle $AMSBIN/ams << EOF

  Task PESScan

  System
  Atoms
    O      0.00000000    0.00000000    0.59372000
```

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```

      H      0.00000000      0.76544000      -0.00836000
      H      0.00000000     -0.76544000     -0.00836000
    End
  End

  PESScan
    ScanCoordinate
      nPoints 25
      Angle 2 1 3 80.0 180.0
    End
  End

  GeometryOptimization
    ! Delocalized coordinates currently have a problem with linear systems.
    ! So we will use cartesian coordinates here.
    CoordinateType Cartesian
  End

  Engine DFTB
    Model DFTB0
    ResourcesDir DFTB.org/mio-1-1
  EndEngine

EOF

echo
echo "======"
echo "Hydrocarbon reaction"
echo "======"
echo

AMS_JOBNAME=hydcarb $AMSBIN/ams << EOF

  Task PESScan

  System
    Atoms
      C      0.14667300     -0.21503500      0.40053800
      C      1.45297400     -0.07836900      0.12424400
      C      2.23119700      1.15868100      0.12912100
      C      1.78331500      2.39701500      0.38779700
      H     -0.48348000      0.63110600      0.67664100
      H     -0.33261900     -1.19332100      0.35411600
      H      2.01546300     -0.97840100     -0.14506700
      H      3.29046200      1.03872500     -0.12139700
      H      2.45728900      3.25301000      0.35150400
      H      0.74193400      2.60120700      0.64028800
      C     -0.75086900      1.37782400     -2.43303700
      C     -0.05392100      2.51281000     -2.41769100
      H     -1.78964800      1.33942600     -2.09651100
      H     -0.30849400      0.43896500     -2.76734700
      H     -0.49177100      3.45043100     -2.06789100
      H      0.98633900      2.54913500     -2.74329400
    End
  End

```

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```

PESScan
  ScanCoordinate
    nPoints 25
    Distance 1 11 3.36 1.538
    Distance 4 12 3.36 1.538
  End
End

Engine DFTB
  Model DFTB0
  ResourcesDir DFTB.org/mio-1-1
EndEngine

EOF

echo
echo "====="
echo "Retinal trans -> 11-cis isomerization"
echo "====="
echo

AMS_JOBNAME=retinal_transcis $AMSBIN/ams << EOF

Task PESScan

System
  Atoms
    H -2.10968473 -1.58238733 0.78224517
    C -2.10306857 -0.54058322 0.46363503
    C -0.89436995 0.04807217 0.25528247
    H -0.85555481 1.05432693 -0.15803658
    C 0.38987539 -0.58661182 0.49038464
    C 1.53213446 0.09657801 0.14394773
    H 1.40518949 1.08783970 -0.29205231
    H 3.05232192 -1.34477492 0.72115301
    C 2.88311454 -0.36358433 0.28105432
    C 3.96024700 0.37378345 -0.12385974
    H 3.77965758 1.35231793 -0.56821856
    C 5.34627719 -0.04025647 -0.02249097
    C 6.32191717 0.80135945 -0.49190463
    H 6.00090638 1.74979100 -0.92101391
    C -4.46825064 -0.90426552 -0.39585925
    C -5.87277429 -0.25303564 -0.45007491
    C -3.41139545 0.06493448 0.19516310
    C -3.67932839 1.38221399 0.41656971
    C -5.81598497 1.19032366 -0.92660753
    C -5.00049358 2.01922634 0.05561242
    C -4.58391145 -2.18782901 0.46346394
    C -4.01729542 -1.30039402 -1.82272212
    C -2.72429960 2.32303313 1.10290124
    C 0.40919453 -1.96244629 1.09501374
    C 5.64155973 -1.38034133 0.59419110
    C 7.76996060 0.56699126 -0.48750226
    O 8.57693167 1.36615612 -0.92976322

```

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```

H      -6.51997817      -0.84904979      -1.10100203
H      -6.32039371      -0.28079023       0.54871092
H      -5.36159995       1.23817633      -1.92112092
H      -6.82595442       1.60207678      -1.01946858
H      -5.58216571       2.18390764       0.97424181
H      -4.81292271       3.01993001      -0.35246294
H      -4.74166770      -1.94289144       1.51126095
H      -5.43008715      -2.78247632       0.12572479
H      -3.69644845      -2.81116549       0.38705593
H      -3.02900804      -1.75403268      -1.79820003
H      -4.71056940      -2.01489741      -2.26202914
H      -3.97070839      -0.42860260      -2.47090348
H      -2.16469005       2.92261100       0.38111736
H      -3.27791517       3.02297911       1.72885233
H      -2.00470188       1.79865198       1.72726573
H      -0.13689001      -1.97717074       2.03825359
H      -0.07664772      -2.68134154       0.43362393
H       1.41837401      -2.31391556       1.28591185
H       5.15278730      -2.17622743       0.03222328
H       6.70436647      -1.59729505       0.62729622
H       5.25700064      -1.42489613       1.61313095
H       8.12614442      -0.41441814      -0.04549414
End
End

PESScan
  ScanCoordinate
    nPoints 25
    Dihedral  6 9 10 12  180  0
    Dihedral  8 9 10 11  180  0
  End
End

Engine DFTB
  Model DFTB0
  ResourcesDir DFTB.org/mio-1-1
EndEngine

EOF

```

11.5.2 Example: 2D PES scan

Download PESScan.run

```

#!/bin/sh

echo "====="
echo "Ethane torsion"
echo "====="
echo

AMS_JOBNAME=ethane_torsion $AMSBIN/ams << EOF

Task PESScan

```

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```

System
  Atoms
    C  0.0      0.0      0.76576
    C  0.0      0.0     -0.76576
    H -0.88668938  0.51193036  1.16677
    H  0.88668938  0.51193036  1.16677
    H  0.0      -1.02386071  1.16677
    H  0.0      1.02386071  -1.16677
    H -0.88668938 -0.51193036 -1.16677
    H  0.88668938 -0.51193036 -1.16677
  End
End

PESScan
  # First scan coordinate: C--C bond distance
  ScanCoordinate
    nPoints 5
    Distance 1 2 1.3 1.7
  End
  # Second scan coordinate: One of the H--C--C--H dihedral angles (others will
↳follow naturally)
  ScanCoordinate
    nPoints 21
    Dihedral 3 1 2 6 60.0 0.0
  End
End

GeometryOptimization
  Convergence Step=1.0e-3
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-3-1
  DispersionCorrection D3-BJ
EndEngine

EOF

echo "======"
echo "Ethene torsion"
echo "======"
echo

AMS_JOBNAME=ethene_torsion $AMSBIN/ams << EOF

Task PESScan

System
  Atoms
    C  0.0  0.0  0.66687
    C  0.0  0.0 -0.66687
    H  0.0  0.92974 -1.23912
    H  0.0  0.92974  1.23912
    H  0.0 -0.92974  1.23912

```

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```

      H   0.0  -0.92974  -1.23912
    End
  End

  PESScan
    # First scan coordinate: C--C bond distance
    ScanCoordinate
      nPoints 5
      Distance 1 2 1.1 1.8
    End
    # Second scan coordinate: Two of the H--C--C--H dihedrals
    ScanCoordinate
      nPoints 21
      Dihedral 4 1 2 3 0.0 60.0
      Dihedral 5 1 2 6 0.0 60.0
    End
  End

  End

  GeometryOptimization
    Convergence Step=1.0e-3
  End

  Engine DFTB
    Model DFTB3
    ResourcesDir DFTB.org/3ob-3-1
    DispersionCorrection D3-BJ
  EndEngine

EOF

# Below are more technical examples, demonstrating the PES scan gap filling.
# The QUASINANO2015 parameter set shows some discontinuities in the PES,
# which leads to problems with convergence. The first job leaves the
# non-converged steps as is while the second job instructs AMS to
# attempt a second optimization for non-converged point starting from
# a different initial geometry.

echo "======"
echo "Ethane gap filling test (1/2)"
echo "======"
echo

AMS_JOBNAME=ethane_nofillgaps $AMSBIN/ams << EOF

  Task PESScan

  System
    Atoms
      C -2.333834610464788 -2.268837915270455 -0.2417723425321957
      C -0.8081611038872945 -2.334371994724881 -0.04271045326758349
      H -0.2505615773096904 -1.473443563856088 -0.38077110593546
      H -0.3249814761083244 -3.235478579439597 -0.3904810245975267
      H -0.583247370537557 -2.349691649662279 1.013499336841977
      H -2.817014238243758 -1.367731330555738 0.1059982287977475
      H -2.891434137042391 -3.129766346139247 0.09628831013568076

```

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```

      H  -2.558748343814525  -2.253518260333056  -1.297982132641757
    End
  End

  GeometryOptimization
    CoordinateType Cartesian
    Convergence Step=1.0e-3
  End

  PESScan
    FillUnconvergedGaps False
    CalcPropertiesAtPESPoints True
    ScanCoordinate
      nPoints 10
      Distance 1 2  1.4 1.7
    End
    ScanCoordinate
      nPoints 10
      Distance 7 1  1.0 1.2
      Dihedral 7 1 2 3  60.0 180.0
    End
  End

  Engine DFTB
    Model SCC-DFTB
    ResourcesDir QUASINANO2015
  EndEngine

EOF

echo "======"
echo "Ethane gap filling test (2/2)"
echo "======"
echo

AMS_JOBNAME=ethane_fillgaps $AMSBIN/ams << EOF

  Task PESScan

  System
    Atoms
      C  -2.333834610464788  -2.268837915270455  -0.2417723425321957
      C  -0.8081611038872945  -2.334371994724881  -0.04271045326758349
      H  -0.2505615773096904  -1.473443563856088  -0.38077110593546
      H  -0.3249814761083244  -3.235478579439597  -0.3904810245975267
      H  -0.583247370537557  -2.349691649662279  1.013499336841977
      H  -2.817014238243758  -1.367731330555738  0.1059982287977475
      H  -2.891434137042391  -3.129766346139247  0.09628831013568076
      H  -2.558748343814525  -2.253518260333056  -1.297982132641757
    End
  End

  GeometryOptimization
    CoordinateType Cartesian
    Convergence Step=1.0e-3
  End

```

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```

PESScan
  FillUnconvergedGaps True
  CalcPropertiesAtPESPoints True
  ScanCoordinate
    nPoints 10
    Distance 1 2 1.4 1.7
  End
  ScanCoordinate
    nPoints 10
    Distance 7 1 1.0 1.2
    Dihedral 7 1 2 3 60.0 180.0
  End
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir QUASINANO2015
EndEngine

EOF

```

11.5.3 Example: PES scan for lattice degrees of freedom

Download PESScan_lattice.run

```

#!/bin/sh

AMS_JOBNAME=aramide_twist_stretch "$AMSBIN/ams" << eor

Task PESScan

PESScan
  ScanCoordinate
    nPoints 11
    Dihedral 28 2 19 25 0 125
    Dihedral 28 2 19 17 180.0 305
  End
  ScanCoordinate
    nPoints 5
    FromLattice
      13.05 0.0 0.0
    End
    ToLattice
      13.25 0.0 0.0
    End
  End
End

System
  Atoms
    C 0.9216531199085832 -0.5454515169645626 -0.2340697410375409
    N 7.445957794299515 -0.01681964756070911 0.06597315465223283
    H 3.355037052904425 -1.688703702390754 -0.8816252752735284

```

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```

H 9.500951967451224 -1.431847829691195 -0.7477789274312976
H 5.95132493510865 1.984563817105728 1.200973659205526
H 12.85473854569853 1.727718149230879 1.067133628354558
H 3.505268840981867 2.045685273157995 1.235853514670207
H 10.46827545285599 2.196297117037482 1.332327137819838
H 5.801094666247189 -1.749824820538445 -0.9165045876907203
H 11.88742341712797 -1.900439221973683 -1.012979952512364
O 1.177299854143639 -1.578051954645684 -0.8209290818960512
H 7.76304211724438 -0.8491313767219947 -0.4061010828807728
H 1.543350207091979 1.145009665092428 0.7254639267720714
O 8.129085729296452 1.87393928672803 1.140288046892258
C 5.295013835525856 -0.9149565254466551 -0.4430653247614506
C 11.56877839022646 -1.000603430504764 -0.4978381858642764
C 3.910823555244332 -0.8828087052616261 -0.4247213344032906
C 10.22040985505902 -0.7280213735372861 -0.3433304227374022
C 6.047229053946179 0.1077887625542279 0.1368149617061501
C 12.54387637027615 -0.133469498676877 5.429319732480154e-05
C 3.259131208138235 0.1880726458368187 0.1825325811252197
C 9.811866044761443 0.4293238039083616 0.3192924938584955
C 5.395538021020841 1.178670009771766 0.7440678521670584
C 12.13529814513992 1.023878258864663 0.662679127884124
C 4.011348680350846 1.210817677954059 0.762411994086449
C 10.78693136481616 1.296462367210578 0.8171881914852902
N 1.860406855610308 0.3126927007099983 0.2533844179661697
C 8.384662974014494 0.8413381653458467 0.553433102061532

End
Lattice
13.04933362476033 0.0 0.0

End

End

Engine DFTB
EndEngine

eor

AMS_JOBNAME=graphene_shear "$AMSBIN/ams" << eor

Task PESScan

PESScan
  ScanCoordinate
    nPoints 21
    FromLattice
      4.92000000      0.00000000      0.00000000
      0.00000000      8.52169000      0.00000000
    End
    ToLattice
      4.92000000      0.00000000      0.00000000
      4.92000000      8.52169000      0.00000000
    End
  End
End

End

GeometryOptimization
Convergence

```

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```

Energy 1.0e-6
Gradients 1.0e-4
Step 1.0e-3
End
End

System
  Atoms
    C   -1.23000000   -0.71014083   0.00000000
    C   -1.23000000   3.55070417   0.00000000
    C    1.23000000   -0.71014083   0.00000000
    C    1.23000000   3.55070417   0.00000000
    C   -2.46000000   -4.26084500   0.00000000
    C   -2.46000000   0.00000000   0.00000000
    C    0.00000000   -4.26084500   0.00000000
    C    0.00000000   0.00000000   0.00000000
    C   -2.46000000   -2.84056333   0.00000000
    C   -2.46000000   1.42028167   0.00000000
    C    0.00000000   -2.84056333   0.00000000
    C    0.00000000   1.42028167   0.00000000
    C   -1.23000000   -2.13042250   0.00000000
    C   -1.23000000   2.13042250   0.00000000
    C    1.23000000   -2.13042250   0.00000000
    C    1.23000000   2.13042250   0.00000000
  End
  Lattice
    4.92000000   0.00000000   0.00000000
    0.00000000   8.52169000   0.00000000
  End
End

Engine ForceField
EndEngine

eor

AMS_JOBNAME=kevlar_compression "$AMSBIN/ams" << eor

Task PESScan

PESScan
  ScanCoordinate
    nPoints 20
    FromLattice
      VEC1   4.46344907   0.00000000   0.00000000
      VEC2   0.00000000  15.00000000   0.00000000
      VEC3  -4.15619754   0.00000000   7.88460768
    End
    ToLattice
      VEC1   4.46344907   0.00000000   0.00000000
      VEC2   0.00000000  10.00000000   0.00000000
      VEC3  -4.15619754   0.00000000   7.88460768
    End
  End
End
End

```

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```

GeometryOptimization
  Convergence
    Energy 1.0e-6
    Gradients 1.0e-4
    Step 1.0e-3
  End
End

System
  Atoms
    H      -2.34574255      10.46947046      6.67609071
    H      -0.21566118      9.39070300      5.31032622
    H      1.86323468      3.63186532      1.36675944
    H      0.91346507      8.66345932      2.72468894
    H      -1.16691150      4.36193098      6.67034725
    O      0.68270622      0.35139274      3.28609533
    O      -1.39626502      12.67182069      7.22653591
    O      -0.38377339      7.08567440      4.63239262
    O      1.69448120      5.93755213      0.69230693
    N      -1.77963457      0.94576156      4.16255748
    N      0.29699209      12.07879149      0.22096612
    N      2.09175597      6.51059740      3.71380310
    N      0.01425402      6.51383083      7.65821075
    C      1.78077337      13.06266669      3.74496897
    C      -0.29869254      -0.03890117      7.68614442
    C      2.15256370      11.62041659      3.86515960
    C      0.07290835      1.40360669      7.80683608
    C      -1.25820404      11.13456872      4.63597235
    C      0.81898860      1.88918756      0.69223960
    C      -1.03413359      9.76886805      4.71156187
    C      1.04382335      3.25459780      0.76864405
    C      -1.84321511      8.85293722      4.03709183
    C      0.23429106      4.17122113      0.09564705
    C      1.56385944      9.33860183      3.26763920
    C      -0.51592344      3.68621895      7.21191051
    C      1.34444793      10.70471794      3.18555782
    C      -0.73592207      2.32019944      7.12929096
    C      -1.95926167      2.34708714      4.02068710
    C      0.11835470      10.67722153      0.08003469
    C      1.48642930      3.00363604      4.70160260
    C      3.56353841      10.02077981      0.76017378
    C      1.37833294      4.38413148      4.62212487
    C      3.45526706      8.64027066      0.68061721
    C      2.27121884      5.11078244      3.84153940
    C      0.19337160      7.91355330      7.78646448
    C      -1.17724825      4.45615536      3.15531864
    C      -3.25414982      8.56800675      7.10151848
    C      -1.05881000      3.07587289      3.25293559
    C      -3.13673047      9.94838835      7.19779875
    C      -1.47236454      7.40647135      4.16074741
    C      0.60580388      5.61750577      0.22026971
    H      -0.81007305      0.64728338      4.20563108
    H      1.26623048      12.37812387      0.26423466
    H      1.12367626      6.80447595      3.64285507
    H      -0.95355823      6.21973701      7.58479288
    H      -0.61732754      11.80995952      5.18500113
    H      1.46048855      1.21353041      1.24041623

```

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```

H      0.52432261      11.08730485      2.59181576
H     -1.55764558       1.93835499      6.53737820
H      0.78524131       2.43214154      5.29441455
H      2.86125712      10.59243593      1.35153830
H      0.59209290       4.90748377      5.15056713
H      2.66790223       8.11715076      1.20764332
H     -0.48947479       5.02445608      2.54346024
H     -2.56564408       7.99935355      6.49077972
H     -0.26677134       2.55599700      2.73158401
End
Lattice
  VEC1      4.46344907      0.00000000      0.00000000
  VEC2      0.00000000     13.02426461      0.00000000
  VEC3     -4.15619754      0.00000000      7.88460768
End
End

Engine ForceField
EndEngine

eor

AMS_JOBNAME=diamond_volumescan "$AMSBIN/ams" << eor

Task PESScan

PESScan
  ScanCoordinate
    nPoints 5
    CellVolumeScalingRange 0.8 1.2
  End
End
System
  Atoms
    C 3.12375 3.12375 3.12375
    C 0.44625 0.44625 0.44625
    C 3.12375 1.33875 1.33875
    C 0.44625 2.23125 2.23125
    C 1.33875 3.12375 1.33875
    C 2.23125 0.44625 2.23125
    C 1.33875 1.33875 3.12375
    C 2.23125 2.23125 0.44625
  End
  Lattice
    3.57 0.0 0.0
    0.0 3.57 0.0
    0.0 0.0 3.57
  End
  BondOrders
    1 2 1.0 1 1 1
    1 4 1.0 1 0 0
    1 6 1.0 0 1 0
    1 8 1.0 0 0 1
    2 3 1.0 -1 0 0
    2 5 1.0 0 -1 0
    2 7 1.0 0 0 -1

```

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```

    3 4 1.0 1 0 0
    3 6 1.0
    3 8 1.0
    4 5 1.0
    4 7 1.0
    5 6 1.0 0 1 0
    5 8 1.0
    6 7 1.0
    7 8 1.0 0 0 1
End
End

Engine DFTB
EndEngine
eor

```

11.6 PES Exploration

11.6.1 Example: Basin Hopping for Ar 13 cluster

Download BasinHopping_Ar13.run

```

#!/bin/sh

# This example shows how the Basin Hopping procedure can be used to find the
# global minimum (and several local minima) of an Argon-13 cluster.
# The LennardJones engine is used for computing energy and gradients.

"$AMSBIN/ams" << EOF

Task PESExploration

System
  Atoms
    Ar      3.19796865788947      1.15934987330252      -1.33239534934505
    Ar      0.77363272043336      0.86005279907579      4.44840472306942
    Ar      6.16557782618638      1.42715657126078      1.00292335487038
    Ar      1.31188973509015      -2.14075518617674     -0.96878076867831
    Ar     -2.41087887202771     -1.38658115989663     -0.47288216008194
    Ar     -0.21272211859964     -2.33529094743978      2.53956949757235
    Ar      0.68146295080450      4.04228262113743     -1.08313269600570
    Ar     -0.30271346683735      0.77172238432013     -2.86122291101125
    Ar     -2.82554186881390      0.46651994777473      2.87593685953916
    Ar      3.25381032839757     -0.76862912920592      2.01893019694943
    Ar     -2.88251373018356      2.43351471156095     -0.54320785580135
    Ar      0.18478571590318      0.93399697546301      0.81886912458718
    Ar      2.90785012175754      3.08435653882379      2.01057298433565
  End
End

PESExploration
  Job BasinHopping

```

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```

RandomSeed 10
Temperature 50.0
NumExpeditions 5
NumExplorers 5
FiniteDifference 1e-7

BasinHopping
  Displacement 5.0
  Steps 50
  DisplacementDistribution gaussian
  WriteUnique T
End

Optimizer
  ConvergedForce 1e-8
  MaxIterations 1000
End

StructureComparison
  DistanceDifference 0.5
  NeighborCutoff 7.6
End
End

#Engine ForceField
#EndEngine
Engine LennardJones
  Rmin 3.81749342630018000 # sigma=3.401*angs, rmin=2**(1.0/6.0)*3.401*angs
  Eps 0.000369915709507261 # eps=116.81*K
  Cutoff 15.00 # 15*angs
EndEngine

EOF

```

11.6.2 Example: PES Exploration, Process Search for alanine with PLAMS

Download ProcessSearch_alanine.plms

```

from tools.plams_test_utils import validate_energy_landscape

config.log.stdout = 0

alanine = from_smiles("CC(C(=O)O)N")

# Let's run a process search job on Alanine:

engine_sett = Settings()
engine_sett.input.ForceField = Settings()

sett = Settings()
sett.input.ams.Task = "PESExploration"
sett.input.ams.PESExploration.Job = "ProcessSearch"
sett.input.ams.PESExploration.NumExpeditions = 32
sett.input.ams.PESExploration.NumExplorers = 16

```

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```

job = AMSJob(name='alanine_process_search', molecule=alanine, settings=set + engine_
↪set)
results = job.run()
energy_landscape = results.get_energy_landscape()
print(energy_landscape)

# Let's run single point calculations on the found states to verify the
# correctness of the results:

validate_energy_landscape(energy_landscape, engine_sett)

```

11.6.3 Example: PES Exploration, Binding Sites for O on Pt 111

Download BindingSites_O+Pt111.run

```

#!/bin/sh

export OMP_NUM_THREADS=1 # Reduce ReaxFF engine noise

AMS_JOBNAME=process_search "$AMSBIN/ams" << EOF

Task PESExploration

System
  Atoms
    O      5.54003937    1.60484089    8.92740946    region=adsorbate
    Pt     8.31521714    4.80239136    7.78926430    region=surface
    Pt     5.54298786    0.00160612    7.79128800    region=surface
    Pt     6.92910250    2.40199874    7.79027615    region=surface
    Pt    11.08707571    4.80244586    7.78854885    region=surface
    Pt     8.31484643    0.00166062    7.79057254    region=surface
    Pt     9.70096096    2.40178486    7.79068672    region=surface
    Pt     5.54335868    4.80260524    7.78885374    region=surface
    Pt     2.77112940    0.00182001    7.79087743    region=surface
    Pt     4.15724404    2.40221263    7.78986559    region=surface
    Pt     9.70154331    5.60130339    5.52585419    region=surface
    Pt     6.92931403    0.80051815    5.52787789    region=surface
    Pt     8.31542867    3.20091077    5.52686604    region=surface
    Pt     4.15782639    5.60173116    5.52503306    region=surface
    Pt     1.38559711    0.80094593    5.52705675    region=surface
    Pt     2.77171175    3.20133854    5.52604491    region=surface
    Pt     6.92968485    5.60151727    5.52544363    region=surface
    Pt     4.15745557    0.80073204    5.52746732    region=surface
    Pt     5.54357021    3.20112466    5.52645547    region=surface
    Pt     6.92989639    4.00003668    3.26303536    region=surface
    Pt     8.31601103    6.40042930    3.26202352    region=surface
    Pt     5.54378174    1.59964406    3.26404721    region=surface
    Pt     9.70175484    3.99982280    3.26344593    region=surface
    Pt    11.08786948    6.40021541    3.26243408    region=surface
    Pt     8.31564020    1.59943018    3.26445778    region=surface
    Pt     4.15803792    4.00025057    3.26262480    region=surface
    Pt     5.54415256    6.40064318    3.26161295    region=surface
    Pt     2.77192328    1.59985795    3.26363664    region=surface
    Pt     1.38639089    2.39871548    1.00094199    region=surface
    Pt     5.54436409    4.79916260    0.99921469    region=surface

```

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```
Pt      6.93024583    7.19969029    1.00043291    region=surface
Pt      4.15824945    2.39876998    1.00022653    region=surface
Pt      8.31622256    4.79894871    0.99962525    region=surface
Pt      9.70210429    7.19947641    1.00084348    region=surface
Pt      6.93010792    2.39855609    1.00063710    region=surface
Pt      2.77250564    4.79937648    0.99880412    region=surface
Pt      4.15838737    7.19990418    1.00002234    region=surface
End
Lattice
  8.31557575    0.00000000    0.00000000
  4.15778787    7.20149984    0.00000000
End
End
Constraints
  FixedRegion surface
End
PESExploration
  Job ProcessSearch

  RandomSeed 100
  NumExpeditions 50
  NumExplorers 5
  DynamicSeedStates T

  Temperature 100.0

  Optimizer
    ConvergedForce 0.0001
  End

  SaddleSearch
    MaxEnergy 2.0
  End

  StructureComparison
    DistanceDifference 0.1
    NeighborCutoff 10.0
    EnergyDifference 0.01
  End
End
End
Engine ReaxFF
  ForceField CHONSFptClNi.ff
  Charges Solver=Direct # Reduce ReaxFF engine noise
EndEngine
EOF

AMS_JOBNAME=binding_sites "$AMSBIN/ams" << EOF

Task PESExploration

System
  Atoms
```

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```

O      5.54003937      1.60484089      8.92740946      region=adsorbate
Pt     8.31521714      4.80239136      7.78926430      region=surface
Pt     5.54298786      0.00160612      7.79128800      region=surface
Pt     6.92910250      2.40199874      7.79027615      region=surface
Pt    11.08707571      4.80244586      7.78854885      region=surface
Pt     8.31484643      0.00166062      7.79057254      region=surface
Pt     9.70096096      2.40178486      7.79068672      region=surface
Pt     5.54335868      4.80260524      7.78885374      region=surface
Pt     2.77112940      0.00182001      7.79087743      region=surface
Pt     4.15724404      2.40221263      7.78986559      region=surface
Pt     9.70154331      5.60130339      5.52585419      region=surface
Pt     6.92931403      0.80051815      5.52787789      region=surface
Pt     8.31542867      3.20091077      5.52686604      region=surface
Pt     4.15782639      5.60173116      5.52503306      region=surface
Pt     1.38559711      0.80094593      5.52705675      region=surface
Pt     2.77171175      3.20133854      5.52604491      region=surface
Pt     6.92968485      5.60151727      5.52544363      region=surface
Pt     4.15745557      0.80073204      5.52746732      region=surface
Pt     5.54357021      3.20112466      5.52645547      region=surface
Pt     6.92989639      4.00003668      3.26303536      region=surface
Pt     8.31601103      6.40042930      3.26202352      region=surface
Pt     5.54378174      1.59964406      3.26404721      region=surface
Pt     9.70175484      3.99982280      3.26344593      region=surface
Pt    11.08786948      6.40021541      3.26243408      region=surface
Pt     8.31564020      1.59943018      3.26445778      region=surface
Pt     4.15803792      4.00025057      3.26262480      region=surface
Pt     5.54415256      6.40064318      3.26161295      region=surface
Pt     2.77192328      1.59985795      3.26363664      region=surface
Pt     1.38639089      2.39871548      1.00094199      region=surface
Pt     5.54436409      4.79916260      0.99921469      region=surface
Pt     6.93024583      7.19969029      1.00043291      region=surface
Pt     4.15824945      2.39876998      1.00022653      region=surface
Pt     8.31622256      4.79894871      0.99962525      region=surface
Pt     9.70210429      7.19947641      1.00084348      region=surface
Pt     6.93010792      2.39855609      1.00063710      region=surface
Pt     2.77250564      4.79937648      0.99880412      region=surface
Pt     4.15838737      7.19990418      1.00002234      region=surface
End
Lattice
      8.31557575      0.00000000
      4.15778787      7.20149984
End
Constraints
  FixedRegion surface
End
PESExploration
  Job BindingSites
  LoadEnergyLandscape
    Path process_search.results/ams.rkf
  End
StatesAlignment
  ReferenceRegion surface
End

```

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```

StructureComparison
  DistanceDifference 0.1
  NeighborCutoff 3.5
  EnergyDifference 0.1
End
End

Engine ReaxFF
  ForceField CHONSFPtClNi.ff
  Charges Solver=Direct # Reduce ReaxFF engine noise
EndEngine

EOF

```

11.6.4 Example: Importing conformers into PES explorations

Download `import_into_pesexp.run`

```

#!/bin/sh

# Step 1: Run the conformer tool to quickly get a set of minima on the PES
# -----

$AMSBIN/conformers << EOF

Generator
  RDKit
  InitialNConformers 100
End
End

System
  Atoms
  N -1.912873733399416 2.022897940092991 -0.1378294583620503
  C -0.871664156578182 3.02960778940094 0.06584379364356192
  C 0.5013812000791015 2.352115382193892 0.0410146984615521
  O 0.812167345172201 1.847076794564962 -1.240836870209463
  H -1.850257440384896 1.675835972092315 -1.088966428216949
  H -2.82010628990089 2.459772455658122 -0.02412199180453132
  H -1.024866752021569 3.492408399687411 1.045420209976512
  H -0.9134720948542179 3.809309747393572 -0.7093004343600406
  H 0.5270488401868264 1.547182041972351 0.7934160458635944
  H 1.275876827761384 3.088526288396493 0.2854207086154862
  H 0.2041922851100986 1.132993293447435 -1.463777763138591
  End
  BondOrders
  1 2 1.0
  1 5 1.0
  1 6 1.0
  2 3 1.0
  2 7 1.0
  2 8 1.0
  3 4 1.0

```

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```

        3 9 1.0
        3 10 1.0
        4 11 1.0
    End
End

Engine DFTB
  Model DFTB0
  ResourcesDir DFTB.org/mio-1-1
EndEngine

RNGSeed 20200512 # Just to make the test output deterministic ...

EOF

# Step 2: Import energy landscape by running a LandscapeRefinement on it
# -----
#
# The energy landscape that is produced by the conformers tool does not contain
# the engine output files of the individual states, which contain e.g. the
# normal modes. It can be used as input to the PESExploration ->
# LandscapeRefinement job, but not for the other PESExploration jobs (e.g.
# ProcessSearch). You should therefore always run the conformers output through
# a quick LandscapeRefinement before proceeding to other PES exploration jobs.
#
# At this point you can also trim down the number of minima loaded from the set
# of conformers. In the example below, we only load the 10 lowest energy
# conformers.

AMS_JOBNAME=refinement $AMSBIN/ams << EOF

Task PESExploration

PESExploration
  Job LandscapeRefinement
  LoadEnergyLandscape
    Path conformers.results/conformers.rkf
  KeepOnly 1:10
  End
End

Engine DFTB
  Model DFTB0
  ResourcesDir DFTB.org/mio-1-1
EndEngine

RNGSeed 20200512 # Just to make the test output deterministic ...

EOF

# Step 3: Run a process search around the lowest energy conformer
# -----
#
# We load all states we got from the LandscapeRefinement and run a single

```

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```
# expedition around the lowest energy conformer. This will give us a set of
# transition states connecting it to other conformers, but possibly also other
# isomers.

AMS_JOBNAME=process_search $AMSBIN/ams << EOF

Task PESExploration

PESExploration
  Job ProcessSearch
  LoadEnergyLandscape
    Path refinement.results
    SeedStates 1
  End
  DynamicSeedStates False
  NumExpeditions 1
  NumExplorers 64
End

LoadSystem
  File refinement.results/ams.rkf
End

Engine DFTB
  Model DFTB0
  ResourcesDir DFTB.org/mio-1-1
EndEngine

RNGSeed 20200512 # Just to make the test output deterministic ...

EOF

# Note that DFTB0 wrongly predicts an energetically favorable proton transfer
# from the OH group to the NH2 group. This would not have happened if we had
# used SCC-DFTB, but it is a nice example to show off the input for these jobs
# and that the PES exploration can discover also isomers, while the conformer
# tool should only produce conformers.
```

11.7 Molecular dynamics

11.7.1 Example: Simple MD for H2

Download MD_hydrogen_longrun.run

```
#!/bin/sh

$AMSBIN/ams << eor

Task MolecularDynamics

MolecularDynamics
  nSteps 1000
```

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```

TimeStep 0.1
InitialVelocities Type=zero
Preserve Momentum=False AngularMomentum=False
Thermostat Type=none
Trajectory SamplingFreq=100
End

System
  Atoms [Bohr]
    H -2.0 0.0 0.0
    H  2.0 0.0 0.0
  End
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir Dresden
  Occupation Strategy=Fermi Temperature=5
  Repulsion
    forcePolynomial true
  End
  DispersionCorrection Auto
EndEngine

eor

```

11.7.2 Example: MD for a box of water

Download [H2O_nreac.run](#)

11.7.3 Example: Lattice deformations in MD

Download [MD_Deformation.run](#)

```

#!/bin/sh

# This example consists of three MD runs exercising the Deformation feature in MD:
# 1. Simple deformations of a 2D slab
# 2. Complex sequence of deformations of a 3D box including multiple simultaneous
↳deformations
# 3. Combination of a uniaxial strain with barostatting the remaining directions

# This run first oscillates the lengths of the lattice vectors of the original non-
↳orthogonal
# lattice of an argon slab to 20 and 12 Angstrom respectively and back to the
↳original values,
# with a period of 125 fs. Afterwards, it linearly morphs the lattice to a 5 by 5
↳Angstrom square.
AMS_JOBNAME=Ar-2D "$AMSBIN/ams" <<EOR
# Set the random number seed to ensure reproducible results for testing. Omit this in
↳normal runs.
RNGSeed -2056449389 -1942239902 -422783941 -563204803 439708673 85320298 1328648683 -
↳688288369

```

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```
Task MolecularDynamics

MolecularDynamics
  nSteps 1000
  TimeStep 0.25
  CalcPressure True
  InitialVelocities Type=Zero
  Trajectory SamplingFreq=10
  Deformation
    StopStep 500
    Type Cosine
    TargetLength 20 12
    Period 125
  End
  Deformation
    StartStep 500
    Type Linear
    TargetLattice
      5 0 0
      0 5 0
    End
  End
  BinLog
    Step
    Time
    PressureTensor
    Pressure
    Volume
    Density
  End
End

System
  Atoms
    Ar 0.5 0.6 0.7
    Ar 3.0 3.2 3.4
  End
  Lattice
    10.0 2.0 0.0
    1.0 10.0 0.0
  End
End

Engine LennardJones
  Rmin 3.753962043231411
  Eps 3.98e-4
  Cutoff 12.0
EndEngine
EOR

# Print the evolution of the lattice parameters in the "fort.59" format
# of old standalone reaxff for testing purposes.
echo "BEGIN fort59 nobarostat"
"$AMSBIN/amspython" "$AMSHOME/scripting/standalone/reaxff-ams/fort59.py" Ar-2D.results
echo "END fort59"
```

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```

# This run applies a sequence of deformations to a box of Lennard-Jones argon atoms.
AMS_JOBNAME=Ar-box "$AMSBIN/ams" <<EOR
# Set the random number seed to ensure reproducible results for testing. Omit this in
↳normal runs.
RNGSeed 1450250278 2029462689 827312839 1518230169 1408825437 1769469410 -406759494 -
↳1006638501

Task MolecularDynamics

MolecularDynamics
  nSteps 10000
  InitialVelocities Type=Random Temperature=300
  Thermostat Type=NHC Temperature=300 Tau=100
  Timestep 1
  Trajectory SamplingFreq=100
  CalcPressure True
  # Compress the a and b vectors to 20 Angstrom and stretch the c vector to 40
↳Angstrom over 2000 steps.
  Deformation
    StartStep 0
    StopStep 2000
    Type Linear
    TargetLength 20 20 40
  End
  # Oscillate the c vector (z axis) from 40 to 30 Angstroms and back again with a
↳period of 1000 fs.
  Deformation
    StartStep 2000
    StopStep 3500
    Type Cosine
    TargetLattice
      20.0 0.0 0.0
      0.0 20.0 0.0
      0.0 0.0 30.0
  End
  Period 1000
End
# Shear the box by tilting the c vector 10 A away from the z axis in the xz plane.
Deformation
  StartStep 3500
  StopStep 4000
  Type Linear
  TargetLattice
    20.0 0.0 0.0
    0.0 20.0 0.0
    10.0 0.0 30.0
  End
End
# The following two blocks apply simultaneous cosine and sine oscillations to the
# x and y components of the c vector. The amplitude of both oscillations is the
↳same,
# indirectly defined by the maximum velocity (velocity at the inflection point).
# The c vector thus traces out a cone around the z axis over 2000 fs.
Deformation
  StartStep 4000
  StopStep 8000
  Type Cosine

```

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```

    LatticeVelocity
      0.0 0.0 0.0
      0.0 0.0 0.0
      -3e-2 0.0 0.0
    End
  Period 2000
End
Deformation
  StartStep 4000
  StopStep 8000
  Type Sine
  LatticeVelocity
    0.0 0.0 0.0
    0.0 0.0 0.0
    0.0 3e-2 0.0
  End
  Period 2000
End
# This un-shears the box again, returning the c vector to the z axis.
Deformation
  StartStep 8000
  StopStep 8500
  Type Linear
  TargetLattice
    20.0 0.0 0.0
    0.0 20.0 0.0
    0.0 0.0 30.0
  End
End
# Finally, apply an exponential ("true") strain by compressing the c vector by 1/
→1000th every step.
Deformation
  StartStep 8500
  Type Exponential
  LengthRate 0.0 0.0 -1e-3
End
End

System
  Atoms
    Ar 22.97333 5.533091 19.78068
    Ar 5.255777 10.75370 3.164254
    Ar 8.594419 0.957110 14.00514
    Ar 8.407438 7.306515 2.762099
    Ar 5.335001 18.10475 11.25000
    Ar 13.84870 24.00523 1.485310
    Ar 18.65495 8.812906 24.08580
    Ar 23.50126 5.372569 24.77962
    Ar 20.32336 23.84153 3.669808
    Ar 7.692337 5.389691 10.57909
    Ar 2.407753 7.779618 0.755645
    Ar 1.520220 15.74803 13.75000
    Ar 2.921397 15.34413 20.41981
    Ar 1.660913 18.10666 3.895263
    Ar 19.54458 18.76246 20.66279
    Ar 3.853819 4.537228 14.15265
    Ar 17.57174 15.47554 17.14501

```

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```

    Ar 8.601399 2.836638 1.872337
    Ar 2.786004 3.601185 22.17957
    Ar 0.047572 18.11282 24.78959
    Ar 0.172965 0.035326 0.223982
    Ar 6.604983 7.254174 21.83257
    Ar 16.63254 15.02432 7.992034
    Ar 7.941898 9.130224 17.89523
    Ar 18.26063 20.70600 5.643385
    Ar 22.63932 15.20789 23.33429
    Ar 1.138343 21.37810 13.97294
    Ar 0.461841 18.99572 6.401096
    Ar 22.67542 22.89935 9.344785
    Ar 7.215648 18.28717 3.411308
End
Lattice
    25.0 0.0 0.0
    0.0 25.0 0.0
    0.0 0.0 25.0
end
end

Engine LennardJones
    Eps 3.67e-4
    RMin 3.4
    Cutoff 12.0
EndEngine
EOR

# Print the evolution of the lattice parameters in the "fort.59" format
# of old standalone reaxff for testing purposes.
echo "BEGIN fort59 nobarostat"
"$AMSBIN/amspython" "$AMSHOME/scripting/standalone/reaxff-ams/fort59.py" Ar-box.
↪results | cut -c 1-86
echo "END fort59"

# This run simulates an experiment to measure the mechanical properties of an argon.
↪box
# by stretching the lattice in the z direction by 100 ppm per timestep (1 fs) while.
↪simultaneously
# keeping the x and y axes relaxed using a barostat.
AMS_JOBNAME=Ar-box-barostat "$AMSBIN/ams" <<EOR
# Set the random number seed to ensure reproducible results for testing. Omit this in.
↪normal runs.
RNGSeed 877404503 1621112889 -559440914 -1857103174 -1082101960 -1842609385 -
↪845245172 -279655974

Task MolecularDynamics

MolecularDynamics
    nSteps 8000
    InitialVelocities Type=Random Temperature=300
    Thermostat Type=NHC Temperature=300 Tau=100
    Barostat Type=MTK Pressure=1e7 Tau=1000 Scale=XY Equal=XY
    Timestep 1
    Trajectory SamplingFreq=100
    Deformation

```

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```

Type Exponential
StrainRate
  0.0 0.0 0.0
  0.0 0.0 0.0
  0.0 0.0 1e-4
End
End
End
System
  Atoms
    Ar 22.97333 5.533091 19.78068
    Ar 5.255777 10.75370 3.164254
    Ar 8.594419 0.957110 14.00514
    Ar 8.407438 7.306515 2.762099
    Ar 5.335001 18.10475 11.25000
    Ar 13.84870 24.00523 1.485310
    Ar 18.65495 8.812906 24.08580
    Ar 23.50126 5.372569 24.77962
    Ar 20.32336 23.84153 3.669808
    Ar 7.692337 5.389691 10.57909
    Ar 2.407753 7.779618 0.755645
    Ar 1.520220 15.74803 13.75000
    Ar 2.921397 15.34413 20.41981
    Ar 1.660913 18.10666 3.895263
    Ar 19.54458 18.76246 20.66279
    Ar 3.853819 4.537228 14.15265
    Ar 17.57174 15.47554 17.14501
    Ar 8.601399 2.836638 1.872337
    Ar 2.786004 3.601185 22.17957
    Ar 0.047572 18.11282 24.78959
    Ar 0.172965 0.035326 0.223982
    Ar 6.604983 7.254174 21.83257
    Ar 16.63254 15.02432 7.992034
    Ar 7.941898 9.130224 17.89523
    Ar 18.26063 20.70600 5.643385
    Ar 22.63932 15.20789 23.33429
    Ar 1.138343 21.37810 13.97294
    Ar 0.461841 18.99572 6.401096
    Ar 22.67542 22.89935 9.344785
    Ar 7.215648 18.28717 3.411308
  End
  Lattice
    25.0 0.0 0.0
    0.0 25.0 0.0
    0.0 0.0 25.0
  end
end

Engine LennardJones
  Eps 3.67e-4
  RMin 3.4
  Cutoff 12.0
EndEngine
EOR

# Print the evolution of the lattice parameters in the "fort.59" format

```

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```
# of old standalone reaxff for testing purposes.
echo "BEGIN fort59 barostat"
"$AMSBIN/amspython" "$AMSHOME/scripting/standalone/reaxff-ams/fort59.py" Ar-box-
↳barostat.results | cut -c 1-86
echo "END fort59"
```

11.7.4 Example: PLUMED spherical constraint on Ion-Water cluster

Download IonWaterClusterPlumed.run

```
#!/bin/sh

#####
# A molecular dynamics simulation of a sodium ion in a small water cluster.
# The oxygen atoms of the water molecules are constrained to be within 0.45 nm of the
↳central ion.
#
# The constraint is a harmonic function  $U(r)=\kappa*(r-0.45)**2$ .
# The constrained value  $r$  is the maximum distance out of the set of Na-O distances.
# It is a continuous function that approximates the maximum out of a set of values.
# The parameter beta determines the gradient of the function.
# Choosing a small beta value results in a better match between the actual
# and approximate maximum values, but also in a less continuous function.
#####

$AMSBIN/ams << eor

Task MolecularDynamics

MolecularDynamics
  NSteps 1000
  TimeStep 0.5
  InitialVelocities
    Temperature 300
  End
  Thermostat
    Type Berendsen
    Temperature 300
    Tau 100
  End
  Trajectory
    SamplingFreq 1
  End
  Plumed
    Input
GROUP ATOMS=2,5,8,11,14,17,20,23,26 LABEL=oxygen
DISTANCES GROUPA=1 GROUPB=oxygen MAX={BETA=0.05} LABEL=wallcv
UPPER_WALLS ARG=wallcv.max AT=0.45 KAPPA=5000.0
PRINT ARG=wallcv.max STRIDE=1 FILE=COLVAR
    End
  End
End

system
  Atoms
```

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```

Na      0.0000000000      0.0000000000      0.0000000000
O      1.7119252402     -2.0080034855      1.0155335456
H      2.5731328659     -2.4678020432      1.2672765294
H      1.4480244399     -2.5303870208      0.1729165635
O      0.6300542373      0.5761441595      2.8226448718
H      1.2391579321     -0.0089304214      2.3349735783
H      0.9338206205      1.4729694268      2.4878846070
O      0.1647045543      2.0208702482     -2.3249601218
H     -0.7307215954      2.0625495942     -2.7797813945
H      0.2097075116      1.0635963204     -2.1125352562
O     -1.7025066874     -1.0780652110     -3.0700032660
H     -2.3616744611     -0.4381207399     -3.4654803274
H     -1.8354437418     -1.8757732529     -3.6203721171
O      3.0658874271      0.7135749531     -2.1674092521
H      3.9052706085      1.2362759268     -2.1017219618
H      2.5231505825      1.3717470880     -2.6845066156
O     -2.8805081861      2.6302885978     -0.3532568156
H     -3.8762635503      2.6712519969     -0.4669367452
H     -2.6280204633      2.2152595735     -1.2369080650
O     -3.5076002124     -1.7860735453     -0.4319799526
H     -3.8213733752     -1.9705946207     -1.3583130388
H     -2.8954116001     -1.0294541930     -0.5563055520
O      2.9868579456      2.5941122968      0.9208652453
H      2.2983746780      3.1353478114      0.4089961955
H      3.1905202107      1.8321429488      0.2760998864
O     -2.9007338617      1.4515370844      2.5612078673
H     -2.1648641984      1.4189029227      1.8879229015
H     -3.6017400767      1.9414536506      2.1086226997

End
BondOrders
  20 21 1.0
  20 22 1.0
  26 27 1.0
  26 28 1.0
  23 24 1.0
  23 25 1.0
  2 3 1.0
  2 4 1.0
  11 12 1.0
  11 13 1.0
  17 18 1.0
  17 19 1.0
  14 15 1.0
  14 16 1.0
  5 6 1.0
  5 7 1.0
  8 9 1.0
  8 10 1.0
End
Charge 1.0
End

Engine ForceField
  Type UFF
EndEngine

RNGSeed 1

```

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```

eor

#####
# The constrained values are stored in the file named COLVAR.
# Below we use Python to read the COLVAR file, and print the average, maximum, and
↳minimum value.
#####

$AMSBIN/amspython << eor
infile = open('COLVAR')
lines = infile.readlines()
infile.close()

values = [float(line.split()[1]) for line in lines[1:]]
print()
print('Average value constraint: ',sum(values)/len(values))
print('Minimum value constraint: ',min(values))
print('Maximum value constraint: ',max(values))
eor

```

11.7.5 Example: MM/MM with constrained ion-water cluster in periodic water box

Download `IonWaterHybridSolvationPlumed.run`

```

#!/bin/sh

#####
# A molecular dynamics simulation of MgCl2 dissolved in a small periodic water box.
# The setup mimics a multi-scale (QM/MM) simulation,
# but with both sides described by the UFF force field.
#
# In an actual QM/MM simulation it is crucial that
# the QM and MM water molecules do not diffuse into one another.
# We accomplish this by constraining the water molecules according to the FIRES_
↳procedure
# (doi: 10.1021/ct300091w).
# The constraint  $f(\{r_O\})$  is a function of the set of distances of
# all oxygen atoms to the central ion.
#  $\{r_O\} = \{r_{QM}\} + \{r_{MM}\}$ 
#  $f(\{r_O\}) = \min(\{r_{MM}\}) - \max(\{r_{QM}\})$ .
# This function is constrained to be greater than zero using a half-harmonic_
↳potential.
#  $U(f) = \kappa * (f)^2$  for  $f < 0$ 
#  $U(f) = 0$  for  $f \geq 0$ 
#
# The min() and max() functions are continuous functions that
# approximate respectively the minimum and the maximum out of a set of values.
# The parameter beta determines the continuity of the function.
# Choosing a beta value further from 1
# (larger and smaller for the min() and max() functions respectively)
# results in a better match between the actual
# and approximate minimum/maximum values, but also in a less continuous function.
#####

```

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```

$AMSBIN/ams << eor

MolecularDynamics
  InitialVelocities
    Temperature 300.0
  End
  NSteps 200
  Plumed
    Input
GROUP ATOMS=27,36,63,93,102,138,198,213,276 LABEL=qm
GROUP ATOMS=3,6,9,12,15,18,21,24,30,33,39,42,45,48,51,54,57,60,66,69,72,75,78,81,84,
↪87,90,96,99,105,108,111,114,117,120,123,126,129,132,135,141,144,147,150,153,156,159,
↪162,165,168,171,174,177,180,183,186,189,192,195,201,204,207,210,216,219,222,225,228,
↪231,234,237,240,243,246,249,252,255,258,261,264,267,270,273,279,282,285,288,291,294,
↪297,300,303,306 LABEL=mm
DISTANCES GROUPA=1 GROUPB=qm MAX={BETA=0.005} LABEL=maxcv
DISTANCES GROUPA=1 GROUPB=mm MIN={BETA=100.0} LABEL=mincv
COMBINE ARG=mincv.min,maxcv.max COEFFICIENTS=1,-1 PERIODIC=NO LABEL=cv
LOWER_WALLS ARG=cv AT=0. KAPPA=5000.0
PRINT ARG=maxcv.max,mincv.min,cv STRIDE=1 FILE=COLVAR
  End
  End
  Thermostat
    Tau 100.0
    Temperature 300.0
    Type Berendsen
  End
  TimeStep 0.5
  Trajectory
    SamplingFreq 1
  End
End

Task MolecularDynamics

system
  Atoms
      Mg      5.7200350720      -2.9328800664      0.7897499036 region=qm
      H       1.8099054637      -4.4220924299      4.8703260963 region=mm
      O       7.1694504052      -8.8515558080     -4.2753237457 region=mm
      H      -7.1267761804      -8.3665468365     -4.8452690067 region=mm
      H       6.7102946636      -8.0997193116     -3.7685132509 region=mm
      O       2.7088914434       1.0610825031      4.6923243683 region=mm
      H       3.3054833375       0.4921267903      5.2402434951 region=mm
      H       1.8233363292       0.6530077196      4.7305392172 region=mm
      O      -1.4764148218      -6.8788850509     -2.6003412213 region=mm
      H      -2.0005170531      -7.6500792651     -2.8620779463 region=mm
      H      -2.1885584491      -6.3289735405     -2.1092174532 region=mm
      O       3.8478147995      -7.4795251060     -6.6736084141 region=mm
      H       4.3989126832      -6.7783144126     -7.0250045541 region=mm
      H       2.9555533860      -7.0654023511     -6.8252343194 region=mm
      O      -4.7471764043      -8.6077953930     -2.2377385210 region=mm
      H      -5.5092008380      -8.5969300931     -2.8802846966 region=mm
      H      -5.2576468285      -8.9527935768     -1.4219979311 region=mm
      O      -4.7772922849      -4.8474333611     -2.1581380915 region=mm
      H      -4.8239240982      -4.7790577136     -3.1075173037 region=mm
      H      -5.0338948567      -5.7924530112     -2.0117434690 region=mm

```

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O	2.4515102733	0.8469564304	-3.2719985082	region=mm
H	2.3774951038	-0.1397894447	-3.4984484181	region=mm
H	1.8468114255	0.8917317291	-2.4779777927	region=mm
O	-3.3840665349	-4.0437270402	4.9817876227	region=mm
H	-4.0089551919	-4.0145592434	5.6903827994	region=mm
H	-2.8889478457	-3.1965528132	5.0436088929	region=mm
O	3.3018776783	-3.8565105302	0.1699379171	region=qm
H	2.8411614398	-2.9527284257	0.2152811292	region=qm
H	3.3278682045	-4.1059629877	-0.8090519740	region=qm
O	-0.3029454571	0.3223547569	3.0869293987	region=mm
H	0.2531700096	0.3756415457	2.2625874250	region=mm
H	-0.6800920306	-0.5897179149	2.9611527639	region=mm
O	-5.3484100952	1.5806960236	0.2989946199	region=mm
H	-4.7381235203	2.3283676440	0.2109523156	region=mm
H	-6.1446741550	2.0700615293	0.6143220874	region=mm
O	-5.9927569909	-4.5445068094	0.7252872361	region=qm
H	-6.1165384480	-5.5153290275	0.4900339104	region=qm
H	-6.2159199095	-4.0455250579	-0.1412140829	region=qm
O	-0.9099199619	-1.8881647338	5.2995851295	region=mm
H	-0.2497687678	-2.4792433544	4.9371760594	region=mm
H	-0.3480512141	-1.3260802954	5.9009948331	region=mm
O	3.6215242959	2.1814508127	1.6874751538	region=mm
H	4.5165073769	2.5415115300	1.9221949954	region=mm
H	3.4064165275	1.6332209215	2.4834093017	region=mm
O	5.1833051040	-1.2908175195	6.4042504661	region=mm
H	5.0111822889	-1.5205203085	7.3487966849	region=mm
H	5.1785123947	-0.3057599544	6.5543696690	region=mm
O	0.4603933279	-1.2441515414	-0.2033532097	region=mm
H	0.7445254512	-0.6039397934	-0.9167026803	region=mm
H	-0.5688268735	-1.2243571151	-0.2572139023	region=mm
O	-5.4968287382	-8.9609194175	1.2499552393	region=mm
H	-5.1571901876	-8.8988514057	2.1941505053	region=mm
H	-6.4529456019	5.8448385545	1.3244900622	region=mm
O	-5.0649038431	-1.5925489571	5.4791046507	region=mm
H	-5.4190296195	-0.6625809652	5.5607319002	region=mm
H	-4.6322521004	-1.5417498356	4.5302003438	region=mm
O	0.3677337844	-8.5810760971	5.8032571443	region=mm
H	-0.1086349973	5.8640829165	5.1172774803	region=mm
H	0.3027415357	-7.6611857343	5.5038587712	region=mm
O	1.5717316961	-8.1886314470	-4.1347530444	region=mm
H	0.6160556952	-7.9037370683	-4.2849423181	region=mm
H	1.5976518950	-8.8465245437	-3.3851806828	region=mm
O	6.0759336250	-1.6447775457	-1.9957055354	region=qm
H	5.0826000738	-1.6154040577	-2.1716448087	region=qm
H	6.2225213454	-0.9240536977	-1.3190154430	region=qm
O	7.0411997183	-6.3306028762	2.6673264477	region=mm
H	7.2603015022	-6.4603061816	3.6331777655	region=mm
H	6.8554828937	-5.4038722790	2.3804719901	region=mm
O	5.4891620764	1.7626392649	5.4506129348	region=mm
H	5.1390437356	2.4184645147	6.1374986521	region=mm
H	5.0532883869	2.1669956638	4.6417895438	region=mm
O	-4.2394186994	0.8168239717	3.3776299556	region=mm
H	-5.1876861457	0.9406435176	3.6467381795	region=mm
H	-4.3280295844	0.9981858500	2.4035538318	region=mm
O	1.6209849652	-6.0322658389	-1.7020131060	region=mm
H	1.9033980535	-6.6148231926	-0.9312205097	region=mm
H	0.6074913843	-6.2050854204	-1.6495119106	region=mm

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O	2.3347829393	-2.1734816277	6.0621168212	region=mm
H	2.3757060915	-2.0614469403	7.0710797559	region=mm
H	3.1815618956	-2.6859727964	5.8159286113	region=mm
O	2.6526456824	-4.5252677481	-6.7120333812	region=mm
H	2.8020328735	-4.0500353548	-5.8761570391	region=mm
H	3.5420462524	-4.3070798418	-7.1561049884	region=mm
O	-5.1041720806	-2.2728098033	-4.3516727544	region=mm
H	-4.3561610138	-2.4109430620	-4.9834336502	region=mm
H	-5.2187295786	-1.2775902805	-4.3031347846	region=mm
O	-6.7183990792	-5.6026203305	5.5769211366	region=mm
H	-6.2276316883	-4.8397127501	6.0169261502	region=mm
H	-6.8644442921	-6.2360671517	6.3313904040	region=mm
O	-0.2997249631	-2.3248611096	-6.0652301268	region=mm
H	0.4480748249	-1.7420695578	-5.7844640285	region=mm
H	-0.2345271923	-3.0579113415	-5.3963109343	region=mm
O	4.4557229323	-4.0321409485	3.4229510135	region=qm
H	4.8228557987	-3.1175556198	3.2353382785	region=qm
H	3.6117875931	-4.0360335014	2.8114358246	region=qm
O	0.0246131293	0.7982683816	6.6958688191	region=mm
H	-0.7298836601	0.7814998411	7.3663632337	region=mm
H	0.8452573517	1.1002106587	7.2018710420	region=mm
O	0.5132549970	-3.4758845845	2.4755554365	region=mm
H	0.7192096520	-4.4568118056	2.3329907178	region=mm
H	-0.4531120524	-3.3351695953	2.3773299504	region=mm
O	3.7669484301	-0.0561634528	-0.5323383617	region=qm
H	3.3380366522	-0.6568105740	0.1454732327	region=qm
H	3.3744123064	0.8333772867	-0.3424611610	region=qm
O	-3.0203045076	4.5213182503	-0.5452112002	region=mm
H	-3.2392487263	4.4060241441	-1.4939704819	region=mm
H	-3.1245969727	5.4811933760	-0.4039600780	region=mm
O	-6.7794338138	0.4373660034	-3.4123297388	region=mm
H	-7.3506733030	1.2324326950	-3.2821835254	region=mm
H	-7.0467839805	-0.1662989127	-2.6296147182	region=mm
O	-7.2132673344	-6.9058350093	-0.9498762639	region=mm
H	-7.4423414731	-7.4598580979	-1.7108459608	region=mm
H	-7.2921175047	-7.5034525041	-0.1967566459	region=mm
O	-3.4217194872	-7.0004057995	0.2176912260	region=mm
H	-4.4126912325	-6.9974370339	0.2326646720	region=mm
H	-3.2536051030	-6.8635041363	1.1841799205	region=mm
O	5.5910174783	2.1763450404	-2.4932345279	region=mm
H	4.6852021649	2.5693050423	-2.2779105192	region=mm
H	5.3066397633	1.4214774177	-3.1080658731	region=mm
O	-2.4065506310	-7.2932513323	5.7623954624	region=mm
H	-2.7119429920	-7.7054547466	6.5983438564	region=mm
H	-2.6278433895	-6.2775197492	5.8969552032	region=mm
O	3.6640031160	1.8922352246	-6.2296569654	region=mm
H	2.8532764044	2.2115544890	-5.7709024750	region=mm
H	4.3856544177	2.5355822019	-5.8712770223	region=mm
O	-2.3745450348	-8.5657562688	2.7265414945	region=mm
H	-2.1735583778	5.4660643939	2.7300346193	region=mm
H	-2.9009994050	-8.4965918575	3.5413436006	region=mm
O	5.8804342009	4.5354240094	7.1325312387	region=mm
H	5.0131973513	4.8751670246	7.4157239493	region=mm
H	5.9002289371	4.7710058802	6.1556779744	region=mm
O	2.7885658031	-0.8611341888	-5.9360278211	region=mm
H	2.1091805613	-0.1354528711	-6.0003389022	region=mm
H	3.5887596075	-0.3300691963	-5.6526108069	region=mm

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O	-7.3714532064	-2.7223839233	-7.2784923252	region=mm
H	-7.1791818261	-2.2678828420	6.8553882382	region=mm
H	-6.4996545488	-2.5177748518	-6.7900553649	region=mm
O	-7.0331348372	-0.9204735428	0.6063230068	region=qm
H	-6.0921468583	-0.5254758737	0.4836642534	region=qm
H	-6.8874090945	-1.8611486055	0.3995170375	region=qm
O	-0.1957946562	-7.2810928977	0.5399018314	region=mm
H	-1.0417531010	-7.4140228543	0.0205629395	region=mm
H	-0.5066511890	-7.1774442433	1.4825039769	region=mm
O	1.8600464739	4.3473997665	-7.1437429628	region=mm
H	1.3996822124	5.0181731916	7.3159348797	region=mm
H	2.3374212908	4.9612352379	-6.5405671664	region=mm
O	-2.6582165538	3.6810647486	6.5096614907	region=mm
H	-1.9090302118	3.2846493549	5.9694982028	region=mm
H	-2.8320470394	4.5572534342	6.1597032487	region=mm
O	-0.9179119719	-7.7641827452	-6.4041108369	region=mm
H	0.0071023946	-7.5564900267	-6.8187063304	region=mm
H	-1.0509730649	-8.7349187187	-6.5113229941	region=mm
O	1.7179882871	4.6867540529	1.8322922929	region=mm
H	1.5287720026	4.0244442843	2.5787414767	region=mm
H	1.2098413206	5.5102132633	2.1367024110	region=mm
O	0.2315235157	5.3955193196	-1.3941386642	region=mm
H	0.9154934397	5.3968616552	-0.6625282811	region=mm
H	-0.6278735028	5.3026017629	-0.9672366771	region=mm
O	-2.6986887017	0.3541447860	5.9851919711	region=mm
H	-3.1402066242	1.0834994773	5.5167535098	region=mm
H	-2.0336367686	0.0007013596	5.3230337832	region=mm
O	7.2680955491	-7.7923878013	-7.0442418879	region=mm
H	-7.4069606746	-8.7072187093	-7.0814921365	region=mm
H	6.3283830672	-7.7710456593	-7.4966591209	region=mm
O	-6.3515739115	1.6766983710	5.5666144799	region=mm
H	-6.9810189288	1.3458684925	6.2898485162	region=mm
H	-6.7899460804	2.4073839912	5.1839051961	region=mm
O	-2.8567695695	-5.4944242037	-4.6438699205	region=mm
H	-2.1548980650	-4.9062145314	-4.9951434742	region=mm
H	-2.5217388050	-6.4735195066	-4.8292651223	region=mm
O	-6.7725880456	-5.3434185943	-4.7758904121	region=mm
H	-6.7069455824	-4.3534970892	-4.8167677162	region=mm
H	-6.7009918221	-5.5232802389	-5.7915052246	region=mm
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H	-6.3730841010	0.7190796050	-6.4056830813	region=mm
O	-1.2158144042	3.0933733381	1.7465428819	region=mm
H	-2.0208343618	3.5624274404	1.2900489033	region=mm
H	-1.6275528675	2.3857289407	2.3167156253	region=mm
O	-1.2518029287	-5.6724338313	3.1188234197	region=mm
H	-0.9850206033	-5.8319014903	4.0612631213	region=mm
H	-2.2290327112	-5.7688269115	3.2007651071	region=mm
O	-4.9043214995	5.6519654141	-5.4508370598	region=mm
H	-4.2942510297	-8.7887223286	-4.9708446990	region=mm
H	-4.4193283168	4.7703067795	-5.4563625441	region=mm
O	-2.5247612340	0.57322653081	0.0472599717	region=mm
H	-3.3924069268	0.1521030415	-0.1584794862	region=mm
H	-2.3892053288	0.2230100537	0.9885150093	region=mm
O	0.3117073158	3.2255479828	4.5437006801	region=mm
H	0.3906039249	2.9422839706	5.4734024052	region=mm
H	0.3838958897	2.3769700045	4.0139213002	region=mm

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O	-2.9873643647	-0.4272529780	-4.2245927340	region=mm
H	-3.3997184963	0.2439643116	-3.6677294861	region=mm
H	-2.3084400234	0.1141270972	-4.6000318007	region=mm
O	-3.6653412109	2.2731181202	-6.1284820314	region=mm
H	-2.7056660816	2.1477099050	-6.3724225625	region=mm
H	-4.1288630092	2.2931913038	-7.0006965934	region=mm
O	4.6410116320	-6.7264988994	0.4616167168	region=qm
H	4.4101166082	-6.1645564534	-0.2934777526	region=qm
H	4.6730614520	-6.0060191761	1.1335922366	region=qm
O	4.3976523416	-7.8892228919	-2.5423896153	region=mm
H	5.0311201352	-7.2835094543	-2.0152830256	region=mm
H	3.5722763512	-7.3542989528	-2.6482867334	region=mm
O	7.0792006923	0.1209931002	3.4993386680	region=mm
H	6.8558318086	-0.2426661313	4.4284878799	region=mm
H	7.0270810501	-0.7659916797	2.9870911033	region=mm
O	6.6224221857	5.1402997862	-1.3156095086	region=mm
H	6.4201527371	4.7330581484	-2.1687204168	region=mm
H	6.3243291309	4.4143694297	-0.6709013361	region=mm
O	5.2683337184	-3.5100535099	-5.2215001164	region=mm
H	5.8186543832	-3.6850578037	-5.9995996723	region=mm
H	5.6184071998	-2.7108787147	-4.7924321672	region=mm
O	-7.6586220330	-3.0339696605	3.7287215092	region=qm
H	7.2504138494	-3.8120801294	4.3111784975	region=qm
H	-6.7267376092	-3.0922749899	3.3936627288	region=qm
O	5.0926753309	-4.7195394906	6.3232718697	region=mm
H	5.0070618688	-5.3058931194	5.5083656859	region=mm
H	5.7226193237	-3.9642093025	6.0597369209	region=mm
O	4.9347540809	-7.5589961366	5.0766107941	region=mm
H	5.0190229119	-7.1138138521	4.1998727672	region=mm
H	4.0768338888	-8.0217682098	4.9892390834	region=mm
O	-1.3396252121	-4.8600195445	7.1634896373	region=mm
H	-1.4362228840	-3.8887325443	6.7864428723	region=mm
H	-0.3747219308	-4.9651044260	7.3167935631	region=mm
O	-0.2275547923	1.9526060878	-5.5664997661	region=mm
H	-0.1338166809	1.7406093835	-4.5841281712	region=mm
H	-0.2484315595	2.9461522919	-5.5385698031	region=mm
O	-4.6688925072	-6.6804128275	3.4621502759	region=mm
H	-5.5204451119	-6.1841221817	3.2712262969	region=mm
H	-4.5417671440	-6.4984155373	4.3985513305	region=mm
O	-1.7613304313	4.8508364057	-4.1901358774	region=mm
H	-0.9490659842	4.6732275830	-3.6375923368	region=mm
H	-2.1008600242	3.9220171023	-4.3346962477	region=mm
O	1.2813806306	3.6942770054	-3.7171813351	region=mm
H	2.1905963115	3.2609579576	-3.8200540205	region=mm
H	0.9663947506	3.5064245036	-2.7884181141	region=mm
O	-1.6491575074	-4.0249870766	0.4625752262	region=mm
H	-2.3793757109	-4.6115566902	0.1880014661	region=mm
H	-0.8619995170	-4.5482091047	0.1181706395	region=mm
O	3.4345393490	4.4656758215	-0.8654721765	region=mm
H	3.3499869346	4.8246344996	0.0656770670	region=mm
H	3.9194874435	5.1825851342	-1.3432740979	region=mm
O	6.0129279769	-0.1231584466	-5.7786542866	region=mm
H	6.9162672527	-0.4111451674	-5.5767296519	region=mm
H	6.1760997496	0.8392847423	-5.9209507268	region=mm
O	-3.9277443861	3.8877115252	3.4225768700	region=mm
H	-3.8512216972	3.1029288422	4.0808853225	region=mm
H	-4.9243236650	3.8119809069	3.1676946984	region=mm

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O	-2.0152094098	-3.5752136096	-2.8775430094	region=mm
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H	-2.4420915432	-4.0420947596	-2.0928745724	region=mm
O	-4.5676885067	-5.7821342384	-7.1960812502	region=mm
H	-4.0359502299	-5.0251773009	-6.7947097709	region=mm
H	-4.3397042788	-6.5601909701	-6.6311674198	region=mm
O	2.3837305449	-7.0019574341	2.8932940349	region=mm
H	1.5843595021	-6.5819302317	3.2063062063	region=mm
H	2.5110710808	-6.4985063424	2.0690005115	region=mm
O	4.3480000521	4.6575725755	-4.8007895809	region=mm
H	3.6918814150	5.3893598759	-4.6122940939	region=mm
H	5.1810645873	5.1658353534	-5.0129492914	region=mm
O	0.9105420244	2.0399129451	-0.2709605351	region=mm
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H	1.7544905017	2.6157672486	-0.3305092813	region=mm
O	6.3707479202	1.9225951795	0.5271756371	region=mm
H	6.1104155087	1.4272322940	-0.2591354170	region=mm
H	6.3108235294	1.1855175540	1.1809221336	region=mm
O	4.9793112969	5.7720777956	2.5371259504	region=mm
H	5.4410948138	-8.6373822889	1.8401865423	region=mm
H	4.0732573198	-8.8547465508	2.6355542548	region=mm
O	-1.5069942574	2.1175389224	-2.6413269953	region=mm
H	-2.2772337306	2.2001260822	-2.0840108235	region=mm
H	-0.8183840708	1.8070130896	-1.9384258703	region=mm
O	-3.1778696685	-2.2850690637	-7.0670100441	region=mm
H	-2.4447728292	-1.6521612371	-6.8766103444	region=mm
H	-3.6202120836	-1.7154370846	7.2497112917	region=mm
O	2.6192086546	-1.2244922235	2.4518195104	region=qm
H	1.8351686207	-1.4137948393	1.8609661449	region=qm
H	2.5964459046	-1.8062454655	3.2887419185	region=qm
O	-7.3321456538	2.9732498807	-5.9518392574	region=mm
H	-6.6099217284	3.5423516492	-5.5423303270	region=mm
H	6.8861073462	3.5653655129	-6.0522063293	region=mm
O	3.5659080357	4.5187085880	5.0152611102	region=mm
H	3.5206873771	4.2674900037	4.0721000327	region=mm
H	2.7215092257	4.1357642662	5.4053293417	region=mm
O	0.0671456473	-1.3384369103	-3.1666600421	region=mm
H	-0.8744551748	-1.6446509153	-3.3302330139	region=mm
H	0.5025521594	-2.2006073634	-2.8295670561	region=mm
O	-4.7331769248	-1.9735610859	-1.1710931100	region=mm
H	-4.1695543501	-2.8050647365	-1.1464150457	region=mm
H	-5.3822945516	-2.0965866117	-1.9311157594	region=mm
O	2.7575468577	-3.0372722381	-2.9953973324	region=mm
H	3.3068657454	-3.8611606289	-3.0419899298	region=mm
H	2.3763274374	-2.9947684277	-3.9059578245	region=mm
O	0.5580418210	-4.9464761608	-4.2804053084	region=mm
H	0.0324857624	-4.8267051729	-3.4837664784	region=mm
H	1.0961942044	-5.7302405505	-4.1506399120	region=mm
O	-7.2757328853	4.1642190639	3.0300970932	region=mm
H	6.9121825713	4.5448659465	3.3081894379	region=mm
H	-7.4863485302	3.2969249860	2.5402164796	region=mm
O	-4.1054878322	-1.9430177652	2.0669797525	region=mm
H	-3.6008873069	-2.6082159778	2.6226459577	region=mm
H	-4.6226134371	-2.6261274449	1.5495079114	region=mm
O	5.3816120650	-5.1804053954	-2.7240970290	region=mm
H	5.9660533434	-4.3648474016	-2.5314171173	region=mm
H	5.7143244302	-5.4848887180	-3.6381896932	region=mm

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O      1.3959632716      -5.2927847809      5.0843716744 region=mm
H      1.7762736990      -5.4289533682      5.9772747488 region=mm
Cl     -5.4680212411      3.4130263189      -2.7136231556 region=mm
Cl     -5.9988494351      5.4081934954      5.7964537819 region=mm

End
BondOrders
 2 306 1.0
 3 4 1.0
 3 5 1.0
 6 7 1.0
 6 8 1.0
 9 10 1.0
 9 11 1.0
12 13 1.0
12 14 1.0
15 16 1.0
15 17 1.0
18 19 1.0
18 20 1.0
21 22 1.0
21 23 1.0
24 25 1.0
24 26 1.0
27 28 1.0
27 29 1.0
30 31 1.0
30 32 1.0
33 34 1.0
33 35 1.0
36 37 1.0
36 38 1.0
39 40 1.0
39 41 1.0
42 43 1.0
42 44 1.0
45 46 1.0
45 47 1.0
48 49 1.0
48 50 1.0
51 52 1.0
51 53 1.0
54 55 1.0
54 56 1.0
57 58 1.0
57 59 1.0
60 61 1.0
60 62 1.0
63 64 1.0
63 65 1.0
66 67 1.0
66 68 1.0
69 70 1.0
69 71 1.0
72 73 1.0
72 74 1.0
75 76 1.0
75 77 1.0
```

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78 79 1.0
78 80 1.0
81 82 1.0
81 83 1.0
84 85 1.0
84 86 1.0
87 88 1.0
87 89 1.0
90 91 1.0
90 92 1.0
93 94 1.0
93 95 1.0
96 97 1.0
96 98 1.0
99 100 1.0
99 101 1.0
102 103 1.0
102 104 1.0
105 106 1.0
105 107 1.0
108 109 1.0
108 110 1.0
111 112 1.0
111 113 1.0
114 115 1.0
114 116 1.0
117 118 1.0
117 119 1.0
120 121 1.0
120 122 1.0
123 124 1.0
123 125 1.0
126 127 1.0
126 128 1.0
129 130 1.0
129 131 1.0
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132 134 1.0
135 136 1.0
135 137 1.0
138 139 1.0
138 140 1.0
141 142 1.0
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144 145 1.0
144 146 1.0
147 148 1.0
147 149 1.0
150 151 1.0
150 152 1.0
153 154 1.0
153 155 1.0
156 157 1.0
156 158 1.0
159 160 1.0
159 161 1.0
162 163 1.0
```

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162	164	1.0
165	166	1.0
165	167	1.0
168	169	1.0
168	170	1.0
171	172	1.0
171	173	1.0
174	175	1.0
174	176	1.0
177	178	1.0
177	179	1.0
180	181	1.0
180	182	1.0
183	184	1.0
183	185	1.0
186	187	1.0
186	188	1.0
189	190	1.0
189	191	1.0
192	193	1.0
192	194	1.0
195	196	1.0
195	197	1.0
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201	202	1.0
201	203	1.0
204	205	1.0
204	206	1.0
207	208	1.0
207	209	1.0
210	211	1.0
210	212	1.0
213	214	1.0
213	215	1.0
216	217	1.0
216	218	1.0
219	220	1.0
219	221	1.0
222	223	1.0
222	224	1.0
225	226	1.0
225	227	1.0
228	229	1.0
228	230	1.0
231	232	1.0
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237	238	1.0
237	239	1.0
240	241	1.0
240	242	1.0
243	244	1.0
243	245	1.0
246	247	1.0
246	248	1.0

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```
249 250 1.0
249 251 1.0
252 253 1.0
252 254 1.0
255 256 1.0
255 257 1.0
258 259 1.0
258 260 1.0
261 262 1.0
261 263 1.0
264 265 1.0
264 266 1.0
267 268 1.0
267 269 1.0
270 271 1.0
270 272 1.0
273 274 1.0
273 275 1.0
276 277 1.0
276 278 1.0
279 280 1.0
279 281 1.0
282 283 1.0
282 284 1.0
285 286 1.0
285 287 1.0
288 289 1.0
288 290 1.0
291 292 1.0
291 293 1.0
294 295 1.0
294 296 1.0
297 298 1.0
297 299 1.0
300 301 1.0
300 302 1.0
303 304 1.0
303 305 1.0
306 307 1.0

End
Lattice
      15.0000000000      0.0000000000      0.0000000000
      0.0000000000     15.0000000000      0.0000000000
      0.0000000000      0.0000000000     15.0000000000

End
End

Engine Hybrid
  Engine ForceField ForceField1
    Type UFF
  EndEngine

  Engine ForceField ForceField2
    Type UFF
  EndEngine

QMMM
```

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```

Embedding Mechanical
mmEngineID ForceField2
qmEngineID ForceField1
qmRegion qm
End

GuessAttributesOnce No
EndEngine

RNGSeed 1
eor

#####
# The constrained values are stored in the file named COLVAR.
# Below we use Python to read the COLVAR file, and print the averages for max({r_QM})
↳and min({r_MM}).
#####

$AMSBIN/amspython << eor
infile = open('COLVAR')
lines = infile.readlines()
infile.close()

maxdist = [float(line.split()[1]) for line in lines[1:]]
mindist = [float(line.split()[2]) for line in lines[1:]]
print()
print('Average of max QM O-Eu distance: ',sum(maxdist)/len(maxdist))
print('Average of min MM O-Eu distance: ',sum(mindist)/len(mindist))
eor

```

11.7.6 Example: Measuring the friction coefficient using NEMD

Download MD_friction.run

```

#!/bin/sh

# This example measures the friction coefficient between two diamond slabs.
#
# The top slab (B) is being pressed onto slab A by a -Z force while being pulled in
↳the +X direction
# with a velocity of 200 m/s. The normal force used in this test is very high (5 nN
↳per atom in B,
# corresponding to a pressure around 20 GPa) to make the friction coefficient
↳measurably nonzero.

"$AMSBIN/ams" << eor
# Set the RNG seed to make results reproducible for regression testing, delete this
↳line for real simulations
RNGSeed 1354700531 -1828372117 1981811283 531897225 -1777170443 -138867001 572543905 -
↳1932870903

Task MolecularDynamics
MolecularDynamics
  NSteps 10000
  TimeStep 2

```

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```

Trajectory
  SamplingFreq 10
  WriteEngineGradients Yes
  WriteVelocities No
  WriteCharges No
  WriteBonds No
  WriteMolecules No
End
InitialVelocities
  Temperature 300
End
Thermostat
  Type NHC
  Temperature 300
  Tau 100
  Region free
End
ApplyVelocity
  Velocity 0.002 0 0
  Components XY
  Region B
End
ApplyForce
  Force 0.0 0.0 -160e-9 [Newton]
  Region B
End
End
System
  Atoms
    C 1.32194823 1.26633023 1.67762819 region=A,free
    C 1.32194823 1.26633023 9.42762819 region=B,free
    C 1.32194823 3.79899068 1.67762819 region=A,free
    C 1.32194823 3.79899068 9.42762819 region=B,free
    C 3.9658447 1.26633023 1.67762819 region=A,free
    C 3.9658447 1.26633023 9.42762819 region=B,free
    C 3.9658447 3.79899068 1.67762819 region=A,free
    C 3.9658447 3.79899068 9.42762819 region=B,free
    C 0.0 1.26633023 0.78253111 region=A,free
    C 0.0 1.26633023 8.532531110000001 region=B,free
    C 0.0 3.79899068 0.78253111 region=A,free
    C 0.0 3.79899068 8.532531110000001 region=B,free
    C 2.64389647 1.26633023 0.78253111 region=A,free
    C 2.64389647 1.26633023 8.532531110000001 region=B,free
    C 2.64389647 3.79899068 0.78253111 region=A,free
    C 2.64389647 3.79899068 8.532531110000001 region=B,free
    C 0.0 0.0 3.48183649 region=A,free
    C 0.0 0.0 11.23183649 region=B,free
    C 0.0 2.53266045 3.48183649 region=A,free
    C 0.0 2.53266045 11.23183649 region=B,free
    C 2.64389647 0.0 3.48183649 region=A,free
    C 2.64389647 0.0 11.23183649 region=B,free
    C 2.64389647 2.53266045 3.48183649 region=A,free
    C 2.64389647 2.53266045 11.23183649 region=B,free
    C 1.32194823 0.0 6.07181582 region=A,free
    C 1.32194823 0.0 13.82181582 region=B,free
    C 1.32194823 2.53266045 6.07181582 region=A,free
    C 1.32194823 2.53266045 13.82181582 region=B,free

```

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```
C 3.9658447 0.0 6.07181582 region=A,free
C 3.9658447 0.0 13.82181582 region=B,free
C 3.9658447 2.53266045 6.07181582 region=A,free
C 3.9658447 2.53266045 13.82181582 region=B,free
C 1.32194823 1.26633023 5.28928471 region=A,free
C 1.32194823 1.26633023 13.03928471 region=B,free
C 1.32194823 3.79899068 5.28928471 region=A,free
C 1.32194823 3.79899068 13.03928471 region=B,free
C 3.9658447 1.26633023 5.28928471 region=A,free
C 3.9658447 1.26633023 13.03928471 region=B,free
C 3.9658447 3.79899068 5.28928471 region=A,free
C 3.9658447 3.79899068 13.03928471 region=B,free
C 0.0 1.26633023 4.39418763 region=A,free
C 0.0 1.26633023 12.14418763 region=B,free
C 0.0 3.79899068 4.39418763 region=A,free
C 0.0 3.79899068 12.14418763 region=B,free
C 2.64389647 1.26633023 4.39418763 region=A,free
C 2.64389647 1.26633023 12.14418763 region=B,free
C 2.64389647 3.79899068 4.39418763 region=A,free
C 2.64389647 3.79899068 12.14418763 region=B,free
C 0.0 0.0 0.0 region=A,fixed
C 0.0 0.0 7.75 region=B,free
C 0.0 2.53266045 0.0 region=A,fixed
C 0.0 2.53266045 7.75 region=B,free
C 2.64389647 0.0 0.0 region=A,fixed
C 2.64389647 0.0 7.75 region=B,free
C 2.64389647 2.53266045 0.0 region=A,fixed
C 2.64389647 2.53266045 7.75 region=B,free
C 1.32194823 0.0 2.58997933 region=A,free
C 1.32194823 0.0 10.33997933 region=B,free
C 1.32194823 2.53266045 2.58997933 region=A,free
C 1.32194823 2.53266045 10.33997933 region=B,free
C 3.9658447 0.0 2.58997933 region=A,free
C 3.9658447 0.0 10.33997933 region=B,free
C 3.9658447 2.53266045 2.58997933 region=A,free
C 3.9658447 2.53266045 10.33997933 region=B,free

End
Lattice
  5.28779292 0.0 0.0
  0.0 5.06532092 0.0

End
BondOrders
  1 9 1.0
  1 13 1.0
  2 10 1.0
  2 14 1.0
  3 11 1.0
  3 15 1.0
  4 12 1.0
  4 16 1.0
  5 9 1.0 1 0
  5 13 1.0
  6 10 1.0 1 0
  6 14 1.0
  7 11 1.0 1 0
  7 15 1.0
  8 12 1.0 1 0
```

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```
8 16 1.0
33 25 1.0
33 27 1.0
33 41 1.0
33 45 1.0
34 26 1.0
34 28 1.0
34 42 1.0
34 46 1.0
35 25 1.0 0 1
35 27 1.0
35 43 1.0
35 47 1.0
36 26 1.0 0 1
36 28 1.0
36 44 1.0
36 48 1.0
37 29 1.0
37 31 1.0
37 41 1.0 1 0
37 45 1.0
38 30 1.0
38 32 1.0
38 42 1.0 1 0
38 46 1.0
39 29 1.0 0 1
39 31 1.0
39 43 1.0 1 0
39 47 1.0
40 30 1.0 0 1
40 32 1.0
40 44 1.0 1 0
40 48 1.0
41 17 1.0
41 19 1.0
42 18 1.0
42 20 1.0
43 17 1.0 0 1
43 19 1.0
44 18 1.0 0 1
44 20 1.0
45 21 1.0
45 23 1.0
46 22 1.0
46 24 1.0
47 21 1.0 0 1
47 23 1.0
48 22 1.0 0 1
48 24 1.0
49 9 1.0
49 11 1.0 0 -1
50 10 1.0
50 12 1.0 0 -1
51 9 1.0
51 11 1.0
52 10 1.0
52 12 1.0
```

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```
53 13 1.0
53 15 1.0 0 -1
54 14 1.0
54 16 1.0 0 -1
55 13 1.0
55 15 1.0
56 14 1.0
56 16 1.0
57 1 1.0
57 3 1.0 0 -1
57 17 1.0
57 21 1.0
58 2 1.0
58 4 1.0 0 -1
58 18 1.0
58 22 1.0
59 1 1.0
59 3 1.0
59 19 1.0
59 23 1.0
60 2 1.0
60 4 1.0
60 20 1.0
60 24 1.0
61 5 1.0
61 7 1.0 0 -1
61 17 1.0 1 0
61 21 1.0
62 6 1.0
62 8 1.0 0 -1
62 18 1.0 1 0
62 22 1.0
63 5 1.0
63 7 1.0
63 19 1.0 1 0
63 23 1.0
64 6 1.0
64 8 1.0
64 20 1.0 1 0
64 24 1.0
End
End
Constraints
  FixedRegion fixed
End
Engine ForceField
EndEngine
eor
"$AMSBIN/amspython" "${TEST_DIRECTORY:-.}/friction_coeff.py" --block 200 ams.results/
echo "END OF TEST"
```

11.7.7 Example: Measuring the viscosity using NEMD

Download MD_shear_viscosity.run

```
#!/bin/sh

# This example performs a NEMD simulation of a water box under a shear acceleration_
↪profile.
# The acceleration profile is cosine-shaped and oriented along the Z axis (so that_
↪atoms with Z=0 are
# pulled in one direction, atoms in the middle of the box are pulled the other way)_
↪The flow direction
# is aligned with the X axis.
#
# This periodic perturbation induces a similarly cosine-shaped flow velocity profile_
↪in the liquid.
# The steady-state average amplitude of the flow velocity is then used to calculate_
↪the viscosity.

"$AMSBIN/ams" << eor
# Set the RNG seed to make results reproducible for regression testing, delete this_
↪line for real simulations
RNGSeed 836841470 1678420146 -1718043284 -369569254 -2053894812 -1628712594 -
↪240676301 -356441007

Task MolecularDynamics
MolecularDynamics
  NSteps 24000
  TimeStep 1
  InitialVelocities
    Type Random
    Temperature 298.15
  End
  Thermostat
    Type NHC
    Temperature 298.15
    Tau 1000
  End
  CosineShear
    Enabled Yes
    Acceleration 0.000004522108063030400
  End
End
System
  Atoms
    O 0.82444444545793177 4.544838021389278 7.080687151044827 ForceField.Type=OW_
↪ForceField.Charge=-0.834
    H 0.3547827848924093 4.719510963847915 7.916536224904227 ForceField.Type=HW_
↪ForceField.Charge=0.417
    H 1.355721739229628 5.344893665481732 6.975525637919818 ForceField.Type=HW_
↪ForceField.Charge=0.417
    O 4.824211318207558 0.8069313216022225 7.759825120988862 ForceField.Type=OW_
↪ForceField.Charge=-0.834
    H 4.514558713823999 1.280197293066311 8.558923240175481 ForceField.Type=HW_
↪ForceField.Charge=0.417
    H 4.033391063195659 0.7201928228115005 7.187127164561153 ForceField.Type=HW_
↪ForceField.Charge=0.417
    O 2.934572969015879 0.626831742380179 5.865967452739235 ForceField.Type=OW_
↪ForceField.Charge=-0.834
```

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```
H 2.151893964459041 1.137329352693095 6.027000900498897 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 3.263433084806719 1.048186940192297 5.040531567587069 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 1.206430947463354 1.856002602957112 9.003428097539595 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 0.7495045796559563 2.685732546074114 9.186271372016726 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 0.5732201719526651 1.426252646404271 8.428676649867203 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 4.00858752820043 4.029996794081304 5.583951652401872 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 4.6767739512274 4.347838022636921 6.162932810282044 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 3.285915055183219 4.655218377978755 5.758534605518392 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 3.563629518129562 1.371347494469859 12.8855840322333 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 3.213171669104573 0.4819670684498465 12.77900015824002 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 3.044964414139814 1.734726370517266 13.59851543041306 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 0.3789251709796683 1.127496658856301 13.2115287736376 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 0.6813483419435356 1.239300575078584 14.13801389632943 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 5.369672396356584 1.083579289595597 13.29812675901156 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 5.466225740442832 5.993496838594383 3.826556322251799 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 4.698727888102344 0.3975271277797332 3.345862980059084 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 5.678590795097077 0.7684784866437412 4.409847532491263 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 5.308923379504553 4.019057754213824 12.30890772203438 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 4.947834409182614 3.130476283899112 12.54309710913415 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 4.507522419442757 4.539019535791192 12.2645840765018 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 0.5246189538877805 2.11444774753437 5.633847854203101 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 0.4798849442749721 2.981151461335371 6.079301327936341 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 0.1746402018766592 1.514431334250879 6.300570842670576 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 0.7532540279197091 1.724451179192218 15.61527324613631 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 1.102056945497837 1.316928430428979 16.4265184790613 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 0.7972987223637659 2.664620455755369 15.82837324135009 ForceField.Type=HW_
↔ForceField.Charge=0.417
O 0.9018681569836331 3.656882816889424 3.402291999454496 ForceField.Type=OW_
↔ForceField.Charge=-0.834
H 0.4026827408969129 4.459281159084593 3.630496065021554 ForceField.Type=HW_
↔ForceField.Charge=0.417
H 0.5526952071471827 3.010307298769798 4.02681327048169 ForceField.Type=HW_
↔ForceField.Charge=0.417
```

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```

O 4.863403687774274 0.9028609469360367 0.558021938995828 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 3.996919626672331 1.319885981099747 0.7021352725814224 ForceField.Type=HW
↔ForceField.Charge=0.417
H 4.689645967466681 5.893899093581502 0.6975454946677974 ForceField.Type=HW
↔ForceField.Charge=0.417
O 0.6125422333973695 4.471658272146462 15.20199530885226 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 5.757700386271314 4.628928071051244 14.72292292770029 ForceField.Type=HW
↔ForceField.Charge=0.417
H 0.4490343750054829 4.454474545873454 16.17738658790725 ForceField.Type=HW
↔ForceField.Charge=0.417
O 0.6366518329200573 4.752909677710202 9.952302751289087 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 0.9300822912913463 5.41930018832904 10.60529619335514 ForceField.Type=HW
↔ForceField.Charge=0.417
H 0.09536209451509015 4.185550544321785 10.53226705454537 ForceField.Type=HW
↔ForceField.Charge=0.417
O 1.973521991893519 4.136851000321193 0.9323878175561867 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 1.958801293505274 4.982561965771234 0.471890391343053 ForceField.Type=HW
↔ForceField.Charge=0.417
H 1.500116599864132 4.339560036883479 1.75645305944565 ForceField.Type=HW
↔ForceField.Charge=0.417
O 4.912922003545703 4.048464241294365 1.122473368577996 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 5.258380821455368 3.682506383808921 1.973193063451997 ForceField.Type=HW
↔ForceField.Charge=0.417
H 3.961611234368922 3.899191033445874 1.229424459523123 ForceField.Type=HW
↔ForceField.Charge=0.417
O 3.68652628868048 1.595323244715648 10.09294194440881 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 2.716738755606992 1.65284789480996 9.785054765941782 ForceField.Type=HW
↔ForceField.Charge=0.417
H 3.717820588318913 1.493830202223642 11.06393026159224 ForceField.Type=HW
↔ForceField.Charge=0.417
O 2.322791158566589 4.525494429167161 13.13712396271713 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 1.684244052546178 4.292584907055148 12.46669482040438 ForceField.Type=HW
↔ForceField.Charge=0.417
H 1.713022179274242 4.656194947137037 13.91280050486365 ForceField.Type=HW
↔ForceField.Charge=0.417
O 1.531573866397418 1.053168936091418 0.3718291838441352 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 1.522293261003647 2.011561261078512 0.5486474226338094 ForceField.Type=HW
↔ForceField.Charge=0.417
H 0.5646086101553838 0.8818604575421908 0.3306918436047358 ForceField.Type=HW
↔ForceField.Charge=0.417
O 3.418411885135323 2.370515151746976 3.6606774188027 ForceField.Type=OW
↔ForceField.Charge=-0.834
H 2.581438388703135 2.63052383259613 3.242613350177665 ForceField.Type=HW
↔ForceField.Charge=0.417
H 3.469669459117304 3.023705121589598 4.375706151452582 ForceField.Type=HW
↔ForceField.Charge=0.417
End
Lattice
5.952918007318143 0.0 0.0

```

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```
0.0 5.952918007318143 0.0
0.0 0.0 17.85875402195457
End
BondOrders
  1 2 1.0
  1 3 1.0
  4 5 1.0
  4 6 1.0
  7 8 1.0
  7 9 1.0
 10 11 1.0
 10 12 1.0
 13 14 1.0
 13 15 1.0
 16 17 1.0
 16 18 1.0
 19 20 1.0
 19 21 1.0 -1 0 0
 22 23 1.0 0 1 0
 22 24 1.0 0 1 0
 25 26 1.0
 25 27 1.0
 28 29 1.0
 28 30 1.0
 31 32 1.0
 31 33 1.0
 34 35 1.0
 34 36 1.0
 37 38 1.0
 37 39 1.0 0 -1 0
 40 41 1.0 -1 0 0
 40 42 1.0
 43 44 1.0
 43 45 1.0
 46 47 1.0
 46 48 1.0
 49 50 1.0
 49 51 1.0
 52 53 1.0
 52 54 1.0
 55 56 1.0
 55 57 1.0
 58 59 1.0
 58 60 1.0
 61 62 1.0
 61 63 1.0
End
End
Engine ForceField
  Type Amber95
EndEngine
eor

# The following script extracts the induced velocity amplitude and calculates the
# corresponding viscosity
#
```

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```
# The --test argument is only useful for regression testing
"$AMSBIN/amspython" "${TEST_DIRECTORY:-.}/analyze_cosine_shear.py" --test --from 41 --
↳block 100 ams.results/
echo "END OF TEST"
```

11.8 Trajectory replay

11.8.1 Example: Trajectory replays for PES scans, NEB and MD calculations

Download `Replay.run`

```
#!/bin/sh

# 1. Replay of PES scans
# =====

AMS_JOBNAME=pesscan "$AMSBIN/ams" << eor

Task PESScan

PESScan
  ScanCoordinate
    nPoints 6
    Dihedral 5 1 2 6 0.0 50
    Dihedral 4 1 2 3 0.0 50
  End
  ScanCoordinate
    nPoints 7
    Distance 1 2 1.2 1.5
  End
End

System
  Atoms
    C 0.0 -0.0 0.66687
    C 0.0 -0.0 -0.33313
    H 0.0 0.92974 -0.90538
    H 0.0 0.92974 1.23912
    H 0.0 -0.92974 1.23912
    H 0.0 -0.92974 -0.90538
  End
End

Engine ForceField
EndEngine

eor

AMS_JOBNAME=replay_pesscan "$AMSBIN/ams" << eor

Task Replay
```

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```

Replay
  File pesscan.results
  StoreAllResultFiles Yes
End

Properties
  Gradients True
End

Engine DFTB
EndEngine

eor

echo "Start extracting data from ams.rkf ..."
echo "Number of frames on file:"
$AMSBIN/amsreport replay_pesscan.results/ams.rkf -r 'History%nEntries'
frame=1
while [ $frame -le 42 ]; do
  echo "Frame: $frame"
  $AMSBIN/amsreport replay_pesscan.results/ams.rkf -r "History%Energy($frame) "
  $AMSBIN/amsreport replay_pesscan.results/ams.rkf -r "History%Gradients($frame) "
  frame=$((expr $frame + 1))
done
echo "Data in PESScan section:"
$AMSBIN/amsreport replay_pesscan.results/ams.rkf -r 'PESScan%PESCoords'
$AMSBIN/amsreport replay_pesscan.results/ams.rkf -r 'PESScan%PES'
$AMSBIN/amsreport replay_pesscan.results/ams.rkf -r 'PESScan%HistoryIndices'
echo "Data extracted."

# 2. Replay of NEB calculations
# =====

AMS_JOBNAME=neb "$AMSBIN/ams" << eor

Task NEB

NEB
  Images 16
End

GeometryOptimization
  Convergence
    Energy 1.0e-4
    Gradients 1.0e-2
  End
End

System
  Atoms
    C -0.04837097189972882 0.002828754545985427 1.099927275387085
    C -0.7231327687579711 -1.264630955508361 1.591341080262239
    C -0.7174118987979032 1.275587203448819 1.585489846719994

```

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```

H -1.758221225827696 -1.294861009536393 1.215612210647893
H -0.7536609466556244 -1.286949469754588 2.689737906089842
H 0.02700743800283175 0.0001348498227195367 0.004547638456250216
H -0.7481941882345999 1.302956664081095 2.683766567353197
H -0.1880537663322776 2.167332127899618 1.228056629315197
H -1.752232117403696 1.308927696210993 1.209290912745431
H -0.1979764470101184 -2.160385916691095 1.237731888775011
Cl 1.710726893919094 4.005547128448699e-05 1.649098041095717

End
End
System final
  Atoms
    C -0.8173023574499557 -0.01408167289928656 0.8544841004283144
    C -1.086263680920393 -1.14724517989661 1.518039806717775
    C -0.8990221290639472 1.362120508644236 1.43231282384412
    H -1.018446188967536 -2.121649215821082 1.03173453221026
    H -1.404982357822256 -1.129945575549278 2.563696578967125
    H -0.5085933307712909 -0.08344191227560969 -0.1948268157146379
    H -1.210244367762068 1.342173382164807 2.485525533439326
    H 0.07413947140246446 1.873805664554979 1.364278897383801
    H -1.616521025856608 1.9769362830809 0.8657976784252567
    H 1.044986335480545 -0.9543604705303219 1.922869894354733
    Cl 2.292729632733364 -1.053331811482705 2.350686966791855

  End
End

Engine DFTB
EndEngine

eor

AMS_JOBNAME=replay_neb "$AMSBIN/ams" << eor

Task Replay
Replay File=neb.results/ams.rkf

Engine ADF
  NumericalQuality Basic
EndEngine

eor

echo "Start extracting data from ams.rkf ..."
echo "Number of frames on file:"
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'History%nEntries'
frame=1
while [ $frame -le 16 ]; do
  echo "Frame: $frame"
  $AMSBIN/amsreport replay_neb.results/ams.rkf -r "History%Energy($frame)"
  frame=$((expr $frame + 1))
done
echo "Data in NEB section:"
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%nebIterations'
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%historyIndex@dim'
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%historyIndex'

```

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```

$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%energy'
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%highestIndex'
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%LeftBarrier'
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%RightBarrier'
$AMSBIN/amsreport replay_neb.results/ams.rkf -r 'NEB%ReactionEnergy'
echo "Data extracted."

# 3. Replay of generic history (e.g. MD)
# =====

AMS_JOBNAME=md "$AMSBIN/ams" << eor

Task MolecularDynamics

MolecularDynamics
  nSteps 1000
  InitialVelocities Type=Zero
  Trajectory SamplingFreq=10
End

System
  Atoms
    O      5.84400000    0.31970000    0.89540000
    H      1.17000000    0.12750000   -2.13090000
    H     -0.61000000   -1.28280000   -1.84810000
    H     -0.57930000   -0.70680000    1.15800000
    C     -3.12520000    0.09550000    0.94430000
    C     -3.19980000   -1.42460000    1.23360000
    C     -2.05280000    0.23760000   -0.14210000
    C     -1.27100000    1.53130000   -0.13370000
    C     -0.13080000    1.46490000   -1.14670000
    C     -2.05030000   -2.08490000    0.42320000
    C     -1.08120000   -0.91390000    0.20520000
    C      0.72590000    0.20890000   -1.09890000
    C     -0.07070000   -1.07000000   -0.90020000
    C      1.91880000    0.37840000   -0.17010000
    C      2.85070000    1.44940000   -0.76420000
    C      4.06090000    1.66070000    0.14280000
    C      0.79940000   -2.27110000   -0.66800000
    C      2.70610000   -0.90160000   -0.05510000
    C      4.70630000    0.33980000    0.46480000
    C      2.06470000   -2.18950000   -0.28730000
    C      4.02370000   -0.86790000    0.26480000
    C      1.49560000    0.82380000    1.22970000
    C     -2.72010000    0.03450000   -1.50220000
    C     -4.44990000    0.59620000    0.43260000
    O     -5.21170000   -0.16370000   -0.11570000
    C     -4.82510000    2.04560000    0.60460000
    H     -2.82710000    0.64000000    1.83720000
    H     -3.05600000   -1.60950000    2.29900000
    H     -4.16120000   -1.82340000    0.91220000
    H     -1.95080000    2.35390000   -0.41170000
    H     -0.90510000    1.74180000    0.87040000
    H     -0.54560000    1.56290000   -2.16020000
    H      0.51310000    2.34310000   -1.00320000
    H     -1.56740000   -2.86790000    1.01220000

```

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```

H      -2.40770000      -2.48600000      -0.52040000
H      3.18420000       1.11610000      -1.74960000
H      2.30420000       2.38610000      -0.86930000
H      4.79290000       2.28810000      -0.38330000
H      3.77550000       2.17310000       1.05860000
H      0.36740000      -3.25490000      -0.82120000
H      2.63690000      -3.09890000      -0.14660000
H      4.55990000      -1.80060000       0.37040000
H      0.83020000       0.07700000       1.66290000
H      2.37890000       0.93230000       1.85900000
H      0.97580000       1.77970000       1.16520000
H     -3.42010000       0.84890000      -1.68870000
H     -1.95890000       0.02380000      -2.28240000
H     -3.25700000      -0.91410000      -1.50550000
H     -4.48270000       2.61460000      -0.25970000
H     -5.90820000       2.13270000       0.69120000
H     -4.35580000       2.43770000       1.50690000
End
End

Engine ReaxFF
  ForceField CHON-2019.ff
EndEngine

eor

AMS_JOBNAME=replay_md "$AMSBIN/ams" << eor

Task Replay
Replay
  File md.results/
  Frames 1:101:10
End

Properties
  Gradients True
  BondOrders True
End

Engine DFTB
EndEngine

eor

echo "Start extracting data from ams.rkf ..."
echo "Number of frames on file:"
$AMSBIN/amsreport replay_md.results/ams.rkf -r 'History%nEntries'
frame=1
while [ $frame -le 11 ]; do
  echo "Frame: $frame"
  $AMSBIN/amsreport replay_md.results/ams.rkf -r "History%Energy($frame) "
  $AMSBIN/amsreport replay_md.results/ams.rkf -r "History%Bonds.Index($frame) "
  $AMSBIN/amsreport replay_md.results/ams.rkf -r "History%Bonds.Atoms($frame) "
  $AMSBIN/amsreport replay_md.results/ams.rkf -r "History%Bonds.Orders($frame) #8.2f"
  frame=$((expr $frame + 1))
done

```

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```
done
echo "Data extracted."
```

11.9 Vibrational analysis

11.9.1 Example: Mode Refinement

Download VAtools_dydrogesterone.run

```
#!/bin/sh

# This example shows a mode refinement of the band associated with the
# C=O and C=C stretch modes in the dydrogesterone molecule. This was one
# of the example calculations in the original paper on mode refinement:
#
#   J. Phys. Chem. Lett., 2018, 9 (23), pp 6878-6882

# Step 1: Get DFTB modes at the optimized DFT geometry
# -----

AMS_JOBNAME=FREQ_DFTB $AMSBIN/ams << EOF

System
Atoms
# Dydrogesterone geometry already optimized with DFT (BP86/TZP).
C 0.179402320119871 1.1462568499773749 -1.34045805553897
C -1.0397129548582973 1.4038864822738149 -0.42742864655449175
C -1.9187723039939633 0.15407663507305838 -0.2887082902723144
C 5.26339021966562 -0.0803229279006518 0.15901574737297627
C 4.387948120190181 -1.2500901532169464 0.1985138671042922
C 3.0305058270434313 -1.2006020082109579 0.06687676611264043
C 2.2733069275281843 0.12162323554336309 -0.08656132560038762
C 3.224495049036027 1.1562588842598234 -0.7427294996476081
C 4.589580248129175 1.2673670000240371 -0.055599205726051454
C -2.593712600512111 -0.1967276203097069 -1.6287069723510241
C -2.011183672049868 -2.0904848406306247 0.6637924766824627
C -3.24333170765593 -1.3040476226855777 1.1949612943873085
C -2.9910039148987044 0.19289628304945772 0.8647395097635705
C 1.8832501895313913 0.6066618903839885 1.3319251022509289
C -1.021215985785471 -0.9883577256376227 0.2595406535945511
C 0.950572917185341 -2.499497885394989 -0.17845795742396
C 2.2618422613458535 -2.429295894019406 0.12998062227671012
C 0.14931427176016024 -1.3398555308999998 -0.6810919840203331
C 1.0424571714734645 -0.11148243146945544 -1.0381151732514977
C -4.261014768367461 0.9709543041281233 0.5302962418813911
C -4.2770282131623745 2.4457823410117943 0.8829249061723259
O -5.23153866013212 0.4348316478674291 0.006835058476534351
O 6.486629619384615 -0.1787206146841789 0.3101830744372818
H 4.496419281348679 1.7413060958817603 0.9361407723186962
H 4.889108126023183 -2.2103967123783246 0.34783394165927906
H -2.5053803890738937 0.6948315694295174 1.7185731459759712
H 2.747947397670055 2.147017249296297 -0.7608107343500633
```

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```

H 3.3788188981072294 0.8618896159833123 -1.7937886227370627
H 5.278515387629924 1.9033945262275014 -0.6280820487414189
H -0.313881863508176 -1.6818474813482587 -1.6263008186833716
H 2.7970964757389787 -3.3338033858599037 0.4312075853898926
H 0.4355882565839679 -3.460258453470549 -0.09628540747796212
H 2.7788926695047853 0.7904363143118734 1.939504792825026
H 1.3142558486724543 1.5445870277271823 1.281760102768146
H 1.2817550339094792 -0.13839730232383732 1.865618408504196
H 1.519857325493626 -0.37989780969443004 -1.9963570252289853
H -3.35526145791249 2.9466219355670638 0.5538746959825623
H -0.5844412872674496 -0.5966200898063014 1.193600037988863
H 0.8128688006525261 2.043605920072621 -1.3496094336049678
H -0.18858319204633375 1.0503960522723468 -2.3730012879550473
H -1.6112343483079186 2.2461900431605373 -0.8495116990527544
H -0.710640496667605 1.7174589936204205 0.5760379282354502
H -1.5937002785491352 -2.7672883134736264 1.4205298630102559
H -2.2836000112559893 -2.709635208733019 -0.2046201598348845
H -3.3761548431942434 -1.4386051747789588 2.276540650869438
H -4.174084527825135 -1.628156544022731 0.7132317870749941
H -1.860827847389362 -0.4325042173503644 -2.4102132115597854
H -3.2757258446436426 -1.0505046678063983 -1.5382984747892279
H -3.1932088604642455 0.6502553019056425 -1.9892714020438331
H -4.314908973244162 2.55066722711135 1.9790476680048945
H -5.155478941054673 2.9311753898910595 0.44480850527661253
End
End

Task SinglePoint

Properties
  NormalModes Yes
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-freq-1-2
EndEngine

EOF

# Step 2: Mode refinement of the DFTB C=O and C=C stretch bands at the DFT level
# -----

AMS_JOBNAME=ModeRefinement $AMSBIN/ams << EOF

  LoadSystem
    File FREQ_DFTB.results/dftb.rkf
  End

Task VibrationalAnalysis

VibrationalAnalysis
  Type ModeRefinement
  NormalModes
    ModeFile FREQ_DFTB.results/dftb.rkf
  ModeSelect

```

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```

        FreqRange 1500 1800
    End
End
End

Engine BAND
# Settings from the paper:
XC
    GGA BP86
End
Basis
    Type DZP
End
Relativity Level=None
# Just to make this test run faster:
NumericalQuality Basic
Convergence Criterion=1e-6 # results quite sensitive to this
SCF Method=DIIS # slightly faster because mix is inherited with restarts, not
↳so for the MultiStepper.
EndEngine

EOF

```

11.9.2 Example: Mode Tracking

Download VATools_cyclohexanone.run

```

#!/bin/sh

# This example demonstrates the usage of the AMS vibrational analysis tools
# on the cyclohexanone molecule.

# 1. Optimization with DFT
# -----

AMS_JOBNAME=DFT $AMSBIN/ams << EOF

System
Atoms
C      0.000000    0.000000    0.000000
C      0.978606    1.950589   -1.251328
C      0.978606    1.950589    1.251328
C      0.812569    2.806732    0.000000
C     -0.039622    0.802151    1.272926
C     -0.039622    0.802151   -1.272926
O      0.062619   -1.251283    0.000000
H      0.123306    0.119861    2.122758
H     -1.060012    1.229063    1.372200
H      0.871524    2.560541    2.167037
H      2.001065    1.521810    1.263746
H     -0.196785    3.268312    0.000000
H      1.549313    3.631809    0.000000
H      0.871524    2.560541   -2.167037
H      2.001065    1.521810   -1.263746

```

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```

      H      0.123306    0.119861   -2.122758
      H     -1.060012    1.229063   -1.372200
    End
  End

  Task GeometryOptimization

  GeometryOptimization
    Convergence Gradients=1.0e-4
  End

  Engine BAND
  EndEngine

EOF

# 2. Obtain DFTB hessian and modes as preconditioner and guess
# -----

AMS_JOBNAME=DFTB $AMSBIN/ams << EOF

  LoadSystem
    File DFT.results/ams.rkf
  End

  Task GeometryOptimization

  GeometryOptimization
    Convergence Gradients=1.0e-4
  End

  Properties
    NormalModes Yes
  End

  Engine DFTB
    Model DFTB3
    ResourcesDir DFTB.org/3ob-freq-1-2
  EndEngine

EOF

# 3. ModeScanning of DFTB C=O stretch mode with DFT
# -----

AMS_JOBNAME=ModeScanning $AMSBIN/ams << EOF

  LoadSystem
    File DFTB.results/ams.rkf
  End
  LoadEngine DFT.results/band.rkf

  Task VibrationalAnalysis

  VibrationalAnalysis

```

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```
Type ModeScanning
NormalModes
  ModeFile DFTB.results/dftb.rkf
  ModeSelect
    HighIR 1 # This should select the C=O stretch
  End
End
End
EOF

# 4. Mode tracking with DFT starting from DFTB C=O stretch mode
# -----

AMS_JOBNAME=ModeTracking $AMSBIN/ams << EOF

LoadSystem
  File DFT.results/ams.rkf
End
LoadEngine DFT.results/band.rkf

Task VibrationalAnalysis

VibrationalAnalysis
  Type ModeTracking
  ModeTracking
    HessianGuess File
    HessianPath DFTB.results
  End
  NormalModes
    ModeInputFormat File
    ModeFile DFTB.results/dftb.rkf
    ModeSelect
      HighIR 1 # This should select the C=O stretch
    End
  End
End
EOF

# 5. Mode tracking with DFT starting from a pure C=O stretch
# -----

AMS_JOBNAME=ModeTracking_COSTretch $AMSBIN/ams << EOF

LoadSystem
  File DFT.results/ams.rkf
End
LoadEngine DFT.results/band.rkf

Task VibrationalAnalysis

VibrationalAnalysis
  Type ModeTracking
  NormalModes
```

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```

ModeInputFormat Inline
ModeInline
  0.0  0.0  0.7071 # This is the C attached to the O
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0 -0.7071 # This is the O
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
  0.0  0.0  0.0
End
ModeSelect
  HighIR 1 # This should select the C=O stretch
End
End
ModeTracking
  HessianGuess File
  HessianPath DFTB.results
  TrackingMethod OverlapPrevious
                #      ^-- Probably better than the default.
                #      Our initial mode is not particularly close yet ...
End
End
EOF

```

11.9.3 Example: Vibronic-Structure Tracking

Download `VST_pyrene.run`

```

#!/bin/sh

# This example demonstrates the usage of vibronic-structure tracking
# on the pyrene molecule. Excited state calculations are performed within AMS and
# at the DFTB level

# 1. Ground state optimization with DFTB
#-----

AMS_JOBNAME=GroundState $AMSBIN/ams << eor

System
  Atoms
    C      -0.01654981      1.36506537      0.00802668
    C      0.00281590      -0.06808050      0.00051978

```

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```
C      1.19835953      2.08859192      0.00127327
C      -1.25056871      2.05539572      0.02157814
C      1.23682878      -0.75840671     -0.01375673
C      -1.21209870     -0.79160461      0.00671225
C      2.44308841      1.35898462     -0.01256813
C      1.16450680      3.48665407      0.00772934
C      -2.47512291      1.29231475      0.02824995
C      -1.25452039      3.45386389      0.02759561
C      2.46138768      0.00467142     -0.01984509
C      1.24076149     -2.15686407     -0.02209661
C      -2.45682219     -0.06199957      0.02121310
C      -1.17826305     -2.18965609     -0.00177638
C      -0.05432386      4.15935390      0.02049748
C      0.04055488     -2.86234799     -0.01620562
H      3.36596464      1.93801392     -0.01731234
H      2.09583666      4.04986513      0.00239299
H      -3.41330596      1.84611463      0.03902307
H      -2.20073438      3.99162601      0.03767421
H      3.39957176     -0.54912830     -0.03053168
H      2.18696724     -2.69462025     -0.03320657
H      -3.37969722     -0.64102946      0.02611688
H      -2.10959908     -2.75286422      0.00274662
H      -0.06904859      5.24837501      0.02503968
H      0.05526108     -3.95135857     -0.02284989
End
End

Task GeometryOptimization

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-freq-1-2
EndEngine

eor

# 2. Get lowest singlet-singlet excitation of pyrene and
# compute the excited state gradient at the optimized GS geometry
#-----

AMS_JOBNAME=ExcitedState $AMSBIN/ams << eor

Task SinglePoint
LoadSystem
  File ./GroundState.results/dftb.rkf
End

Properties
  Gradients yes
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-freq-1-2
  Properties
    Excitations
      TDDFTB
```

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```

        Calc Singlet
        Lowest 1
    End
    TDDFTBGradients
        Excitation 1
    End
End
End
EndEngine

eor

# 3. Vibronic-structure tracking for this excitation
# -----

AMS_JOBNAME=VibronicStructure $AMSBIN/ams << eor

LoadSystem
    File ./GroundState.results/dftb.rkf
End

Task VibrationalAnalysis

VibrationalAnalysis
    Type VibronicStructureTracking
    ExcitationSettings
        ExcitationInputFormat File
        ExcitationFile ./ExcitedState.results/dftb.rkf
        Singlet
        A 1
    End
End
AbsorptionSpectrum
    AbsorptionRange -500.0 4000.0
    LineWidth 100
    FrequencyGridPoints 181
End
End

Engine DFTB
    Model DFTB3
    ResourcesDir DFTB.org/3ob-freq-1-2
EndEngine

eor

# 4. Restart the VST run from the previous one
# We have changed our mind and we want
# the peaks to be a little sharper
# -----

AMS_JOBNAME=VibronicStructureRestart $AMSBIN/ams << eor

LoadSystem
    File ./GroundState.results/dftb.rkf
End

```

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```

Task VibrationalAnalysis

VibrationalAnalysis
  Type VibronicStructureTracking
  ExcitationSettings
    ExcitationInputFormat File
    ExcitationFile ./ExcitedState.results/dftb.rkf
    Singlet
      A 1
    End
  End
  VSTRestartFile ./VibronicStructure.results/ams.rkf
  AbsorptionSpectrum
    AbsorptionRange -500.0 4000.0
    LineWidth 50
    FrequencyGridPoints 181
  End
End

Engine DFTB
  Model DFTB3
  ResourcesDir DFTB.org/3ob-freq-1-2
EndEngine

eor

```

11.10 PES point properties

11.10.1 Example: Phonons for graphene

Download Phonons_Graphene.run

```

#!/bin/sh
AMS_JOBNAME=graphene $AMSBIN/ams << EOF

Task GeometryOptimization

GeometryOptimization
!   CoordinateType Cartesian
    OptimizeLattice True
    Convergence Gradients=1.0e-5
    Method Quasi-Newton
End

Properties
  Phonons True
End

NumericalPhonons
  SuperCell
    2 0
    0 2

```

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```

End
End

System
  Atoms
    C      0.000000000   -0.000000000   0.00000
    C      0.000000000   -1.420281662   0.00000
  End

  Lattice
    1.230000000   -2.130422493   0.000000000
    1.230000000    2.130422493   0.000000000
  End
End

Engine DFTB
  ResourcesDir Dresden
  Model DFTB0
  KSpace
    Type Symmetric
    Symmetric KInteg=9
  End
  Technical AnalyticalStressTensor=False # Not yet supported with symmetric k-
↪space grid ...
EndEngine

EOF

echo ""
echo "Begin TOC of result file"

$AMSBIN/dmpkf -n 1 graphene.results/dftb.rkf --toc

echo "End TOC of result file"

```

11.10.2 Example: Phonons with isotopes

Download Phonons_Isotopes.run

```

#!/bin/sh

# =====
# Phonons with default nuclear masses:
# =====

AMS_JOBNAME=defmasses $AMSBIN/ams << EOF

  Task SinglePoint

  Properties
    Phonons True
  End

  NumericalPhonons

```

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```
StepSize 0.01
SuperCell
  4
End
End

System
  Atoms
    C -2.42906152 -0.3445528299 -0.1353492062
    C -1.146891508 -1.134644249 0.1353492061
    H -2.429062041 0.004468895147 -1.185797304
    H -2.429062011 0.5753101439 0.4803683017
    H -1.146891017 -2.054507222 -0.4803683019
    H -1.146890987 -1.483665974 1.185797304
  End

  Lattice
    2.564338467 0.0 0.0
  End
End

Engine DFTB
  ResourcesDir QUASINANO2015
  Model DFTB0
  KSpace
    Type Symmetric
    Symmetric KInteg=9
  End
EndEngine

EOF

echo ""
echo "Begin TOC of result file"
$AMSBIN/dmpkf -n 1 defmasses.results/dftb.rkf --toc
echo "End TOC of result file"

# =====
# Phonons with two deuterium atoms:
# =====

AMS_JOBNAME=usermasses $AMSBIN/ams << EOF

  Task SinglePoint

  Properties
    Phonons true
  End

  NumericalPhonons
    StepSize 0.01
    SuperCell
      4
    End
  End
End
```

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```

System
  Atoms
    C  -2.42906152  -0.3445528299  -0.1353492062
    C  -1.146891508 -1.134644249    0.1353492061
    H  -2.429062041  0.004468895147  -1.185797304
    H  -2.429062011  0.5753101439   0.4803683017
    H  -1.146891017  -2.054507222    -0.4803683019  mass=2.014
    H  -1.146890987  -1.483665974    1.185797304   mass=2.014
  End
  Lattice
    2.564338467  0.0  0.0
  End
End

Engine DFTB
  ResourcesDir QUASINANO2015
  Model DFTB0
  KSpace
    Type Symmetric
    Symmetric KInteg=9
  End
EndEngine

EOF

echo ""
echo "Begin TOC of result file"
$AMSBIN/dmpkf -n 1 usermasses.results/dftb.rkf --toc
echo "End TOC of result file"

```

11.10.3 Example: User-defined Brillouin zone for phonon dispersion

Download Phonons_UserBZPath.run

```

#!/bin/sh

# This example shows how to specify a user-defined path through the
# Brillouin zone (BZ) when computing the phonon dispersion curves.

# Note: when computing the phonons, you should first run a geometry
# optimization (including relaxation of lattice vectors).
# Here we use a pre-optimized structure.

AMS_JOBNAME=BoronNitride $AMSBIN/ams << eor

Task SinglePoint

System
  Atoms
    B 0.0 0.0 0.0
    N 0.92538708336681 0.92538708336681 0.92538708336681
  End
  Lattice
    0.0 1.8507741667336 1.8507741667336
    1.8507741667336 0.0 1.8507741667336

```

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```
1.8507741667336 1.8507741667336 0.0
End
End
Properties
  Phonons Yes
End
NumericalPhonons
  SuperCell
    2 0 0
    0 2 0
    0 0 2
  End
  # Disable the automatically generated path though the BZ
  AutomaticBZPath No
  BZPath
    # In each 'Path' block you should define the vertices of the path
    # in fractional coordinates (with respect to the reciprocal lattice
    # vectors)
    # First segment: Gamma-X-W-K
    Path
      0.0 0.0 0.0 G
      0.5 0.0 0.5 X
      0.5 0.25 0.75 W
      0.375 0.375 0.75 K
    End
    # Second segment: Gamma-SomeRandomPoint
    Path
      0.0 0.0 0.0 G
      0.1 0.2 0.3 RandomPoint
    End
  End
End
End
Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/matsci-0-3
  KSpace Quality=Basic
EndEngine
eor
echo 'Content of phonon_curves section'
$AMSBIN/dmpkf BoronNitrade.results/dftb.rkf 'phonon_curves'
echo 'End content of phonon_curves section'
```


11.10.4 Example: Elastic tensor

Download ElasticTensor.run

```

#!/bin/sh

# === Diamond ===
AMS_JOBNAME=Diamond $AMSBIN/ams << EOF

Task GeometryOptimization

Properties
  ElasticTensor Yes
End

System
  Atoms
    C 0.44625 0.44625 2.23125
    C 2.23125 2.23125 2.23125
    C -2.23125 -2.23125 -2.23125
    C -0.44625 -0.44625 -2.23125
    C -0.44625 -2.23125 -0.44625
    C 1.33875 -0.44625 -0.44625
    C -2.23125 -0.44625 -0.44625
    C -0.44625 1.33875 -0.44625
    C -0.44625 -0.44625 1.33875
    C 1.33875 1.33875 1.33875
    C -1.33875 -1.33875 -1.33875
    C 0.44625 0.44625 -1.33875
    C 0.44625 -1.33875 0.44625
    C 2.23125 0.44625 0.44625
    C -1.33875 0.44625 0.44625
    C 0.44625 2.23125 0.44625
  End
  Lattice
    0.0 3.57 3.57
    3.57 0.0 3.57
    3.57 3.57 0.0
  End
End

GeometryOptimization
  OptimizeLattice Yes
  Convergence Quality=Good
End

Symmetry Tolerance=1e-6

Engine DFTB
  Model DFTB
  ResourcesDir DFTB.org/mio-1-1
  KSpace
    Type Symmetric
    Symmetric KInteg=3
  End
  Technical AnalyticalStressTensor=False # Not yet supported with symmetric k-
↔space grid.

```

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```
EndEngine

EOF

# === Boron-Nitride sheet ===

# 3x3 super-cell, default k-space sampling

AMS_JOBNAME=BN_sheet $AMSBIN/ams << EOF

Task GeometryOptimization

Properties
  ElasticTensor Yes
End

System
  Atoms
    N 3.76095075 0.723795 0.0
    N 5.01460112 2.89518114 0.0
    B -3.76095112 -2.17138614 0.0
    B -2.50730075 0.0 0.0
    B -1.25365038 2.17138614 0.0
    B -1.25365037 -2.17138614 0.0
    B 0.0 0.0 0.0
    B 1.25365037 2.17138614 0.0
    B 1.25365038 -2.17138614 0.0
    B 2.50730075 0.0 0.0
    B 3.76095112 2.17138614 0.0
    N -2.50730112 -1.44759114 0.0
    N -1.25365075 0.723795 0.0
    N -3.8e-07 2.89518114 0.0
    N -3.7e-07 -1.44759114 0.0
    N 1.25365 0.723795 0.0
    N 2.50730037 2.89518114 0.0
    N 2.50730038 -1.44759114 0.0
  End
  Lattice
    7.52190225 0.0
    3.76095111 6.51415842
  End
End

GeometryOptimization
  OptimizeLattice Yes
  Convergence Quality=Good
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/matsci-0-3
EndEngine

EOF
```

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```

# === Polyoxyethylene ===
# primitive cell with k-space sampling
AMS_JOBNAME=Polyoxyethylene $AMSBIN/ams << EOF

Task GeometryOptimization

Properties
  ElasticTensor Yes
End

ElasticTensor
  StrainStepSize 0.002
End

System
  Atoms
    C  -0.279368361  -0.125344097  -0.026221791
    O   0.840592835  -0.919621431  -0.193214154
    H  -0.279527057   0.337014408   0.997733792
    H  -0.281697417   0.707951120  -0.778297849
  End
  Lattice
    2.240292981
  End
End

GeometryOptimization
  OptimizeLattice Yes
  Convergence Quality=Good
End

Engine DFTB
  Model SCC-DFTB
  ResourcesDir DFTB.org/3ob-3-1
  KSpace
    Type Symmetric
    Symmetric KInteg=5
  End
  Technical AnalyticalStressTensor=False # Not yet supported with symmetric k-
→space grid.
  EndEngine

EOF

# Note: the elastic tensor is also printed to standard output.

echo ""
echo "Extract the elastic tensor of Diamond from the rkf file:"
$AMSBIN/amsreport Diamond.results/dftb.rkf -r "AMSResults%ElasticTensor#12.4f##6"

echo ""
echo "Extract the elastic tensor of Boron-Nitride from the rkf file:"
$AMSBIN/amsreport BN_sheet.results/dftb.rkf -r "AMSResults%ElasticTensor#12.4f##3"

```

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```

echo ""
echo "Extract the elastic tensor of Polyoxyethylene from the rkf file:"
$AMSBIN/amsreport Polyoxyethylene.results/dftb.rkf -r "AMSResults%ElasticTensor#12.4f#
↪#1"

```

11.11 Pipe interface

11.11.1 Example: ASE calculator as a pipe worker

Download Pipe_ASEWorker.run

```

#!/bin/sh
# This example uses a Python pipe worker based on ASE to evaluate the Lennard-Jones_
↪potential.
# First we do a single-point calculation including the gradients and the stress_
↪tensor and then
# a short MD run similar to the Pipe_AMSonAMS example.

export SCM_DISABLE_MPI=1

AMS_JOBNAME=SP "$AMSBIN/ams" << eor
RNGSeed -538839488 972444872 -468448621 535232319 -953628259 777353319 -1036072_
↪387155213

Task SinglePoint

Properties
  Gradients True
  StressTensor True
End

System
  Atoms
    Ar    0.03374714   -0.02579634   -0.03864485
    Ar   -2.47202773   -2.57754100   -0.02505375
    Ar   -2.54465030   -0.00587811   -2.49637860
    Ar   -4.98237672   -2.60930954   -2.49495517
    Ar   -0.03221746   -2.51967081   -2.47883073
    Ar   -2.52675554   -5.12905072   -2.48152312
    Ar   -2.54445364   -2.45619404   -5.02601013
    Ar   -4.95645981   -5.14903666   -4.95752059
  End
  Lattice
    0.00000000    5.00000000    5.00000000
    5.00000000    0.00000000    5.00000000
    5.00000000    5.20000000    0.00000000
  End
End

Engine Pipe
  WorkerCommand "$AMSBIN/amspython" "$TEST_DIRECTORY/ASE-LJ-worker.py"
EndEngine

```

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```
eor
AMS_JOBNAME=MD "$AMSBIN/ams" << eor
RNGSeed -538839488 972444872 -468448621 535232319 -953628259 777353319 -1036072_
↪387155213

Task MolecularDynamics

MolecularDynamics
  nSteps 200
  TimeStep 5.0
  Thermostat Type=NHC Temperature=298.15 Tau=100
  Trajectory SamplingFreq=20
  InitialVelocities Type=random Temperature=200
End

System
  Atoms
    Ar 0.0 0.0 0.0
    Ar 1.605 0.9266471820493496 2.605
  End
  Lattice
    3.21 0.0 0.0
    1.605 2.779941546148048 0.0
    0.0 0.0 5.21
  End
  SuperCell 4 4 4
End

Engine Pipe
  WorkerCommand "$AMSBIN/amspython" "$TEST_DIRECTORY/ASE-LJ-worker.py"
EndEngine

eor
```

Download ASE-LJ-worker.py

```
from scm.amspipe import ASEPipeWorker
from ase.calculators.lj import LennardJones

calculator = LennardJones()
calculator.parameters.epsilon = 0.0102996
calculator.parameters.sigma = 3.4
calculator.parameters.rc = 12.0

engine = ASEPipeWorker(calculator=calculator)
engine.run()
```

11.11.2 Example: AMS as a pipe worker

Download Pipe_AMSonAMS.run

```
#!/bin/sh
# This example runs two separate AMS processes communicating over AMSPipe. One of
↳them is the PipeWorker
# calculating Lennard-Jones energies and the other as the PipeMaster drives the MD
↳simulation.

export SCM_DISABLE_MPI=1
export NSCM_AMSEXTERNAL=1

cat - > worker.in << eor
Task Pipe

Engine LennardJones
  Rmin 3.81637
  Eps 3.785e-4
  Cutoff 12.0
EndEngine
eor

"$AMSBIN/ams" << eor
RNGSeed -538839488 972444872 -468448621 535232319 -953628259 777353319 -1036072
↳387155213

Task MolecularDynamics

MolecularDynamics
  nSteps 200
  TimeStep 5.0
  Thermostat Type=NHC Temperature=298.15 Tau=100
  Trajectory SamplingFreq=20
  InitialVelocities Type=random Temperature=200
End

System
  Atoms
    Ar 0.0 0.0 0.0
    Ar 1.605 0.9266471820493496 2.605
  End
  Lattice
    3.21 0.0 0.0
    1.605 2.779941546148048 0.0
    0.0 0.0 5.21
  End
  SuperCell 4 4 4
End

Engine Pipe
  WorkerCommand "$AMSBIN/ams" < ../../worker.in > worker.out 2>&1
EndEngine
eor

echo "Worker output:"
cat ams.results/*/worker.out
```

12.1 Extended XYZ file format

The `.xyz` file format is a simple text based format for molecular geometries. `.xyz` files have the number of atoms in the first line, followed by a comment line, followed by one line per atom, specifying the element as well as the x, y, and z coordinates of this atom.

However, the standard `.xyz` file format does not include lattice vectors. AMS therefore uses an extended `.xyz` file format which is also suitable for periodic systems. In this extended format the lattice vectors are specified at the end of the `.xyz` file via the keys `VEC1`, `VEC2` and `VEC3`. For 1D periodic systems (chains) only `VEC1` is needed. For 2D periodic systems (slabs) only `VEC1` and `VEC2` are needed. An example extended `.xyz` for graphene looks like this:

```
2
C      0.0  0.0  0.0
C      1.23 0.71014 0.0
VEC1   2.46 0.0  0.0
VEC2   1.23 2.13042 0.0
```

Note that the extended `.xyz` format is also understood by the AMS GUI for importing and exporting geometries from/to `.xyz` files.

12.2 Developer options

```
Print
  Timers [None | Normal | Detail | TooMuchDetail]
End
```

Print

Type Block

Description This block controls the printing of additional information to stdout.

Timers

Type Multiple Choice

Default value None

Options [None, Normal, Detail, TooMuchDetail]

Description Printing timing details to see how much time is spend in which part of the code.

```
EngineDebugging
  AlwaysClaimSuccess Yes/No
  CheckInAndOutput Yes/No
  ForceContinousPES Yes/No
  IgnoreGradientsRequest Yes/No
  IgnorePreviousResults Yes/No
  IgnoreStressTensorRequest Yes/No
  NeverQuiet Yes/No
  RandomFailureChance float
  RandomNoiseInEnergy float
  RandomNoiseInGradients float
  RandomStopChance float
End
```

EngineDebugging

Type Block

Description This block contains some options useful for debugging the computational engines.

AlwaysClaimSuccess

Type Bool

Default value No

Description If an engine fails, pretend that it worked. This can be useful when you know that an SCF might fail.

CheckInAndOutput

Type Bool

Default value No

Description Enables some additional checks on the input and output of an engine, e.g. for NaN values.

ForceContinousPES

Type Bool

Default value No

Description If this option is set, the engine will always run in continuous PES mode. For many engines this disables the use of symmetry, as this one always leads to a discontinuous PES around the symmetric points: Basically there is jump in the PES at the point where the symmetry detection starts classifying the system as symmetric. Normally the continuous PES mode of the engine (often disabling the symmetry) is only used when doing numerical derivatives, but this flag forces the engine to continuously run in this mode.

IgnoreGradientsRequest

Type Bool

Default value No

Description If this option is set, the engine will not do analytical gradients if asked for it, so that gradients will have to be evaluated numerically by AMS.

IgnorePreviousResults

Type Bool

Default value No

Description If this option is set, the engine will not receive information from previous calculations. Typically this information is used to restart the self consistent procedure of the engine.

IgnoreStressTensorRequest

Type Bool

Default value No

Description If this option is set, the engine will not calculate an analytical stress tensor if asked for it, so that the stress tensor will have to be evaluated numerically by AMS.

NeverQuiet

Type Bool

Default value No

Description Makes the engine ignore the request to work quietly.

RandomFailureChance

Type Float

Default value 0.0

Description Makes the engine randomly report failures, even though the results are actually fine. Useful for testing error handling on the application level.

RandomNoiseInEnergy

Type Float

Default value 0.0

Unit Hartree

Description Adds a random noise to the energy returned by the engine. The random contribution is drawn from $[-r,r]$ where r is the value of this keyword.

RandomNoiseInGradients

Type Float

Default value 0.0

Unit Hartree/Angstrom

Description Adds a random noise to the gradients returned by the engine. A random number in the range $[-r,r]$ (where r is the value of this keyword) is drawn and added separately to each component of the gradient.

RandomStopChance

Type Float

Default value 0.0

Description Makes the engine randomly stop. Can be used to simulate crashes.

12.3 Symmetry

12.3.1 Schönfliess symbols and symmetry labels

A survey of all molecular point groups that are recognized by AMS is given below. The table contains the Schönfliess symbols together with the names of the subspecies of the irreducible representations as they are used by AMS to label normal modes.

Table 12.1: Schönfliess symbols and the labels of the irreducible representations.

Point Group	Schönfliess Symbol in AMS	Irreducible representations
C_1	NOSYM	A
$C_{\infty v}$	C(LIN)	Sigma Pi
$D_{\infty h}$	D(LIN)	Sigma.g Sigma.u Pi.g Pi.u
I	I	A T1 T2 G H
I_h	I(H)	A.g A.u T1.g T1.u T2.g T2.u G.g G.u H.g H.u
O	O	A1 A2 E T1 T2
O_h	O(H)	A1.g A1.u A2.g A2.u E.g E.u T1.g T1.u T2.g T2.u
T	T	A E T
T_h	T(H)	A.g A.u E.g E.u T.g T.u
T_d	T(D)	A1 A2 E T1 T2
C_i	C(I)	A.g A.u
S_n	S(N)	n=4: A B E
		n=6: A.g A.u E.g E.u
		n=8: A B E1 E2 E3
C_n	C(N)	n=2: A B
		n=4: A B E
		even n: A B E1 E2 ...
		n=3: A E
		odd n: A E1 E2 ...
C_{nv}	C(NV)	n=2: A1 A2 B1 B2
		n=4: A1 A2 B1 B2 E
		even n: A1 A2 B1 B2 E1 E2 ...
		n=3: A1 A2 E
		odd n: A1 A2 E1 E2 ...
C_s	C(S)	A' A''
C_{nh}	C(NH)	n=2: A.g A.u B.g B.u
		n=4: A.g A.u B.g B.u E.g E.u
		even n: A.g A.u B.g B.u E1.g E1.u E2.g E2.u ...
		n=3: A' A'' E' E''
		odd n: A' A'' E1' E1'' E2' E2'' ...
D_n	D(N)	n=2: A B1 B2 B3
		n=4: A1 A2 B1 B2 E
		even n: A1 A2 B1 B2 E1 E2 ...
		n=3: A1 A2 E
		odd n: A1 A2 E1 E2 ...
D_{nd}	D(ND)	n=2: A1 A2 B1 B2 E
		even n: A1 A2 B1 B2 E1 E2 ...
		n=3: A1.g A1.u A2.g A2.u E.g E.u

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Table 12.1 – continued from previous page

		odd n: A1.g A1.u A2.g A2.u E1.g E1.u E2.g E2.u ...
D_{nh}	D(NH)	n=2: A.g A.u B1.g B1.u B2.g B2.u B3.g B3.u
		n=4: A.g A.u B1.g B1.u B2.g B2.u B3.g B3.u E.g E.u
		even n: A.g A.u B1.g B1.u B2.g B2.u B3.g B3.u E1.g E1.u E2.g E2.u ...
		n=3: A1' A1'' A2' A2'' E' E''
		odd n: A1' A1'' A2' A2'' E1' E1'' E2' E2'' ...

The symmetry labeling may depend on the choice of coordinate system. For instance, B1 and B2 representations in C_{nv} are interchanged when you rotate the system by 90 degrees around the z-axis so that x-axis becomes y-axis and vice-versa (apart from sign).

12.3.2 Molecular orientation requirements

In order that AMS recognizes the (sub)symmetry of a molecule, the molecule has to have a specific orientation in space.

- The origin is a fixed point of the symmetry group.
- The z-axis is the main rotation axis.
- xy is the σ_h -plane (axial groups, $C(s)$).
- The x-axis is a C_2 axis (D symmetries).
- The xz-plane is a σ_v -plane (C_{nv} symmetries).
- In T_d and O_h the z-axis is a fourfold axis (S_4 and C_4 , respectively) and the (111)-direction is a threefold axis.

If the system is symmetrized (and no symmetry is given in the System block key) the molecular structure is rotranslated into this standard orientation.

REQUIRED CITATIONS

13.1 General references

When you publish results in the scientific literature that were obtained through the AMS driver program, you are required to include a reference to the program package with the appropriate release number:

AMS 2023.1, SCM, Theoretical Chemistry, Vrije Universiteit, Amsterdam, The Netherlands, <http://www.scm.com>. Optionally, you may add the following list of authors and contributors: R. Rüger, M. Franchini, T. Trnka, A. Yakovlev, E. van Lenthe, P. Philipsen, T. van Vuren, B. Klumpers, T. Soini

The engine used for a particular calculation might require you to include other references. Please refer to the specific *engine manuals* (page 251) for required citations.

In addition to these general references, certain AMS features require additional citations, in case you have used them. An overview of these is given in the *Feature references* section below.

Note: If you have used a modified (by yourself, for instance) version of the code, you should mention in the citation that a modified version has been used.

13.2 Feature references

13.2.1 Frequencies, IR Intensities, Raman, VCD

Mode tracking M. Reiher, J. Neugebauer, *A mode-selective quantum chemical method for tracking molecular vibrations applied to functionalized carbon nanotubes*, *Journal of Chemical Physics* 118, 1634 (2003) (<https://doi.org/10.1063/1.1523908>)

M. Reiher, J. Neugebauer, *Convergence characteristics and efficiency of mode-tracking calculations on pre-selected molecular vibrations*, *Physical Chemistry Chemical Physics* 6, 4621 (2004) (<http://dx.doi.org/10.1039/B406134A>)

C. Herrmann, M. Reiher, J. Neugebauer, *Finding a needle in a haystack: direct determination of vibrational signatures in complex systems*, *New Journal of Chemistry* 31, 818 (2007) (<http://dx.doi.org/10.1039/B618769M>)

Mode tracking based on intensities M. Reiher, J. Neugebauer, *A mode-selective quantum chemical method for tracking molecular vibrations applied to functionalized carbon nanotubes*, *Journal of Chemical Physics* 118, 1634 (2003) (<https://doi.org/10.1063/1.1523908>)

S. Luber, J. Neugebauer, M. Reiher, *Intensity tracking for theoretical infrared spectroscopy of large molecules*, *Journal of Chemical Physics* 130, 064105 (2009) (<https://doi.org/10.1063/1.3069834>)

- Mode refinement** T.Q. Teodoro, M.A.J. Koenis, S.E. Galembeck, V.P. Nicu, W.J. Buma, L. Visscher, *A frequency range selection method for vibrational spectra*, *J. Phys. Chem. Lett.*, 9 (23), 6878 (2018) (<https://doi.org/10.1021/acs.jpcllett.8b02963>)
- Mobile Block Hessian (MBH)** A. Ghysels, D. Van Neck, V. Van Speybroeck, T. Verstraelen and M. Waroquier, *Vibrational Modes in partially optimized molecular systems* *Journal of Chemical Physics* 126, 224102 (2007) (<https://doi.org/10.1063/1.2737444>)
- Raman scattering** S.J.A. van Gisbergen, J.G. Snijders and E.J. Baerends, *Application of time-dependent density functional response theory to Raman scattering*, *Chemical Physics Letters* 259, 599 (1996) ([https://doi.org/10.1016/0009-2614\(96\)00858-5](https://doi.org/10.1016/0009-2614(96)00858-5))
- Resonance Raman: excited-state finite lifetime** L. Jensen, L. Zhao, J. Autschbach and G.C. Schatz, *Theory and method for calculating resonance Raman scattering from resonance polarizability derivatives*, *Journal of Chemical Physics* 123, 174110 (2005) (<https://doi.org/10.1063/1.2046670>)
- Resonance Raman: excited-state gradient** J. Neugebauer, E.J. Baerends, E. Efremov, F. Ariese and C. Gooijer, *Combined Theoretical and Experimental Deep-UV Resonance Raman Studies of Substituted Pyrenes*, *Journal of Physical Chemistry A* 109, 2100 (2005) (<https://doi.org/10.1021/jp045360d>)
- VROA: (Resonance) vibrational Raman optical activity** L. Jensen, J. Autschbach, M. Krykunov, and G.C. Schatz, *Resonance vibrational Raman optical activity: A time-dependent density functional theory approach*, *Journal of Chemical Physics* 127, 134101 (2007) (<https://doi.org/10.1063/1.2768533>)
- Vibrational Circular Dichroism (VCD)** V.P. Nicu J. Neugebauer S.K. Wolff and E.J. Baerends, *A vibrational circular dichroism implementation within a Slater-type-orbital based density functional framework and its application to hexa- and hepta-helicenes*, *Theoretical Chemical Accounts* 119, 245 (2008) (<https://doi.org/10.1007/s00214-006-0234-x>)
- VCD analysis: VCDtools** V.P. Nicu, J. Neugebauer and E.J. Baerends, *Effects of Complex Formation on Vibrational Circular Dichroism Spectra*, *Journal of Physical Chemistry A* 112, 6978 (2008) (<https://doi.org/10.1021/jp710201q>)
- M.A.J. Koenis, O. Visser, L. Visscher, W.J. Buma, V.P. Nicu, *GUI Implementation of VCDtools, A Program to Analyze Computed Vibrational Circular Dichroism Spectra*, *J. Chem. Inf. Model* 60, 259 (2020) (<https://pubs.acs.org/doi/abs/10.1021/acs.jcim.9b00956>)
- V.P. Nicu, *Revisiting an old concept: the coupled oscillator model for VCD. Part 1: the generalised coupled oscillator mechanism and its intrinsic connection to the strength of VCD signals*, *Physical Chemistry Chemical Physics* 18, 21202 (2016) (<https://doi.org/10.1039/C6CP01282E>).
- Franck-Condon factors** J.S. Seldenthuis, H.S.J. van der Zant, M.A. Ratner and J.M. Thijssen, *Vibrational Excitations in Weakly Coupled Single-Molecule Junctions: A Computational Analysis*, *ACS Nano* 2, 1445 (2008) (<https://doi.org/10.1021/nn800170h>)

13.2.2 PES Exploration

Samuel T Chill, Matthew Welborn, Rye Terrell, Liang Zhang, Jean-Claude Berthet, Andreas Pedersen, Hannes Jónsson and Graeme Henkelman *EON: software for long time simulations of atomic scale systems*, *Modelling Simul. Mater. Sci. Eng.* 22 055002 (2014) (<https://doi.org/10.1088/0965-0393/22/5/055002>)

EXTERNAL PROGRAMS AND LIBRARIES

[Click here](#) for the list of programs and/or libraries used in the AMS package. On some platforms optimized libraries have been used and/or vendor specific MPI implementations.

KEYWORDS

15.1 Links to manual entries

ams:

- *BondOrders* (page 246)
- *Constraints* (page 53)
- *ElasticTensor* (page 184)
- *Engine* (page 251)
- *EngineAddons* (page 263)
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- *GCMC* (page 146)
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15.2 Summary of all keywords

BondOrders

Type Block

Description Configures details regarding the calculation/guessing of bond orders. To request the calculation of bond orders, use the 'Properties%BondOrders' key.

Method

Type Multiple Choice

Default value EngineWithGuessFallback

Options [Engine, Guess, EngineWithGuessFallback]

Description How to compute the bond orders when they are requested via the 'Properties%BondOrders' key.

'Engine': let the engine compute the bond orders. The specific method used to compute the bond orders depends on the engine selected, and it may be configurable in the engine's input. Note: the calculation may stop if the engine cannot compute bond orders.

'Guess': Use a bond guessing algorithm based on the system's geometry. This is the same algorithm that is used by the Graphical User Interface to guess bonds.

'EngineWithGuessFallback': let the engine compute the bond orders (same as in 'Engine' option) but if the engine did not produce any bond orders, use the bond guessing algorithm as a fallback option.

Constraints

Type Block

Description The Constraints block allows geometry optimizations and potential energy surface scans with constraints. The constraints do not have to be satisfied at the start of the calculation.

All

Type String

Recurring True

Description Fix multiple distances using one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 as well as the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then any bond between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk '*' denoting any atom. If the distance is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at the start of the simulation can be constrained, which means that the bonds may need to be specified in the System block.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

Angle

Type String

Recurring True

Description Fix the angle between three atoms. Three atom indices followed by an angle in degrees.

Atom

Type Integer

Recurring True

Description Fix the position of an atom. Just one integer referring to the index of the atom in the [System%Atoms] block.

AtomList

Type Integer List

Recurring True

Description Fix positions of the specified atoms. A list of integers referring to indices of atoms in the [System%Atoms] block.

Block

Type String

Recurring True

Description Name of the region to constrain as a rigid block. Regions are specified in the System%Atoms block.

BlockAtoms

Type Integer List

Recurring True

Description List of atom indices for a block constraint, where the internal degrees of freedom are frozen.

Coordinate

Type String

Recurring True

Description Fix a particular coordinate of an atom. Atom index followed by (x|y|z).

DifDist

Type String

Recurring True

Description Four atom indices i j k l followed by the distance in Angstrom. This will constrain the difference $R(ij)-R(kl)$ at the given value.

Dihedral

Type String

Recurring True

Description Fix the dihedral angle between four atoms. Four atom indices followed by an angle in degrees.

Distance

Type String

Recurring True

Description Fix the distance between two atoms. Two atom indices followed by the distance in Angstrom.

EqualStrain

Type String

Description Exclusively for lattice optimizations:

Accepts a set of strain components [xx, xy, xz, yy, yz, zz] which are to be kept equal.

The applied strain will be determined by the average of the corresponding stress tensors components.

In AMSinput just check the corresponding check buttons.

FixedRegion

Type String

Recurring True

Description Fix positions of all atoms in a region.

FreezeStrain

Type String

Description Exclusively for lattice optimizations:

Freezes any lattice deformation corresponding to a particular component of the strain tensor.

Accepts a set of strain components [xx, xy, xz, yy, yz, zz] to be frozen.

In AMSinput just check the corresponding check buttons.

SumDist

Type String

Recurring True

Description Four atom indices i j k l followed by the distance in Angstrom. This will constrain the sum $R(ij)+R(kl)$ at the given value.

ElasticTensor

Type Block

Description Options for numerical evaluation of the elastic tensor.

ConvergenceQuality

Type Multiple Choice

Default value Good

Options [Normal, Good, VeryGood]

GUI name Convergence

Description The tightness of the convergence of the geometry optimizations for each strain deformation. This should not be set higher than the overall convergence quality of the preceding geometry optimization configured by the `GeometryOptimization%Convergence%Quality` keyword.

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

StrainStepSize

Type Float

Default value 0.001

Description Step size (relative) of strain deformations used for computing the elastic tensor numerically.

Engine

Type Block

Description The input for the computational engine. The header of the block determines the type of the engine.

EngineAddons

Type Block

Description This block configures all the engine add-ons.

AtomEnergies

Type Non-standard block

Description Add an element-dependent energy per atom. On each line, give the chemical element followed by the energy (in atomic units).

D3Dispersion

Type Block

Description This block configures the add-on that adds the Grimme D3 dispersion correction to the engine's energy, gradients, and stress tensor.

Damping

Type Multiple Choice

Default value BJ

Options [BJ, Zero]

Description Type of damping: BJ (Becke-Johnson) or Zero. BJ is recommended for most applications.

Enabled

Type Bool

Default value No

Description Enables the D3 dispersion correction add-on.

Functional

Type String

Default value PBE

Description Use the D3 parameterization by Grimme for a given xc-functional. Accepts the same values as the `-func` command line option of the official `dftd3` program. Note: the naming convention is different from elsewhere in the AMS suite. For example, BLYP should be called `b-lyp`.

a1

Type Float

Description The `a1` parameter. Only used if Damping is set to BJ. If set, it overwrites the `a1` value for the chosen functional.

a2

Type Float

Description The `a2` parameter. Only used if Damping is set to BJ. If set, it overwrites the `a2` value for the chosen functional.

s6

Type Float

Description The `s6` parameter, global scaling parameter. If set, it overwrites the `s6` value for the chosen functional.

s8

Type Float

Description The `s8` parameter. If set, it overwrites the `s8` value for the chosen functional.

sr6

Type Float

Description The `sr6` parameter. Only used if Damping is set to Zero. If set, it overwrites the `sr6` value for the chosen functional.

D4Dispersion

Type Block

Description This block configures the addon that adds the Grimme D4(EEQ) dispersion correction to the engine's energy, gradients, stress tensor and Hessian.

Enabled

Type Bool

Default value No

Description Enables the D4 dispersion correction addon.

Functional

Type Multiple Choice

Default value PBE

Options [HF, BLYP, BPBE, BP86, BPW, LB94, MPWLYP, MPWPW91, OLYP, OPBE, PBE, RPBE, REVPBE, PW86PBE, RPW86PBE, PW91, PW91P86, XLYP, B97, TPSS, REVTPSS, SCAN, B1LYP, B3LYP, BHLYP, B1P86, B3P86, B1PW91, B3PW91, O3LYP, REVPBE0, REVPBE38, PBE0, PWP1, PW1PW, MPW1PW91, MPW1LYP, PW6B95, TPSSH, TPSS0, X3LYP, M06L, M06, OMEGAB97, OMEGAB97X, CAM-B3LYP, LC-BLYP, LH07TSVWN, LH07SSVWN, LH12CTSSIRPW92, LH12CTSSIFPW92,

LH14TCALPBE, B2PLYP, B2GPPLYP, MPW2PLYP, PWPB95, DSDBLYP, DSDPBE, DSDPBEB95, DSDPBEP86, DSDSVWN, DODBLYP, DODPBE, DODPBEB95, DODPBEP86, DODSVWN, PBE02, PBE0DH, DFTB(3ob), DFTB(mio), DFTB(pbc), DFTB(matsci), DFTB(ob2), B1B95, MPWB1K, REVTPSSH, GLYP, REVPBE0DH, REVTPSS0, REVSDPBEP86, REVSDPBEPBE, REVSDBLYP, REVDODPBEP86, B97M, OMEGAB97M, R2SCAN]

Description Use the D4 parameterization by Grimme for a given xc-functional.

Verbosity

Type Multiple Choice

Default value Silent

Options [Silent, Normal, Verbose, VeryVerbose]

Description Controls the verbosity of the dftd4 code. Equivalent to the `-silent` and `-verbose` command line switches of the official dftd4 program.

a1

Type Float

Description The a1 parameter, see D4 article. The physically reasonable range for a1 is [0.0,1.0]. If set, it overwrites the a1 value for the chosen functional.

a2

Type Float

Description The a2 parameter, see D4 article. The physically reasonable range for a2 is [0.0,7.0]. If set, it overwrites the a2 value for the chosen functional.

s6

Type Float

Description The s6 parameter, see D4 article. The physically reasonable range for s6 is [0.0,1.0]. If set, it overwrites the s6 value for the chosen functional.

s8

Type Float

Description The s8 parameter, see D4 article. The physically reasonable range for s8 is [0.0,3.0]. If set, it overwrites the s8 value for the chosen functional.

s9

Type Float

Description The s9 parameter, see D4 article. If set, it overwrites the s9 value for the chosen functional.

ExternalEngine

Type Block

Description External engine as an addon

Execute

Type String

GUI name Execute

Description execute command

ExternalStress**Type** Block**Description** This block configures the addon that adds external stress term to the engine's energy and stress tensor.**StressTensorVoigt****Type** Float List**Unit** a.u.**GUI name** External stress tensor**Description** The elements of the external stress tensor in Voigt notation. One should specify 6 numbers for 3D periodic system (order: xx,yy,zz,yz,xz,xy), 3 numbers for 2D periodic systems (order: xx,yy,xy) or 1 number for 1D periodic systems.**UpdateReferenceCell****Type** Bool**Default value** No**Description** Whether or not the reference cell should be updated every time the system changes (see documentation).**PipeEngine****Type** Block**Description** Pipe engine as an addon**WorkerCommand****Type** String**GUI name** Worker command**Description** pipe worker command**Pressure****Type** Float**Default value** 0.0**Unit** GPa**Description** Add a hydrostatic pressure term to the engine's energy and stress tensor. Can only be used for 3D periodic boundary conditions.**WallPotential****Type** Block**Description** This block configures the addon that adds a spherical wall potential to the engine's energy and gradients.**Enabled****Type** Bool**Default value** No

Description Enables the wall potential add-on. When enabled, a spherical wall of radius [Radius] around the origin will be added. The force due to the potential will decay exponentially inside the wall, will be close to [Prefactor*Gradient] outside and exactly half of that at the wall.

Gradient

Type Float

Default value 10.0

Unit 1/Angstrom

Description The radial gradient outside the sphere.

Prefactor

Type Float

Default value 0.01

Unit Hartree

Description The multiplier for the overall strength of the potential.

Radius

Type Float

Default value 30.0

Unit Angstrom

Description The radius of the sphere, wherein the potential is close to zero.

EngineDebugging

Type Block

Description This block contains some options useful for debugging the computational engines.

AlwaysClaimSuccess

Type Bool

Default value No

Description If an engine fails, pretend that it worked. This can be useful when you know that an SCF might fail.

CheckInAndOutput

Type Bool

Default value No

Description Enables some additional checks on the input and output of an engine, e.g. for NaN values.

ForceContinuousPES

Type Bool

Default value No

Description If this option is set, the engine will always run in continuous PES mode. For many engines this disables the use of symmetry, as this one always leads to a discontinuous PES around the symmetric points: Basically there is a jump in the PES at the point where the symmetry detection starts classifying the system as symmetric. Normally the continuous PES mode of the

engine (often disabling the symmetry) is only used when doing numerical derivatives, but this flag forces the engine to continuously run in this mode.

IgnoreGradientsRequest

Type Bool

Default value No

Description If this option is set, the engine will not do analytical gradients if asked for it, so that gradients will have to be evaluated numerically by AMS.

IgnorePreviousResults

Type Bool

Default value No

Description If this option is set, the engine will not receive information from previous calculations. Typically this information is used to restart the self consistent procedure of the engine.

IgnoreStressTensorRequest

Type Bool

Default value No

Description If this option is set, the engine will not calculate an analytical stress tensor if asked for it, so that the stress tensor will have to be evaluated numerically by AMS.

NeverQuiet

Type Bool

Default value No

Description Makes the engine ignore the request to work quietly.

RandomFailureChance

Type Float

Default value 0.0

Description Makes the engine randomly report failures, even though the results are actually fine. Useful for testing error handling on the application level.

RandomNoiseInEnergy

Type Float

Default value 0.0

Unit Hartree

Description Adds a random noise to the energy returned by the engine. The random contribution is drawn from $[-r,r]$ where r is the value of this keyword.

RandomNoiseInGradients

Type Float

Default value 0.0

Unit Hartree/Angstrom

Description Adds a random noise to the gradients returned by the engine. A random number in the range $[-r,r]$ (where r is the value of this keyword) is drawn and added separately to each component of the gradient.

RandomStopChance

Type Float

Default value 0.0

Description Makes the engine randomly stop. Can be used to simulate crashes.

EngineRestart

Type String

Description The path to the file from which to restart the engine.

Should be a proper engine result file (like adf.rkf, band.rkf etc), or the name of the results directory containing it.

ExitCondition

Type Block

Recurring True

Description If any of the specified exitconditions are met, the AMS driver will exit cleanly.

AtomsTooClose

Type Block

Description If any pair of atoms is closer than the specified minimum value, the program will exit cleanly.

MinimumDistance

Type Float

Default value 0.7

Unit Angstrom

Description Two atoms closer than this threshold value are considered too close.

PairCalculation

Type Multiple Choice

Default value NeighborList

Options [NeighborList, DistanceMatrix]

Description Two atoms closer than this threshold value are considered too close.

Type

Type Multiple Choice

Default value AtomsTooClose

Options [AtomsTooClose]

Description The type of exitcondition specified

FallbackSolveAfterEngineFailure

Type Bool

Default value Yes

Description If the engine fails to Solve, try to re-run the Solve without restarting the engine from the previous results. This generally decreases the engine failure rate. Only relevant certain tasks, such as GeometryOptimization, MolecularDynamics, Replay, IRC.

GCMC

Type Block

Description This block controls the Grand Canonical Monte Carlo (GCMC) task.

By default, molecules are added at random positions in the simulation box. The initial position is controlled by

AccessibleVolume

Type Float

Default value 0.0

Description Volume available to GCMC, in cubic Angstroms. AccessibleVolume should be specified for “Accessible” and “FreeAccessible” [VolumeOption].

Box

Type Block

Description Boundaries of the insertion space, i.e. coordinates of the origin of an inserted molecule (coordinates of an atom of the inserted system may fall outside the box).

For a periodic dimension it is given as a fraction of the simulation box (the full 0 to 1 range by default). For a non-periodic dimension it represents absolute Cartesian coordinates in Angstrom (the system’s bounding box extended by the MaxDistance value by default).

Amax

Type Float

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Description Coordinate of the lower bound along the third axis.

Ensemble

Type Multiple Choice

Default value Mu-VT

Options [Mu-VT, Mu-PT]

Description Select the MC ensemble: Mu-VT for fixed volume or Mu-PT for variable volume. When the Mu-PT ensemble is selected the [Pressure] and [VolumeChangeMax] should also be specified.

Iterations

Type Integer

GUI name Number of GCMC iterations

Description Number of GCMC moves.

MapAtomsToOriginalCell

Type Bool

Default value Yes

Description Keeps the atom (mostly) in the original cell by mapping them back before the geometry optimizations.

MaxDistance

Type Float

Default value 3.0

Unit Angstrom

GUI name Add molecules within

Description The max distance to other atoms of the system when adding the molecule.

MinDistance

Type Float

Default value 0.3

Unit Angstrom

GUI name Add molecules not closer than

Description Keep the minimal distance to other atoms of the system when adding the molecule.

Molecule

Type Block

Recurring True

GUI name Molecules

Description This block defines the molecule (or atom) that can be inserted/moved/deleted with the MC method. The coordinates should form a reasonable structure. The MC code uses these coordinates during the insertion step by giving them a random rotation, followed by a random translation to generate a random position of the molecule inside the box. Currently, there is no check to make sure all atoms of the molecule stay inside the simulation box. The program does check that the MaxDistance/MinDistance conditions are satisfied.

ChemicalPotential

Type Float

Unit Hartree

Description Chemical potential of the molecule (or atom) reservoir.

It is used when calculating the Boltzmann accept/reject criteria after a MC move is executed. This value can be derived from first principles using statistical mechanics, or equivalently, it can be determined from thermochemical tables available in literature sources. For example, the proper chemical potential for a GCMC simulation in which single oxygen atoms are exchanged with a reservoir of O₂ gas, should equal 1/2 the chemical potential of O₂ at the temperature and pressure of the reservoir:

$$\text{cmpot} = \mu_{\text{O}}(T,P) = 1/2 * \mu_{\text{O}_2}(T,P) = 1/2 * [\mu_{\text{ref}}(T,P_{\text{ref}}) + kT * \log(P/P_{\text{ref}}) - E_{\text{diss}}]$$

where the reference chemical potential [$\mu_{\text{ref}}(T,P_{\text{ref}})$] is the experimentally determined chemical potential of O₂ at T and P_{ref}; $kT * \log(P/P_{\text{ref}})$ is the pressure correction to the free energy, and E_{diss} is the dissociation energy of the O₂ molecule.

NoAddRemove

Type Bool

Default value No

GUI name Fix molecule

Description Set to True to tell the GCMC code to keep the number of molecules/atoms of this type fixed.

It will thus disable Insert/Delete moves on this type, meaning it can only do a displacement move, or volume change move (for an NPT ensemble).

SystemName

Type String

GUI name Molecule

Description String ID of a named [System] to be inserted. The lattice specified with this System, if any, is ignored and the main system's lattice is used instead.

NonAccessibleVolume

Type Float

Default value 0.0

GUI name Non-accessible volume

Description Volume not available to GCMC, in cubic Angstroms. NonAccessibleVolume may be specified for the "Free" [VolumeOption] to reduce the accessible volume.

NumAttempts

Type Integer

Default value 1000

GUI name Max tries

Description Try inserting/moving the selected molecule up to the specified number of times or until all constraints are satisfied. If all attempts fail a message will be printed and the simulation will stop. If the MaxDistance-MinDistance interval is small this number may have to be large.

Pressure

Type Float

Default value 0.0

Unit Pascal

Description Pressure used to calculate the energy correction in the Mu-PT ensemble. Set it to zero for incompressible solid systems unless at very high pressures.

Removables

Type Non-standard block

Description The Removables can be used to specify a list of molecules that can be removed or moved during this GCMC calculation. Molecules are specified one per line in the format following format: MoleculeName atom1 atom2 ... The MoleculeName must match a name specified in one of the [Molecule] blocks. The atom indices refer to the whole input System and the number of atoms must match that in the specified Molecule. A suitable Removables block is written to the standard output after each accepted MC move. If you do so then you should also replace the initial atomic coordinates with the ones found in the same file. If a [Restart] key is present then the Removables block is ignored.

Restart

Type String

Description Name of an RKF restart file. Upon restart, the information about the GCMC input parameters, the initial system (atomic coordinates, lattice, charge, etc.) and the MC molecules (both already inserted and to be inserted) are read from the restart file. The global GCMC input parameters and the MC Molecules can be modified from input. Any parameter not specified in the input will use its value from the restart file (i.e. not the default value). Molecules found in the restart file do not have to be present as named Systems in the input, however if there is a System present that matches the name of a molecule from restart then the System's geometry will replace that found in the restart file. It is also possible to specify new Molecules in the input, which will be added to the pool of the MC molecules from restart.

SwapAtoms

Type Block

Description Experimental: Occasionally swap the coordinates of a random pair of atoms from two regions.

Probability

Type Float

Default value 0.0

Description Probability of performing a swap move instead of any other GCMC move in a single GCMC iteration.

Regions

Type String

Description Names of two regions to swap between (separated by a space).

Temperature

Type Float

Default value 300.0

Unit Kelvin

Description Temperature of the simulation. Increase the temperature to improve the chance of accepting steps that result in a higher energy.

UseGCPreFactor

Type Bool

Default value Yes

GUI name Use GC prefactor

Description Use the GC pre-exponential factor for probability.

VolumeChangeMax

Type Float

Default value 0.05

Description Fractional value by which logarithm of the volume is allowed to change at each step. The new volume is then calculated as $V_{\text{new}} = \exp(\text{random}(-1:1) * \text{VolumeChangeMax}) * V_{\text{old}}$

VolumeOption

Type Multiple Choice

Default value Free

Options [Free, Total, Accessible, FreeAccessible]

GUI name Volume method

Description Specifies the method to calculate the volume used to calculate the GC pre-exponential factor and the energy correction in the Mu-PT ensemble: Free: $V = \text{totalVolume} - \text{occupiedVolume} - \text{NonAccessibleVolume}$; Total: $V = \text{totalVolume}$; Accessible: $V = \text{AccessibleVolume}$; FreeAccessible: $V = \text{AccessibleVolume} - \text{occupiedVolume}$. The AccessibleVolume and NonAccessibleVolume are specified in the input, the occupiedVolume is calculated as a sum of atomic volumes.

GeometryOptimization

Type Block

Description Configures details of the geometry optimization and transition state searches.

CalcPropertiesOnlyIfConverged

Type Bool

Default value Yes

Description Compute the properties requested in the 'Properties' block, e.g. Frequencies or Phonons, only if the optimization (or transition state search) converged. If False, the properties will be computed even if the optimization did not converge.

Convergence

Type Block

Description Convergence is monitored for up to 4 quantities: the energy change, the Cartesian gradients, the Cartesian step size, and for lattice optimizations the stress energy per atom. Convergence criteria can be specified separately for each of these items.

Energy

Type Float

Default value 1e-05

Unit Hartree

GUI name Energy convergence

Description The criterion for changes in the energy. The energy is considered converged when the change in energy is smaller than this threshold times the number of atoms.

Gradients

Type Float

Default value 0.001

Unit Hartree/Angstrom

GUI name Gradient convergence

Description Threshold for nuclear gradients.

Quality

Type Multiple Choice

Default value Custom

Options [VeryBasic, Basic, Normal, Good, VeryGood, Custom]

GUI name Convergence

Description A quick way to change convergence thresholds: 'Good' will reduce all thresholds by an order of magnitude from their default value. 'VeryGood' will tighten them by two orders of magnitude. 'Basic' and 'VeryBasic' will increase the thresholds by one or two orders of magnitude respectively.

Step

Type Float

Default value 0.01

Unit Angstrom

GUI name Step convergence

Description The maximum Cartesian step allowed for a converged geometry.

StressEnergyPerAtom

Type Float

Default value 0.0005

Unit Hartree

Description Threshold used when optimizing the lattice vectors. The stress is considered 'converged' when the maximum value of $\text{stress_tensor} * \text{cell_volume} / \text{number_of_atoms}$ is smaller than this threshold (for 2D and 1D systems, the cell_volume is replaced by the cell_area and cell_length respectively).

CoordinateType

Type Multiple Choice

Default value Auto

Options [Auto, Delocalized, Cartesian]

GUI name Optimization space

Description Select the type of coordinates in which to perform the optimization. ‘Auto’ automatically selects the most appropriate CoordinateType for a given Method.

If ‘Auto’ is selected, Delocalized coordinates will be used for the Quasi-Newton and SCMGO methods, while Cartesian coordinates will be used for all other methods.

EngineAutomations

Type Block

Description The optimizer can change some settings of the engine, based for instance on the error. The idea is to allow the engine to be a bit quicker at the start, and more accurate towards the end. Automations are always engine specific.

Enabled

Type Bool

Default value Yes

Description Whether or not autotions are enabled at all.

Gradient

Type Block

Recurring True

Description A gradient-based automation.

FinalValue

Type Float

Description This value will be used whenever the gradient is less than GradientLow

HighGradient

Type Float

Default value 1.0

Unit Hartree/Angstrom

Description Defines a large gradient. When the actual gradient is between GradientHigh and GradientLow a linear interpolation scheme is used for kT (on a log scale).

InitialValue

Type Float

Description This value will be used at the first geometry, and whenever the gradient is higher than GradientHigh

LowGradient

Type Float

Default value 1.0

Unit Hartree/Angstrom

Description Defines a small gradient, see GradientHigh

UseLogInterpolation

Type Bool

Default value Yes

Description Whether to use interpolation on a log (y) scale or not

Variable

Type String

Default value

Description variable to be tweaked for the engine.

Iteration

Type Block

Recurring True

Description Geometry step based automation.

FinalValue

Type Float

Description

FirstIteration

Type Integer

Default value 1

Description When the actual gradient is between the first and last iteration, a linear interpolation is used.

InitialValue

Type Float

Description This value will be used when the iteration number is smaller or equal to FirstIteration

LastIteration

Type Integer

Default value 10

Description Where the automation should reach the FinalValue

UseLogInterpolation

Type Bool

Default value Yes

Description Whether to use interpolation on a log (y) scale or not

Variable

Type String

Default value

Description variable to be tweaked for the engine.

FIRE

Type Block

Description This block configures the details of the FIRE optimizer. The keywords name correspond to the symbols used in the article describing the method, see PRL 97, 170201 (2006).

AllowOverallRotation**Type** Bool**Default value** Yes**Description** Whether or not the system is allowed to freely rotate during the optimization. This is relevant when optimizing structures in the presence of external fields.**AllowOverallTranslation****Type** Bool**Default value** No**Description** Whether or not the system is allowed to translate during the optimization. This is relevant when optimizing structures in the presence of external fields.**MapAtomsToUnitCell****Type** Bool**Default value** No**Description** Map the atoms to the central cell at each geometry step.**NMin****Type** Integer**Default value** 5**Description** Number of steps after stopping before increasing the time step again.**alphaStart****Type** Float**Default value** 0.1**Description** Steering coefficient.**dtMax****Type** Float**Default value** 1.0**Unit** Femtoseconds**Description** Maximum time step used for the integration. For ReaxFF and APPLE&P, this value is reduced by 50%.**dtStart****Type** Float**Default value** 0.25**Unit** Femtoseconds**Description** Initial time step for the integration.**fAlpha****Type** Float**Default value** 0.99**Description** Reduction factor for the steering coefficient.

fDec**Type** Float**Default value** 0.5**Description** Reduction factor for reducing the time step in case of uphill movement.**fInc****Type** Float**Default value** 1.1**Description** Growth factor for the integration time step.**strainMass****Type** Float**Default value** 0.5**Description** Fictitious relative mass of the lattice degrees of freedom. This controls the stiffness of the lattice degrees of freedom relative to the atomic degrees of freedom, with smaller values resulting in a more aggressive optimization of the lattice.**HessianFree****Type** Block**Description** Configures details of the Hessian-free (conjugate gradients or L-BFGS) geometry optimizer.**Step****Type** Block**Description****MaxCartesianStep****Type** Float**Default value** 0.1**Unit** Angstrom**Description** Limit on a single Cartesian component of the step.**MinRadius****Type** Float**Default value** 0.0**Unit** Angstrom**Description** Minimum value for the trust radius.**TrialStep****Type** Float**Default value** 0.0005**Unit** Angstrom**Description** Length of the finite-difference step when determining curvature. Should be smaller than the step convergence criterion.

TrustRadius**Type** Float**Default value** 0.2**Unit** Angstrom**Description** Initial value of the trust radius.**InitialHessian****Type** Block**Description** Options for initial model Hessian when optimizing systems with either the Quasi-Newton or the SCMGO method.**File****Type** String**GUI name** Initial Hessian from**Description** KF file containing the initial Hessian (or the results dir. containing it). This can be used to load a Hessian calculated in a previously with the [Properties%Hessian] keyword.**Type****Type** Multiple Choice**Default value** Auto**Options** [Auto, UnitMatrix, Swart, FromFile, Calculate, CalculateWithFastEngine]**GUI name** Initial Hessian**Description** Select the type of initial Hessian. Auto: let the program pick an initial model Hessian. UnitMatrix: simplest initial model Hessian, just a unit matrix in the optimization coordinates. Swart: model Hessian from M. Swart. FromFile: load the Hessian from the results of a previous calculation (see InitialHessian%File). Calculate: compute the initial Hessian (this may be computationally expensive and it is mostly recommended for TransitionStateSearch calculations). CalculateWithFastEngine: compute the initial Hessian with a faster engine.**KeepIntermediateResults****Type** Bool**Default value** No**Description** Whether the full engine result files of all intermediate steps are stored on disk. By default only the last step is kept, and only if the geometry optimization converged. This can easily lead to huge amounts of data being stored on disk, but it can sometimes be convenient to closely monitor a tricky optimization, e.g. excited state optimizations going through conical intersections, etc. ...**MaxIterations****Type** Integer**GUI name** Maximum number of iterations**Description** The maximum number of geometry iterations allowed to converge to the desired structure.**MaxRestarts**

Type Integer

Default value 0

Description If a geometry optimization of a system with no symmetry operators (or with explicitly disabled symmetry: `UseSymmetry False`) and enabled PES point characterization converges to a transition state (or higher order saddle point), it can be restarted automatically after a small displacement along the imaginary vibrational mode. In case the restarted optimization again does not find a minimum, this can happen multiple times in succession. This keyword sets the maximum number of restarts. The default value is 0, so the automatic restarting is disabled by default.

Method

Type Multiple Choice

Default value Auto

Options [Auto, Quasi-Newton, SCMGO, FIRE, L-BFGS, ConjugateGradients]

GUI name Optimization method

Description Select the optimization algorithm employed for the geometry relaxation. Currently supported are:

the Hessian-based Quasi-Newton-type BFGS algorithm,

the experimental SCMGO optimizer,

the fast inertial relaxation method (FIRE),

the limited-memory BFGS method,

and the conjugate gradients method. The default is to choose an appropriate method automatically based on the engine's speed, the system size and the supported optimization options.

OptimizeLattice

Type Bool

Default value No

Description Whether to also optimize the lattice for periodic structures. This is currently only supported with the Quasi-Newton, FIRE, L-BFGS and SCMGO optimizers.

PretendConverged

Type Bool

Default value No

Description Normally a non-converged geometry optimization is considered an error. If this keyword is set to True, the optimizer will only produce a warning and still claim that the optimization is converged. (This is mostly useful for scripting applications, where one might want to consider non-converged optimizations still successful jobs.)

Quasi-Newton

Type Block

Description Configures details of the Quasi-Newton geometry optimizer.

MaxGDIISVectors

Type Integer

Default value 0

Description Sets the maximum number of GDIIS vectors. Setting this to a number >0 enables the GDIIS method.

Step

Type Block

Description**TrustRadius**

Type Float

Description Initial value of the trust radius.

VaryTrustRadius

Type Bool

Description Whether to allow the trust radius to change during optimization. By default True during energy minimization and False during transition state search.

UpdateTSVectorEveryStep

Type Bool

Default value Yes

GUI name Update TSRC vector every step

Description Whether to update the TS reaction coordinate at each step with the current eigenvector.

RestartDisplacement

Type Float

Default value 0.05

Unit Angstrom

Description If a geometry optimization of a system with no symmetry operators (or with explicitly disabled symmetry: `UseSymmetry False`) and enabled PES point characterization converges to a transition state (or higher order saddle point), it can be restarted automatically after a small displacement along the imaginary vibrational mode. This keyword sets the size of the displacement for the furthest moving atom.

SCMGO

Type Block

Description Configures details SCMGO.

ContractPrimitives

Type Bool

Default value Yes

Description Form non-redundant linear combinations of primitive coordinates sharing the same central atom

NumericalBMatrix

Type Bool

Default value No

Description Calculation of the B-matrix, i.e. Jacobian of internal coordinates in terms of numerical differentiations

Step

Type Block

Description

TrustRadius

Type Float

Default value 0.2

Description Initial value of the trust radius.

VariableTrustRadius

Type Bool

Default value Yes

Description Whether or not the trust radius can be updated during the optimization.

logSCMGO

Type Bool

Default value No

Description Verbose output of SCMGO internal data

testSCMGO

Type Bool

Default value No

Description Run SCMGO in test mode.

IRC

Type Block

Description Configures details of the Intrinsic Reaction Coordinate optimization.

Convergence

Type Block

Description Convergence at each given point is monitored for two items: the Cartesian gradient and the calculated step size. Convergence criteria can be specified separately for each of these items. The same criteria are used both in the inner IRC loop and when performing energy minimization at the path ends.

Gradients

Type Float

Default value 0.001

Unit Hartree/Angstrom

GUI name Gradient convergence

Description Convergence criterion for the max component of the residual energy gradient.

Step

Type Float

Default value 0.001

Unit Angstrom

GUI name Step convergence

Description Convergence criterion for the max component of the step in the optimization coordinates.

CoordinateType

Type Multiple Choice

Default value Cartesian

Options [Cartesian, Delocalized]

GUI name Coordinates used for optimization

Description Select the type of coordinates in which to perform the optimization. Note that the Delocalized option should be considered experimental.

Direction

Type Multiple Choice

Default value Both

Options [Both, Forward, Backward]

Description Select direction of the IRC path. The difference between the Forward and the Backward directions is determined by the sign of the largest component of the vibrational normal mode corresponding to the reaction coordinate at the transition state geometry. The Forward path correspond to the positive sign of the component. If Both is selected then first the Forward path is computed followed by the Backward one.

InitialHessian

Type Block

Description Options for initial Hessian at the transition state. The first eigenvalue of the initial Hessian defines direction of the first forward or backward step. This block is ignored when restarting from a previous IRC calculation because the initial Hessian found in the restart file is used.

File

Type String

GUI name File

Description If 'Type' is set to 'FromFile' then in this key you should specify the RKF file containing the initial Hessian (or the ams results dir. containing it). This can be used to load a Hessian calculated previously with the 'Properties%Hessian' keyword. If you want to also use this file for the initial geometry then also specify it in a 'LoadSystem' block.

Type

Type Multiple Choice

Default value Calculate

Options [Calculate, FromFile]

GUI name Initial Hessian

Description Calculate the exact Hessian for the input geometry or load it from the results of a previous calculation.

KeepConvergedResults

Type Bool

Default value Yes

Description Keep the binary RKF result file for every converged IRC point. These files may contain more information than the main ams.rkf result file.

MaxIRCSteps

Type Integer

GUI name Maximum IRC steps

Description Soft limit on the number of IRC points to compute in each direction. After the specified number of IRC steps the program will switch to energy minimization and complete the path. This option should be used when you are interested only in the reaction path area near the transition state. Note that even if the soft limit has been hit and the calculation has completed, the IRC can still be restarted with a 'RedoBackward' or 'RedoForward' option.

MaxIterations

Type Integer

Default value 300

GUI name Maximum iterations

Description The maximum number of geometry iterations allowed to converge the inner IRC loop. If optimization does not converge within the specified number of steps, the calculation is aborted.

MaxPoints

Type Integer

Default value 100

GUI name Maximum points

Description Hard limit on the number of IRC points to compute in each direction. After the specified number of IRC steps the program will stop with the current direction and switch to the next one. If both 'MaxPoints' and 'MaxIRCSteps' are set to the same value then 'MaxPoints' takes precedence, therefore this option should be used to set a limit on the number of IRC steps if you intend to use the results later for a restart.

MinEnergyProfile

Type Bool

Default value No

GUI name Minimum energy profile

Description Calculate minimum energy profile (i.e. no mass-weighting) instead of the IRC.

MinPathLength

Type Float

Default value 0.1

Unit Angstrom

Description Minimum length of the path required before switching to energy minimization. Use this to overcome a small kink or a shoulder on the path.

Restart

Type Block

Description Restart options. Upon restart, the information about the IRC input parameters and the initial system (atomic coordinates, lattice, charge, etc.) is read from the restart file. The IRC input parameters can be modified from input. Except for 'MaxPoints' and 'Direction' all parameters not specified in the input will use their values from the restart file. The 'MaxPoints' and 'Direction' will be reset to their respective default values if not specified in the input. By default, the IRC calculation will continue from the point where it left off. However, the 'RedoForward' and/or 'RedoBackward' option can be used to enforce recalculation of a part of the reaction path, for example, using a different 'Step' value.

File

Type String

GUI name Restart

Description Name of an RKF restart file generated by a previous IRC calculation. Do not use this key to provide an RKF file generated by a TransitionStateSearch or a SinglePoint calculation, use the 'LoadSystem' block instead.

RedoBackward

Type Integer

Default value 0

Description IRC step number to start recalculating the backward path from. By default, if the backward path has not been completed then start after the last completed step. If the backward path has been completed and the 'RedoBackward' is omitted then no point on the backward path will be recomputed.

RedoForward

Type Integer

Default value 0

Description IRC step number to start recalculating the forward path from. By default, if the forward path has not been completed then start after the last completed step. If the forward path has been completed and the 'RedoForward' is omitted then no point on the forward path will be recomputed.

Step

Type Float

Default value 0.2

GUI name Step size

Description IRC step size in mass-weighted coordinates, $\sqrt{\text{amu}} \cdot \text{bohr}$. One may have to increase this value when heavy atoms are involved in the reaction, or decrease it if the reactant or products are very close to the transition state.

LoadEngine

Type String

Description The path to the file from which to load the engine configuration. Replaces the Engine block.

LoadSystem

Type Block

Recurring True

Description Block that controls reading the chemical system from a KF file instead of the [System] block.

File

Type String

Description The path of the KF file from which to load the system. It may also be the results directory containing it.

Section

Type String

Default value Molecule

Description The section on the KF file from which to load the system.

Log

Type Non-standard block

Description Configures the debugging loggers. Syntax: 'Level LoggerName'. Possible Levels: All, Debug, Info, Warning, Error, Fatal.

MolecularDynamics

Type Block

Description Configures molecular dynamics (with the velocity-Verlet algorithm) with and without thermostats. This block allows to specify the details of the molecular dynamics calculation.

AddMolecules

Type Block

Recurring True

GUI name Add molecules

Description This block controls adding molecules to the system (a.k.a. the Molecule Gun). Multiple occurrences of this block are possible.

By default, molecules are added at random positions in the simulation box with velocity matching the current system temperature. The initial position can be modified using one of the following keywords: Coords, CoordsBox, FractionalCoords, FractionalCoordsBox. The Coords and FractionalCoords keys can optionally be accompanied by CoordsSigma or FractionalCoordsSigma, respectively.

AtomTemperature

Type Float

Default value 0.0

Unit Kelvin

Description Add random velocity corresponding to the specified temperature to individual atoms of the molecule. This only affects rotational and internal degrees of freedom, not the net translational velocity of the inserted molecule as set by the other options.

ContactDistance

Type Float

Default value 0.0

Unit Angstrom

Description Translate the bullet along the velocity vector until it comes within ContactDistance of any other atom.

Coords

Type Float List

Unit Angstrom

Description Place molecules at or around the specified Cartesian coordinates.

This setting takes precedence over other ways to specify initial coordinates of the molecule: [CoordsBox], [FractionalCoords], and [FractionalCoordsBox].

CoordsBox

Type Float List

Unit Angstrom

Description Place molecules at random locations inside the specified box in Cartesian coordinates.

Coordinates of the box corners are specified as: Xmin, Xmax, Ymin, Ymax, Zmin, Zmax. This setting is ignored if Coords is used.

In AMSinput, if this field is not empty it will be used instead of the default Coords.

CoordsSigma

Type Float List

Unit Angstrom

Description Sigma values (one per Cartesian axis) for a Gauss distribution of the initial coordinates. Can only be used together with Coords.

DeviationAngle

Type Float

Default value 0.0

Unit Degree

Description Randomly tilt the shooting direction up to this angle away from the VelocityDirection vector.

Energy

Type Float

Unit Hartree

Description Initial kinetic energy of the molecule in the shooting direction.

EnergySigma

Type Float

Default value 0.0

Unit Hartree

Description Sigma value for the Gauss distribution of the initial kinetic energy around the specified value. Should only be used together with Energy.

FractionalCoords

Type Float List

Description Place molecules at or around the specified fractional coordinates in the main system's lattice. For non-periodic dimensions a Cartesian value in Angstrom is expected. This setting is ignored if [Coords] or [CoordsBox] is used.

FractionalCoordsBox

Type Float List

Description Place molecules at random locations inside the box specified as fractional coordinates in the main system's lattice.

Coordinates of the box corners are specified as: Xmin, Xmax, Ymin, Ymax, Zmin, Zmax.

For non-periodic dimensions the Cartesian value in Angstrom is expected.

This setting is ignored if [Coords], [CoordsBox], or [FractionalCoords] is used.

FractionalCoordsSigma

Type Float List

Description Sigma values (one per axis) for a Gauss distribution of the initial coordinates. For non-periodic dimensions the Cartesian value in Angstrom is expected. Can only be used together with FractionalCoords.

Frequency

Type Integer

Default value 0

Description A molecule is added every [Frequency] steps after the StartStep.

There is never a molecule added at step 0.

MinDistance

Type Float

Default value 0.0

Unit Angstrom

Description Keep the minimal distance to other atoms of the system when adding the molecule.

MoleFraction

Type Float

Description Defines a mixture to be deposited using one AddMolecules block per component.

AMS will randomly alternate between any guns that have MoleFraction set. These need to all have the same settings for StartStep, StopStep and Frequency. Any additional AddMolecules blocks without MoleFraction will remain completely independent.

NumAttempts

Type Integer

Default value 10

Description Try adding the molecule up to the specified number of times or until the MinDistance constraint is satisfied. If all attempts fail a message will be printed and the simulation will continue normally.

Rotate

Type Bool

Default value No

Description Rotate the molecule randomly before adding it to the system.

StartStep

Type Integer

Default value 0

Description Step number when the first molecule should be added. After that, molecules are added every Frequency steps.

For example, ff StartStep=99 and Frequency=100 then a molecule will be added at steps 99, 199, 299, etc...

No molecule will be added at step 0, so if StartStep=0 the first molecule is added at the step number equal to [Frequency].

StopStep

Type Integer

Description Do not add this molecule after the specified step.

System

Type String

Description String ID of the [System] that will be added with this 'gun'.

The lattice specified with this System is ignored and the main system's lattice is used instead.

AMSinput adds the system at the coordinates of the System (thus setting Coords to the center of the System).

Temperature

Type Float

Unit Kelvin

Description Initial energy of the molecule in the shooting direction will correspond to the given temperature.

TemperatureSigma

Type Float

Default value 0.0

Unit Kelvin

Description Sigma value for the Gauss distribution of the initial temperature the specified value. Should only be used together with Temperature.

Velocity

Type Float

Unit Angstrom/fs

Description Initial velocity of the molecule in the shooting direction.

VelocityDirection

Type Float List

Description Velocity direction vector for aimed shooting. It will be random if not specified.

In AMSinput add one or two atoms (which may be dummies).

One atom: use vector from center of the system to add to that atom.

Two atoms: use vector from the first to the second atom.

VelocitySigma

Type Float

Default value 0.0

Unit Angstrom/fs

Description Sigma value for the Gauss distribution of the initial velocity around the specified value. Should only be used together with Velocity.

ApplyForce

Type Block

Recurring True

Description The ApplyForce keyword can be used to apply an arbitrary constant force to a certain (subgroups of) atoms in the system

Force

Type Float List

Unit Hartree/Bohr

Description Defines the constant force vector

PerAtom

Type Bool

Default value No

Description If enabled, the Force vector is applied separately to every atom in the selected Region, so that the total net force on the Region equals the value of Force times the number of atoms in Region. This was the behaviour of ApplyForce in AMS2022. By default, with PerAtom disabled, the Force vector defines the total net force on the Region, so the force applied to each atom equals the value of Force divided by the number of atoms in Region.

Region

Type String

Recurring True

Description Apply the constant force to all atoms in this region.

ApplyVelocity

Type Block

Recurring True

Description The ApplyVelocity keyword can be used to move an arbitrary group of atoms in the system with a constant net velocity

Components

Type Multiple Choice

Default value XY

Options [X, Y, Z, XY, YZ, XZ, XYZ]

Description Select which components of the Velocity vector are used to set the corresponding components of the net velocity of the specified set of atoms. Any other components of Velocity are ignored and the motion of the selected atoms in those directions is unaffected by ApplyVelocity.

Region

Type String

Recurring True

Description Applies the defined velocity to all atoms in this region.

Velocity

Type Float List

Unit Angstrom/fs

Recurring False

Description The constant velocity that will be applied to the specified atoms.

Barostat

Type Block

Description This block allows to specify the use of a barostat during the simulation.

BulkModulus

Type Float

Default value 2200000000.0

Unit Pascal

Description An estimate of the bulk modulus (inverse compressibility) of the system for the Berendsen barostat.

This is only used to make Tau correspond to the true observed relaxation time constant. Values are commonly on the order of 10-100 GPa (1e10 to 1e11) for solids and 1 GPa (1e9) for liquids (2.2e9 for water). Use 1e9 to match the behavior of standalone ReaxFF.

ConstantVolume

Type Bool

Default value No

Description Keep the volume constant while allowing the box shape to change.

This is currently supported only by the MTK barostat.

Duration

Type Integer List

Description Specifies how many steps should a transition from a particular pressure to the next one in sequence take.

Equal

Type Multiple Choice

Default value None

Options [None, XYZ, XY, YZ, XZ]

Description Enforce equal scaling of the selected set of dimensions. They will be barostatted as one dimension according to the average pressure over the components.

Pressure

Type Float List

Unit Pascal

Description Specifies the target pressure.

You can specify multiple pressures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one p to the next p (using a linear ramp).

Scale

Type Multiple Choice

Default value XYZ

Options [XYZ, Shape, X, Y, Z, XY, YZ, XZ]

Description Dimensions that should be scaled by the barostat to maintain pressure. Selecting Shape means that all three dimensions and also all the cell angles are allowed to change.

Tau

Type Float

Unit Femtoseconds

GUI name Damping constant

Description Specifies the time constant of the barostat.

Type

Type Multiple Choice

Default value None

Options [None, Berendsen, MTK]

GUI name Barostat

Description Selects the type of the barostat.

BinLog

Type Block

Description This block controls writing the BinLog section in ams.rkf, which contains the selected MD state scalars and tensors from every MD step. No per-atom data is written. If you need the per-atom data then you can set the sampling frequency to 1 and get the required data from the MDHistory section. The tensors are written per component, that is, the pressure tensor is

written as six variables: PressureTensor_xx, PressureTensor_yy, etc.. To reduce the file size, all data is written in blocks.

BiasEnergy

Type Bool

Default value No

Description Write the CVDH bias energy.

BoostFactor

Type Bool

Default value No

Description Write the CVDH boost factor.

ConservedEnergy

Type Bool

Default value No

Description Write the conserved energy value.

Density

Type Bool

Default value No

Description Write the density.

Hypertime

Type Bool

Default value No

Description Write the CVDH hypertime.

KineticEnergy

Type Bool

Default value No

Description Write the kinetic energy value.

MaxBiasEnergy

Type Bool

Default value No

Description Write the max CVDH bias energy.

MaxBoostFactor

Type Bool

Default value No

Description Write the max CVDH boost factor.

PotentialEnergy

Type Bool

Default value No

Description Write the potential energy value.

Pressure

Type Bool

Default value No

Description Write the pressure.

PressureTensor

Type Bool

Default value No

Description Write the pressure tensor in Voigt notation. Each component of the tensor is written in its own variable.

Step

Type Bool

Default value No

Description Write the step index during the simulation.

Temperature

Type Bool

Default value No

Description Write the temperature.

Time

Type Bool

Default value No

Description Write the simulation time (fs).

TotalEnergy

Type Bool

Default value No

Description Write the total energy value.

Volume

Type Bool

Default value No

Description Write the simulation cell volume, area or length, depending on the system periodicity.

BondBoost

Type Block

Recurring True

Description Forced reaction (bond boost) definitions. Multiple BondBoost blocks may be specified, which will be treated independently.

Chain**Type** Block**Description** Specifications of a chain of atoms. When a chain is detected the distance restraints will be activated. No other chain of this type will be detected while any restraints for this chain is active.**AtomNames****Type** String**Description** Atom names specifying the chain. An atom name can optionally be followed by '@' and a region name, in this case only atoms of this type from the given region will be matched. A leading '@' followed by a number indicates that this position in the chain must be occupied by the atom found earlier at the specified position in the chain. For example "O H N C @1" indicates that the last atom in the chain of the five atoms must be the first oxygen, thus defining a 4-membered ring. This is the only way to define a ring because implicit rings will not be detected. For example, "O H N C O" does not include rings.**MaxDistances****Type** Float List**Unit** Angstrom**Description** Maximum distances for each pair of atoms in the chain. The number of distances must be one less than the number of AtomNames.**MinDistances****Type** Float List**Unit** Angstrom**Description** Minimum distances for each pair of atoms in the chain. The number of distances must be one less than the number of AtomNames.**DistanceRestraint****Type** String**Recurring** True**Description** Specify two atom indices followed by the optimum distance in Angstrom, the first parameter and, optionally, the profile type and the second parameter.

This restraint will try to keep the distance between the two specified atoms at the given value. For periodic systems this restraint follows the minimum image convention.

Each atom index indicates a position of the corresponding atom in the AtomNames key. Currently recognized restraint profile types: Harmonic (default), Hyperbolic, Erf, GaussianWell. The first parameter is the force constant for the Harmonic, Hyperbolic, and Erf profiles, or well depth for GaussianWell. The second parameter is the asymptotic force value F(Inf) for Hyperbolic and Erf profiles, or the factor before x^2 in the exponent for GaussianWell.

Note: the GaussianWell restraint should be used with the Moving flag.

Moving**Type** Bool**Default value** No**GUI name** Move restraint

Description Move the restraints created with this BondBoost. The restraint value will start at the current coordinate's value and will move towards the optimum during the restraint's lifetime. The increment is calculated from the initial deviation and the [NSteps] parameter.

This feature should be used with the GaussianWell restraint types.

NSteps

Type Integer

GUI name Boost lifetime

Description Number of steps the restraints will remain active until removed. Atoms participating in one reaction are not available for the given number of steps.

NumInstances

Type Integer

Default value 1

GUI name Number of instances

Description Number of reactions of this type taking place simultaneously.

Units

Type Multiple Choice

Default value Default

Options [Default, MD]

GUI name Restr. parameter units

Description Change energy, force and force constant units in the DistanceRestraint key from the default (atomic units) to those often used in the MD community (based on kcal/mol and Angstrom). Units for the optimum distances are not affected.

CRESTMTD

Type Block

GUI name CREST_MTD

Description Input for CREST metadynamics simulation.

AddEnergy

Type Bool

Default value No

Description Add the bias energy to the potential energy (to match the gradients)

GaussianScaling

Type Block

Description Options for gradual introduction of the Gaussians

ScaleGaussians

Type Bool

Default value Yes

Description Introduce the Gaussians gradually, using a scaling function

ScalingSlope

Type Float

Default value 0.03

Description Slope of the scaling function for the Gaussians with respect to time

Height

Type Float

Unit Hartree

Description The height of the Gaussians added

NGaussiansMax

Type Integer

Description Maximum number of Gaussians stored

NSteps

Type Integer

Description Interval of Gaussian placement

Region

Type String

Default value *

Description Restrict the range of atoms for RMSD calculation to the specified region.

RestartFile

Type String

Description Filename for file from which to read data on Gaussians placed previously.

Width

Type Float

Unit Bohr

Description The width of the Gaussians added in terms of the RMSD

CVHD

Type Block

Recurring True

GUI name CVHD

Description Input for the Collective Variable-driven HyperDynamics (CVHD).

Bias

Type Block

Description The bias is built from a series of Gaussian peaks deposited on the collective variable axis every [Frequency] steps during MD. Each peak is characterized by its (possibly damped) height and the RMS width (standard deviation).

DampingTemp

Type Float

Default value 0.0

Unit Kelvin

GUI name Bias damping T

Description During well-tempered hyperdynamics the height of the added bias is scaled down with an $\exp(-E/kT)$ factor [PhysRevLett 100, 020603 (2008)], where E is the current value of the bias at the given CV value and T is the damping temperature DampingTemp. If DampingTemp is zero then no damping is applied.

Delta

Type Float

Description Standard deviation parameter of the Gaussian bias peak.

Height

Type Float

Unit Hartree

Description Height of the Gaussian bias peak.

ColVarBB

Type Block

Recurring True

GUI name Collective Variable

Description Description of a bond-breaking collective variable (CV) as described in [Bal & Neyts, JCTC, 11 (2015)]. A collective variable may consist of multiple ColVar blocks.

at1

Type Block

Description Specifies the first bonded atom in the collective variable.

region

Type String

Default value *

Description Restrict the selection of bonded atoms to a specific region. If this is not set, atoms anywhere in the system will be selected.

symbol

Type String

Description Atom type name of the first atom of the bond. The name must be as it appears in the System block. That is, if the atom name contains an extension (e.g C.1) then the full name including the extension must be used here.

at2

Type Block

Description Specifies the second bonded atom in the collective variable.

region

Type String

Default value *

Description Restrict the selection of bonded atoms to a specific region. If this is not set, atoms anywhere in the system will be selected.

symbol

Type String

Description Atom type name of the second atom of the bond. The value is allowed to be the same as [at1], in which case bonds between atoms of the same type will be included.

cutoff

Type Float

Default value 0.3

GUI name Bond order cutoff

Description Bond order cutoff. Bonds with BO below this value are ignored when creating the initial bond list for the CV. The bond list does not change during lifetime of the variable even if some bond orders drop below the cutoff.

p

Type Integer

Default value 6

GUI name Exponent p

Description Exponent value p used to calculate the p-norm for this CV.

rmax

Type Float

Unit Angstrom

GUI name R max

Description Max bond distance parameter Rmax used for calculating the CV. It should be close to the transition-state distance for the corresponding bond.

rmin

Type Float

Unit Angstrom

GUI name R min

Description Min bond distance parameter Rmin used for calculating the CV. It should be close to equilibrium distance for the corresponding bond.

Frequency

Type Integer

Description Frequency of adding a new bias peak, in steps. New bias is deposited every [Frequency] steps after [StartStep] if the following conditions are satisfied: the current CV value is less than 0.9 (to avoid creating barriers at the transition state), the step number is greater than or equal to [StartStep], and the step number is less than or equal to [StopStep].

StartStep

Type Integer

Description If this key is specified, the first bias will be deposited at this step. Otherwise, the first bias peak is added at the step number equal to the Frequency parameter. The bias is never deposited at step 0.

StopStep

Type Integer

Description No bias will be deposited after the specified step. The already deposited bias will continue to be applied until the reaction event occurs. After that no new CVHD will be started. By default, the CVHD runs for the whole duration of the MD calculation.

WaitSteps

Type Integer

Description If the CV value becomes equal to 1 and remains at this value for this many steps then the reaction event is considered having taken place. After this, the collective variable will be reset and the bias will be removed.

CalcPressure

Type Bool

Default value No

GUI name Calculate pressure

Description Calculate the pressure in periodic systems.

This may be computationally expensive for some engines that require numerical differentiation.

Some other engines can calculate the pressure for negligible additional cost and will always do so, even if this option is disabled.

Checkpoint

Type Block

Description Sets the frequency for storing the entire MD state necessary for restarting the calculation.

Frequency

Type Integer

Default value 1000

GUI name Checkpoint frequency

Description Write the MD state and engine-specific data to the respective .rkf files once every N steps.

WriteProperties

Type Bool

Default value No

Description Write the properties from the properties section to the ChecoPoint file once every N steps.

CopyRestartTrajectory

Type Bool

Default value No

Description If the keyword Restart is present, the content of the restartfile is copied to the ams.rkf file.

CosineShear

Type Block

Description Apply an external acceleration to all atoms of a fluid using a periodic (cosine) function along a selected coordinate axis. This induces a periodic shear flow profile which can be used to determine the viscosity.

Acceleration

Type Float

Default value 5e-06

Unit Angstrom/fs²

Description Amplitude of the applied cosine shear acceleration profile. The default value should be a rough first guess for water and it needs to be adjusted by experimentation for other systems.

Enabled

Type Bool

Default value No

GUI name Enable cosine shear

Description Apply a cosine shear acceleration profile for a NEMD calculation of viscosity.

FlowDirection

Type Float List

Default value [1.0, 0.0, 0.0]

Description The direction in which to apply the shear acceleration, in Cartesian coordinates. The magnitude of this vector is ignored (AMS will normalize it internally). FlowDirection has to be perpendicular to ProfileAxis.

ProfileAxis

Type Multiple Choice

Default value Z

Options [X, Y, Z]

Description The Cartesian coordinate axis along which the cosine wave runs

Deformation

Type Block

Recurring True

Description Deform the periodic lattice of the system during the simulation.

LatticeVelocity

Type Non-standard block

Description Velocity of individual lattice vector components in Angstrom/fs. The format is identical to the System%Lattice block. For Type Sine and Cosine, this defines the maximum velocity (at the inflection point).

LengthRate**Type** Float List**Default value** [0.0, 0.0, 0.0]**Description** Relative rate of change of each lattice vector per step.**LengthVelocity****Type** Float List**Default value** [0.0, 0.0, 0.0]**Unit** Angstrom/fs**Description** Change the length of each lattice vector with this velocity. With Type=Exponential, LengthVelocity is divided by the current lattice vector lengths on Start-Step to determine a LengthRate, which is then applied on all subsequent steps. For Type Sine and Cosine, this defines the maximum velocity (at the inflection point).**Period****Type** Float**Unit** Femtoseconds**Description** Period of oscillation for Type Sine and Cosine.**ScaleAtoms****Type** Bool**Default value** Yes**Description** Scale the atomic positions together with the lattice vectors. Disable this to deform only the lattice, keeping the coordinates of atoms unchanged.**StartStep****Type** Integer**Default value** 1**Description** First step at which the deformation will be applied.**StopStep****Type** Integer**Default value** 0**Description** Last step at which the deformation will be applied. If unset or zero, nSteps will be used instead.**StrainRate****Type** Non-standard block**Description** Strain rate matrix to be applied on every step. The format is identical to the System%Lattice block.**TargetLattice****Type** Non-standard block**Description** Target lattice vectors to be achieved by StopStep. The format is identical to the System%Lattice block.

TargetLength**Type** Float List**Default value** [0.0, 0.0, 0.0]**Unit** Angstrom**Description** Target lengths of each lattice vector to be achieved by StopStep. The number of values should equal the periodicity of the system. If a value is zero, the corresponding lattice vector will not be modified.**Type****Type** Multiple Choice**Default value** Linear**Options** [Linear, Exponential, Sine, Cosine]**Description** Function defining the time dependence of the deformed lattice parameters.

Linear increments the lattice parameters by the same absolute amount every timestep. Exponential multiplies the lattice parameters by the same factor every timestep. Only StrainRate, LengthRate, and LengthVelocity are supported for Type=Exponential. Sine deforms the system from the starting lattice to TargetLattice/TargetLength and then by the same amount to the opposite direction, while Cosine deforms the system from the starting lattice to the target and back.

Gravity**Type** Block**Description** Apply a constant acceleration in -z.**Acceleration****Type** Float**Default value** 0.0**Unit** Angstrom/fs²**Description** Magnitude of the applied acceleration.**HeatExchange****Type** Block**Recurring** True**GUI name** Heat exchange**Description** Input for the heat-exchange non-equilibrium MD (T-NEMD).**HeatingRate****Type** Float**Unit** Hartree/fs**Description** Rate at which the energy is added to the Source and removed from the Sink. A heating rate of 1 Hartree/fs equals to about 0.00436 Watt of power being transferred through the system.**Method****Type** Multiple Choice

Default value Simple

Options [Simple, HEX, eHEX]

Description Heat exchange method used.

Simple: kinetic energy of the atoms of the source and sink regions is modified irrespective of that of the center of mass (CoM) of the region (recommended for solids).

HEX: kinetic energy of the atoms of these regions is modified keeping that of the corresponding CoM constant.

eHEX: an enhanced version of HEX that conserves the total energy better (recommended for gases and liquids).

Sink

Type Block

Description Defines the heat sink region (where the heat will be removed).

AtomList

Type Integer List

GUI name Sink region

Description The atoms that are part of the sink.

This key is ignored if the [Box] block or [Region] key is present.

Box

Type Block

Description Part of the simulation box (in fractional cell coordinates) defining the heat sink.

If this block is specified, then by default, the whole box in each of the three dimensions is used, which usually does not make much sense. Normally, you will want to set the bounds along one of the axes.

Amax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the third axis.

Region

Type String

GUI name Sink region

Description The region that is the sink.

This key is ignored if the [Box] block is present.

Source

Type Block

Description Defines the heat source region (where the heat will be added).

AtomList

Type Integer List

GUI name Source region

Description The atoms that are part of the source.

This key is ignored if the [Box] block or [Region] key is present.

Box

Type Block

Description Part of the simulation box (in fractional cell coordinates) defining the heat source.

If this block is specified, then by default, the whole box in each of the three dimensions is used, which usually does not make much sense. Normally, you will want to set the bounds along one of the axes. This block is mutually exclusive with the FirstAtom/LastAtom setting.

Amax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Default value 1.0

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Default value 0.0

Description Coordinate of the lower bound along the third axis.

Region

Type String

GUI name Source region

Description The region that is the source.

This key is ignored if the [Box] block is present.

StartStep

Type Integer

Default value 0

Description Index of the MD step at which the heat exchange will start.

StopStep

Type Integer

Description Index of the MD step at which the heat exchange will stop.

InitialVelocities

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

File

Type String

Description AMS RKF file containing the initial velocities.

RandomVelocitiesMethod

Type Multiple Choice

Default value Exact

Options [Exact, Boltzmann, Gromacs]

GUI name Velocity randomization method

Description Specifies how are random velocities generated. Three methods are available.

Exact: Velocities are scaled to exactly match set random velocities temperature.

Boltzmann: Velocities are not scaled and sample Maxwell-Boltzmann distribution. However, the distribution is not corrected for constraints.

Gromacs: Velocities are scaled to match set random velocities temperature, but removal of net momentum is performed only after the scaling. Resulting kinetic energy is lower based on how much net momentum the system had.

Temperature

Type Float

Unit Kelvin

GUI name Initial temperature

Description Sets the temperature for the Maxwell-Boltzmann distribution when the type of the initial velocities is set to random, in which case specifying this key is mandatory.

AMSinput will use the first temperature of the first thermostat as default.

Type

Type Multiple Choice

Default value Random

Options [Zero, Random, FromFile, Input]

GUI name Initial velocities

Description Specifies the initial velocities to assign to the atoms. Three methods to assign velocities are available.

Zero: All atom are at rest at the beginning of the calculation.

Random: Initial atom velocities follow a Maxwell-Boltzmann distribution for the temperature given by the [MolecularDynamics%InitialVelocities%Temperature] keyword.

FromFile: Load the velocities from a previous ams result file.

Input: Atom's velocities are set to the values specified in the [MolecularDynamics%InitialVelocities%Values] block, which can be accessed via the Expert AMS panel in AMSinput.

Values

Type Non-standard block

Description This block specifies the velocity of each atom, in Angstrom/fs, when [MolecularDynamics%InitialVelocities%Type] is set to Input. Each row must contain three floating point values (corresponding to the x,y,z component of the velocity vector) and a number of rows equal to the number of atoms must be present, given in the same order as the [System%Atoms] block.

NSteps

Type Integer

Default value 1000

GUI name Number of steps

Description The number of steps to be taken in the MD simulation.

Plumed

Type Block

Description Input for PLUMED. The parallel option is still experimental.

Input

Type Non-standard block

Description Input for PLUMED. Contents of this block is passed to PLUMED as is.

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

Preserve

Type Block

Description Periodically remove numerical drift accumulated during the simulation to preserve different whole-system parameters.

AngularMomentum

Type Bool

Default value Yes

GUI name : Angular momentum

Description Remove overall angular momentum of the system. This option is ignored for 2D and 3D-periodic systems.

CenterOfMass

Type Bool

Default value No

GUI name : Center of mass

Description Translate the system to keep its center of mass at the coordinate origin. This option is not very useful for 3D-periodic systems.

Momentum

Type Bool

Default value Yes

GUI name Preserve: Total momentum

Description Remove overall (linear) momentum of the system.

Print

Type Block

Description This block controls the printing of additional information to stdout.

System

Type Bool

Default value No

Description Print the chemical system before and after the simulation.

Velocities

Type Bool

Default value No

Description Print the atomic velocities before and after the simulation.

Reactor

Type Block

Recurring True

Description Define one phase of the nanoreactor. A reactor is a region of space surrounded by an elastic wall. Atoms inside the region are not affected. Atoms outside it will be pushed back with force depending on the [ForceConstant] and the [MassScaled] flag.

ForceConstant

Type Float

GUI name Reactor force constant

Description Force constant of the reactor wall in Hartree/Bohr² (or Hartree/Bohr²/Dalton if [MassScaled] is true).

MassScaled

Type Bool

Default value Yes

GUI name Scale force by mass

Description If this flag is disabled the force on an atom outside of the reactor depends only on the atomic coordinates and the force constant. Otherwise, the force is also multiplied by the mass of the atom. This means that atoms at the same distance from the wall will receive the same accelerate due to the wall potential.

NSteps

Type Integer

GUI name Reactor lifetime

Description Number of steps for which the reactor will remain active until disabled. The next reactor will be activated immediately after this. After the last reactor is disabled the cycle will repeat.

Radius

Type Float

Unit Angstrom

GUI name Reactor radius

Description Radius of the reactor sphere.

ReflectiveWall

Type Block

Recurring True

Description Apply a reflective wall in space

Axis

Type Float List

Unit Angstrom

Description Defines the normal vector perpendicular to the plane of the reflective wall. Any particle moving in this direction will be reflected back.

Region

Type String

Recurring True

Description Apply the reflective wall to all atoms in this region.

Threshold

Type Float

Unit Angstrom

Description Defines the threshold value determining the position of the reflective wall. If the dot product of a position of a particle with Axis exceeds Threshold, the particle will be reflected. This means that the plane of the wall passes through a point given by Axis times Threshold.

Remap

Type Block

Description Control periodic remapping (backtranslation) of atoms into the PBC box.

Type**Type** Multiple Choice**Default value** Atoms**Options** [None, Atoms]**Description** Select the method used to remap atoms into the unit cell.

None: Disable remapping completely.

Atoms: Remap any atoms that leave the unit cell.

RemoveMolecules**Type** Block**Recurring** True**GUI name** Remove molecules**Description** This block controls removal of molecules from the system. Multiple occurrences of this block are possible.**Formula****Type** String**Description** Molecular formula of the molecules that should be removed from the system.

The order of elements in the formula is very important and the correct order is: C, H, all other elements in the strictly alphabetic order. Element names are case-sensitive, spaces in the formula are not allowed. Digit '1' must be omitted.

Valid formula examples: C2H6O, H2O, O2S. Invalid formula examples: C2H5OH, H2O1, OH, SO2. Invalid formulas are silently ignored.

Use * to remove any molecule, which must be combined with SinkBox or SafeBox.

Frequency**Type** Integer**Default value** 0**Description** The specified molecules are removed every so many steps after the StartStep. There is never a molecule removed at step 0.**SafeBox****Type** Block**Description** Part of the simulation box where molecules may not be removed. Only one of the SinkBox or SafeBox blocks may be present. If this block is present the molecule will not be removed if any of its atoms is within the box. For a periodic dimension it is given as a fraction of the simulation box (the full 0 to 1 range by default). For a non-periodic dimension it represents absolute Cartesian coordinates in Angstrom.**Amax****Type** Float**Description** Coordinate of the upper bound along the first axis.**Amin****Type** Float

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Description Coordinate of the lower bound along the third axis.

FractionalCoordsBox

Type Float List

GUI name Safe box

Description Do not remove molecules that are (partly) inside the safe box.

Borders of the safe box specified as: Amin, Amax, Bmin, Bmax, Cmin, Cmax.

For periodic dimensions fractional coordinates between 0 and 1 and for non-periodic dimensions Cartesian values in Angstrom are expected.

SinkBox

Type Block

Description Part of the simulation box where matching molecules will be removed. By default, molecules matching the formula will be removed regardless of their location. If this block is present then such a molecule will only be removed if any of its atoms is within the box. For a periodic dimension it is given as a fraction of the simulation box (the full 0 to 1 range by default). For a non-periodic dimension it represents absolute Cartesian coordinates in Angstrom.

Amax

Type Float

Description Coordinate of the upper bound along the first axis.

Amin

Type Float

Description Coordinate of the lower bound along the first axis.

Bmax

Type Float

Description Coordinate of the upper bound along the second axis.

Bmin

Type Float

Description Coordinate of the lower bound along the second axis.

Cmax

Type Float

Description Coordinate of the upper bound along the third axis.

Cmin

Type Float

Description Coordinate of the lower bound along the third axis.

FractionalCoordsBox

Type Float List

GUI name Sink box

Description Remove molecules that are (partly) inside the sink box.

Borders of the sink box specified as: Amin, Amax, Bmin, Bmax, Cmin, Cmax.

For periodic dimensions fractional coordinates between 0 and 1 and for non-periodic dimensions Cartesian values in Angstrom are expected.

StartStep

Type Integer

Default value 0

Description Step number when molecules are removed for the first time. After that, molecules are removed every [Frequency] steps.

For example, if StartStep=99 and Frequency=100 then molecules will be removed at steps 99, 199, 299, etc...

No molecule will be removed at step 0, so if StartStep=0 the first molecules are removed at the step number equal to [Frequency].

StopStep

Type Integer

Description Do not remove the specified molecules after this step.

ReplicaExchange

Type Block

Description This block is used for (temperature) Replica Exchange MD (Parallel Tempering) simulations.

AllowWrongResults

Type Bool

Default value No

Description Allow combining Replica Exchange with other features when the combination is known to produce physically incorrect results.

EWMALength

Type Integer

Default value 10

Description Length of the exponentially weighted moving average used to smooth swap probabilities for monitoring.

This value is equal to the inverse of the EWMA mixing factor.

SwapFrequency

Type Integer

Default value 100

Description Attempt an exchange every N steps.

TemperatureFactors

Type Float List

Description This is the ratio of the temperatures of two successive replicas.

The first value sets the temperature of the second replica with respect to the first replica, the second value sets the temperature of the third replica with respect to the second one, and so on. If there are fewer values than nReplicas, the last value of TemperatureFactor is used for all the remaining replicas.

Temperatures

Type Float List

Description List of temperatures for all replicas except for the first one.

This is mutually exclusive with TemperatureFactors. Exactly nReplicas-1 temperature values need to be specified, in increasing order. The temperature of the first replica is given by [Thermostat%Temperature].

nReplicas

Type Integer

Default value 1

GUI name Number of replicas

Description Number of replicas to run in parallel.

Restart

Type String

GUI name Restart from

Description The path to the ams.rkf file from which to restart the simulation.

Shake

Type Block

Description Parameters of the Shake/Rattle algorithm.

All

Type String

Recurring True

GUI name Constrain all

Description Constraint description in one the following formats: All [bondOrder] bonds at1 at2 [to distance] All triangles at1 at2 at3

The first option constrains all bonds between atoms at1 at2 to a certain length, while the second - bonds at1-at2 and at2-at3 and the angle between them.

The [bondOrder] can be a number or a string such as single, double, triple or aromatic. If it's omitted then all bonds between specified atoms will be constrained. Atom names are case-sensitive and they must be as they are in the Atoms block, or an asterisk '*' denoting any atom. The distance, if present, must be in Angstrom. If it is omitted then the bond length from the initial geometry is used.

Important: only the bonds present in the system at certain points of the simulation (at the start or right after adding/removing atoms) can be constrained, which means that the bonds may need to be specified in the System block.

Warning: the triangles constraint should be used with care because each constrained bond or angle means removing one degree of freedom from the dynamics. When there are too many constraints (for example, "All triangles H C H" in methane) some of them may be linearly dependent, which will lead to an error in the temperature computation.

Valid examples: All single bonds C C to 1.4 All bonds O H to 0.98 All bonds O H All bonds H * All triangles H * H

ConvergeR2

Type Float

Default value 1e-08

Description Convergence criterion on the max squared difference, in atomic units.

ConvergeRV

Type Float

Default value 1e-08

Description Convergence criterion on the orthogonality of the constraint and the relative atomic velocity, in atomic units.

Iterations

Type Integer

Default value 100

Description Number of iterations.

ShakeInitialCoordinates

Type Bool

Default value Yes

Description Apply constraints before computing the first energy and gradients.

Thermostat

Type Block

Recurring True

Description This block allows to specify the use of a thermostat during the simulation. Depending on the selected thermostat type, different additional options may be needed to characterize the specific thermostat' behavior.

BerendsenApply**Type** Multiple Choice**Default value** Global**Options** [Local, Global]**GUI name** Apply Berendsen**Description** Select how to apply the scaling correction for the Berendsen thermostat:

- per-atom-velocity (Local) - on the molecular system as a whole (Global).

ChainLength**Type** Integer**Default value** 10**GUI name** NHC chain length**Description** Number of individual thermostats forming the NHC thermostat**Duration****Type** Integer List**GUI name** Duration(s)**Description** Specifies how many steps should a transition from a particular temperature to the next one in sequence take.**Region****Type** String**Default value** ***Description** The identifier of the region to thermostat. The default '*' applies the thermostat to the entire system. The value can be a plain region name, or a region expression, e.g. '*-myregion' to thermostat all atoms that are not in myregion, or 'regionA+regionB' to thermostat the union of the 'regionA' and 'regionB'. Note that if multiple thermostats are used, their regions may not overlap.**Tau****Type** Float**Unit** Femtoseconds**GUI name** Damping constant**Description** The time constant of the thermostat.**Temperature****Type** Float List**Unit** Kelvin**GUI name** Temperature(s)**Description** The target temperature of the thermostat.

You can specify multiple temperatures (separated by spaces). In that case the Duration field specifies how many steps to use for the transition from one T to the next T (using a linear ramp). For NHC thermostat, the temperature may not be zero.

Type

Type Multiple Choice

Default value None

Options [None, Berendsen, NHC]

GUI name Thermostat

Description Selects the type of the thermostat.

TimeStep

Type Float

Default value 0.25

Unit Femtoseconds

Description The time difference per step.

Trajectory

Type Block

Description Sets the frequency for printing to stdout and storing the molecular configuration on the .rkf file.

PrintFreq

Type Integer

GUI name Printing frequency

Description Print current thermodynamic properties to the output every N steps. By default this is done every SamplingFreq steps.

SamplingFreq

Type Integer

Default value 100

GUI name Sample frequency

Description Write the the molecular geometry (and possibly other properties) to the .rkf file once every N steps.

TProfileGridPoints

Type Integer

Default value 0

Description Number of points in the temperature profile. If TProfileGridPoints > 0, a temperature profile along each of the three lattice axes will be written to the .rkf file. The temperature at a given profile point is calculated as the total temperature of all atoms inside the corresponding slice of the simulation box, time-averaged over all MD steps since the previous snapshot. By default, no profile is generated.

WriteBonds

Type Bool

Default value Yes

Description Write detected bonds to the .rkf file.

WriteCharges

Type Bool

Default value Yes

Description Write current atomic point charges (if available) to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze charges.

WriteCoordinates

Type Bool

Default value Yes

Description Write atomic coordinates to the .rkf file.

WriteEngineGradients

Type Bool

Default value No

Description Write atomic gradients (negative of the atomic forces, as calculated by the engine) to the History section of ams.rkf.

WriteMolecules

Type Bool

Default value Yes

Description Write the results of molecule analysis to the .rkf file.

WriteVelocities

Type Bool

Default value Yes

Description Write velocities to the .rkf file. Disable this to reduce trajectory size if you do not need to analyze the velocities.

fbMC

Type Block

Recurring True

GUI name fbMC

Description This block sets up force bias Monte Carlo interleaved with the molecular dynamics simulation.

Frequency

Type Integer

Default value 1

Description Run the fbMC procedure every Frequency MD steps.

MassRoot

Type Float

Default value 2.0

Description Inverse of the exponent used to mass-weight fbMC steps.

MolecularMoves**Type** Block**Description** Move molecules as rigid bodies in addition to normal atomic moves.**Enabled****Type** Bool**Default value** No**GUI name** Enable molecular moves**Description** Enable moving molecules as rigid bodies based on net forces and torques. Ordinary per-atom displacements will then be based on residual atomic forces.**RotationStepAngle****Type** Float**Default value** 0.1**Unit** Radian**Description** Maximum allowed angle of rotation of each molecule in one fbMC step.**TranslationStepLength****Type** Float**Default value** 0.1**Unit** Angstrom**Description** Maximum allowed displacement of each molecule in each Cartesian coordinate in one fbMC step.**NSteps****Type** Integer**GUI name** Number of steps**Description** Number of fbMC steps to perform on every invocation of the procedure.**PrintFreq****Type** Integer**GUI name** Printing frequency**Description** Print current thermodynamic properties to the output every N fbMC steps. This defaults to the PrintFreq set in the Trajectory block. Setting this to zero disables printing fbMC steps.**StartStep****Type** Integer**Default value** 1**Description** First step at which the fbMC procedure may run.**StepLength****Type** Float**Default value** 0.1

Unit Angstrom

Description Maximum allowed displacement of the lightest atom in the system in each Cartesian coordinate in one fbMC step.

StopStep

Type Integer

Default value 0

Description Last step at which the fbMC procedure may run. If unset or zero, there is no limit.

Temperature

Type Float

Unit Kelvin

Description Temperature used for fbMC.

Molecules

Type Block

Description Configures details of the molecular composition analysis enabled by the Properties%Molecules block.

AdsorptionSupportRegion

Type String

GUI name Adsorption support region

Description Select region that will represent a support for adsorption analysis. Adsorbed molecules will receive an '(ads)' suffix after name of the element bonded to the support. Such elements will be listed separate from atoms of the same element not bonded to the support, for example, HOH(ads) for a water molecule bonded to a surface via one of its H atoms.

BondOrderCutoff

Type Float

Default value 0.5

Description Bond order cutoff for analysis of the molecular composition. Bonds with bond order smaller than this value are neglected when determining the molecular composition.

NEB

Type Block

Description Configures details of the Nudged Elastic Band optimization.

Climbing

Type Bool

Default value Yes

GUI name Climb highest image to TS

Description Use the climbing image algorithm to drive the highest image to the transition state.

ClimbingThreshold

Type Float

Default value 0.0

Unit Hartree/Bohr

GUI name CI force threshold

Description Climbing image force threshold. If `ClimbingThreshold > 0` and the max perpendicular force component is above the threshold then no climbing is performed at this step. This entry can be used to get a better approximation for the reaction path before starting the search for the transition state. A typical value is 0.01 Hartree/Bohr.

Images

Type Integer

Default value 8

GUI name Number of images

Description Number of NEB images (not counting the chain ends). Using more images will result in a smoother reaction path and can help with convergence problems, but it will also increase the computation time.

InterpolateInternal

Type Bool

Default value Yes

GUI name Interpolate in Internal coordinates

Description The initial NEB image geometries are calculated by interpolating between the initial and the final state. By default, for non-periodic systems the interpolation is performed in Internal coordinates but the user can choose to do it in the Cartesian ones. For periodic systems the interpolation is always done in Cartesian coordinates.

InterpolateShortest

Type Bool

Default value Yes

GUI name Interpolate across cell boundary

Description Allow interpolation across periodic cell boundaries. Set to false if an atom is intended to move more than half across the simulation box during reaction.

Iterations

Type Integer

GUI name Maximum number of iterations

Description Maximum number of NEB iterations. The default value depends on the number of degrees of freedom (number of images, atoms, periodic dimensions).

Jacobian

Type Float

GUI name Jacobian value

Description Scaling factor used to convert the lattice strain to a NEB coordinate value. Default value: $\sqrt{N} \cdot (V/N)^{1/d}$, where V - lattice volume (area for 2D, length for 1D), N - number of atoms, and d - number of periodic dimensions.

LoadPath

Type Block

Description Provide details about the trajectory to get the initial NEB path from. PESScan and NEB trajectories are supported. Only the last geometry for each point on the trajectory is considered.

File

Type String

GUI name Initial path file

Description Provide an ams.rkf file to load the initial path from. All geometries of this calculation, including initial and final, will be taken from the History section of the file.

Note that for a PESScan it should be a 1D path.

Geometries

Type Integer List

GUI name Raw geometry indices

Description Raw indices of the geometries from the History section. By default the last geometry of each path point is used.

Points

Type Integer List

GUI name Path points

Description By default the whole path is used, which may sometimes be not desirable. For example when a PESScan revealed multiple barriers. In this case one can specify indices of the path points to be used. The last geometry of the specified path point will be loaded.

MapAtomsToCell

Type Bool

Default value Yes

GUI name Map atoms to cell

Description Translate atoms to the $[-0.5,0.5]$ cell before every step. This option cannot be disabled for SS-NEB.

OldTangent

Type Bool

Default value No

GUI name Use old tangent

Description Turn on the old central difference tangent.

OptimizeEnds

Type Bool

Default value Yes

GUI name Optimize reactants/products

Description Start the NEB with optimization of the reactant and product geometries.

OptimizeLattice

Type Bool

Default value No

GUI name Optimize lattice

Description Turn on the solid-state NEB (SS-NEB).

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

ReOptimizeEnds

Type Bool

Default value No

GUI name Re-optimize reactants/products

Description Re-optimize reactant and product geometries upon restart.

Restart

Type String

GUI name Restart from

Description Provide an ams.rkf file from a previous NEB calculation to restart from. It can be an unfinished NEB calculation or one performed with different engine parameters.

Skewness

Type Float

Default value 1.0

GUI name Skewness

Description Degree of how much images are shifted towards or away from the TS, which may help tackle problems with a long reaction path (for example involving a loose adsorption complex) without needing too many images. A value greater than 1 will make sure that images are concentrated near the transition state. The optimal value depends on the path length, the number of images (larger [Skewness] may be needed for a longer path and fewer images). Technically [Skewness] is equal to the ratio between the optimized distances to the lower and the higher neighbor image on the path.

Spring

Type Float

Default value 1.0

Unit Hartree/Bohr²

GUI name Spring value

Description Spring force constant in atomic units.

NormalModes

Type Block

Description Configures details of a normal modes calculation.

BlockDisplacements

Type Block

Description Configures details of a Block Normal Modes (a.k.a. Mobile Block Hessian, or MBH) calculation.

AngularDisplacement

Type Float

Default value 0.5

Unit Degree

Description Relative step size for rotational degrees of freedom during Block Normal Modes finite difference calculations. It will be scaled with the characteristic block size.

BlockAtoms

Type Integer List

Recurring True

Description List of atoms belonging to a block. You can have multiple BlockAtoms.

BlockRegion

Type String

Recurring True

Description The region to be considered a block. You can have multiple BlockRegions, also in combination with BlockAtoms.

Parallel

Type Block

Description Configuration for how the individual displacements are calculated in parallel.

nCoresPerGroup

Type Integer

Description Number of cores in each working group.

nGroups

Type Integer

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Cores per task

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

RadialDisplacement

Type Float

Default value 0.005

Unit Angstrom

Description Step size for translational degrees of freedom during Block Normal Modes finite difference calculations.

Displacements

Type Multiple Choice

Default value Cartesian

Options [Cartesian, Symmetric, Block]

GUI name Displacements

Description Type of displacements.

In case of symmetric displacements it is possible to choose only the modes that have non-zero IR or Raman intensity.

Block displacements take rigid blocks into account.

Hessian

Type Multiple Choice

Default value Auto

Options [Auto, Analytical, Numerical]

Description Default Auto means that if possible by the engine the Hessian will be calculated analytically, else the Hessian will be calculated numerically by AMS.

ReScanFreqRange

Type Float List

Default value [-10000000.0, 10.0]

Unit cm-1

Recurring True

GUI name Re-scan range

Description Specifies a frequency range within which all modes will be scanned. 2 numbers: an upper and a lower bound.

ReScanModes

Type Bool

Default value Yes

GUI name Re-scan modes

Description Whether or not to scan imaginary modes after normal modes calculation has concluded.

SymmetricDisplacements

Type Block

Description Configures details of the calculation of the frequencies and normal modes of vibration in symmetric displacements.

Type

Type Multiple Choice

Default value All

Options [All, Infrared, Raman, InfraredAndRaman]

GUI name Symm Frequencies

Description For symmetric molecules it is possible to choose only the modes that have non-zero IR or Raman intensity (or either of them) by symmetry.

In order to calculate the Raman intensities the Raman property must be requested.

NumericalDifferentiation

Type Block

Description Define options for numerical differentiations, that is the numerical calculation of gradients, Hessian and the stress tensor for periodic systems.

NuclearStepSize

Type Float

Default value 0.005

Unit Bohr

Description Step size for numerical nuclear gradient calculation.

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups**Type** Integer**GUI name** Number of groups**Description** Total number of processor groups. This is the number of tasks that will be executed in parallel.**nNodesPerGroup****Type** Integer**GUI name** Nodes per group**Description** Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.**StrainStepSize****Type** Float**Default value** 0.001**Description** Step size (relative) for numerical stress tensor calculation.**NumericalPhonons****Type** Block**Description** Configures details of a numerical phonons calculation.**AutomaticBZPath****Type** Bool**Default value** Yes**GUI name** Automatic BZ path**Description** If True, compute the phonon dispersion curve for the standard path through the Brillouin zone. If False, you must specify your custom path in the [BZPath] block.**BZPath****Type** Block**Description** If [NumericalPhonons%AutomaticBZPath] is false, the phonon dispersion curve will be computed for the user-defined path in the [BZPath] block. You should define the vertices of your path in fractional coordinates (with respect to the reciprocal lattice vectors) in the [Path] sub-block. If you want to make a jump in your path (i.e. have a discontinuous path), you need to specify a new [Path] sub-block.**Path****Type** Non-standard block**Recurring** True**Description** A section of a k space path. This block should contain multiple lines, and in each line you should specify one vertex of the path in fractional coordinates. Optionally, you can add text labels for your vertices at the end of each line.**BornEffCharge****Type** Float**Default value** 0.0

Description Input option to give the Born effective charges of the species.

DielectricConst

Type Float

Default value 1.0

Description Input option to give the static dielectric constant of the species.

DoubleSided

Type Bool

Default value Yes

Description By default a two-sided (or quadratic) numerical differentiation of the nuclear gradients is used. Using a single-sided (or linear) numerical differentiation is computationally faster but much less accurate. Note: In older versions of the program only the single-sided option was available.

Interpolation

Type Integer

Default value 100

Description Use interpolation to generate smooth phonon plots.

NDosEnergies

Type Integer

Default value 1000

Description Nr. of energies used to calculate the phonon DOS used to integrate thermodynamic properties. For fast compute engines this may become time limiting and smaller values can be tried.

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

StepSize

Type Float

Default value 0.04

Unit Angstrom

Description Step size to be taken to obtain the force constants (second derivative) from the analytical gradients numerically.

SuperCell

Type Non-standard block

Description Used for the phonon run. The super lattice is expressed in the lattice vectors. Most people will find a diagonal matrix easiest to understand.

PESExploration

Type Block

Description Configures details of the automated PES exploration methods.

BasinHopping

Type Block

Description Configures the details of the Basin Hopping subtask.

DisplaceAtomsInRegion

Type String

Default value

Description If you specify a region name here, only the atoms belonging to this region will be displaced during the basin hopping procedure. For more details on regions, see the documentation on the System definition.

Displacement

Type Float

Default value 0.5

Unit Angstrom

Description Displacement in each degree of freedom.

PushApartDistance

Type Float

Default value 0.4

Unit Angstrom

Description Push atoms apart until no atoms are closer than this distance. This criterion is enforced for the initial structure and all those generated by random displacements.

Steps

Type Integer

Default value 20

Description Number of displace & optimize Monte-Carlo steps to take.

BindingSites

Type Block

Description Options related to the calculation of binding sites.

Calculate

Type Bool

Default value No

Description Calculate binding sites at the end of a job. Not needed for Binding Sites job.

DistanceDifference

Type Float

Default value -1.0

Unit Angstrom

Description If the distance between two mapped binding-sites is larger than this threshold, the binding-sites are considered different. If not specified, its value will set equal to [PESExploration%StructureComparison%DistanceDifference]

MaxCoordinationShellsForLabels

Type Integer

Default value 3

Description The binding site labels are given based on the coordination numbers of shells in the reference region, using the following format: N<int><int>..., e.g., the label 'N334' means 3 atoms in the first coordination shell, 3 in the second one, and 4 in the third one. This parameter controls the maximum number of shells to include.

NeighborCutoff

Type Float

Default value -1.0

Unit Angstrom

Description Atoms within this distance of each other are considered neighbors for the calculation of the binding sites. If not specified, its value will set equal to [PESExploration%StructureComparison%NeighborCutoff]

ReferenceRegion

Type String

Default value

Description Defines the region that is considered as the reference for binding sites detection. Binding sites are projected on this region using the geometry from the reference system. If not specified, its value will set equal to [PESExploration%StatesAlignment%ReferenceRegion]

CalculateFragments

Type Bool

Default value No

Description Must be used together with an adsorbent set as the StatesAlignment%ReferenceRegion. Runs a final calculation of the adsorbate and adsorbent (marked by the ReferenceRegion) individually. The fragmented state is included in the energy landscape.

Debug

Type Block

Description ???.

DynamicSeedStates

Type Bool

Default value Yes

Description Whether subsequent expeditions may start from states discovered by previous expeditions. This should lead to a more comprehensive exploration of the potential energy surface. Disabling this will focus the PES exploration around the initial seed states.

Dynamics

Type Block

Description ???.

Andersen

Type Block

Description ???.

Alpha

Type Float

Default value 1.0

Description ???.

CollisionPeriod

Type Float

Default value 100.0

Description ???.

Langevin

Type Block

Description ???.

Friction

Type Float

Default value 0.01

Description ???.

Nose

Type Block

Description ???.

Mass

Type Float

Default value 1.0

Description ???.

Thermostat

Type Multiple Choice

Default value none

Options [andersen, nose_hoover, langevin, none]

Description ???.

Time

Type Float

Default value 1000.0

Description ???.

TimeStep

Type Float

Default value 1.0

Description ???.

FiniteDifference

Type Float

Default value 0.0026458861

Unit Angstrom

Description The finite difference distance to use for Dimer, Hessian, Lanczos, and optimization methods.

Hessian

Type Block

Description ???.

AtomList

Type String

Default value all

Description ???.

ZeroFreqValue

Type Float

Default value 1e-06

Description ???.

Job

Type Multiple Choice

Options [ProcessSearch, BasinHopping, SaddleSearch, LandscapeRefinement, BindingSites]

Description Specify the PES exploration job to perform.

LandscapeRefinement

Type Block

Description Configures details of the energy landscape refinement job.

IgnoreFinalPESPointCharacter

Type Bool

Default value No

Description At the end of the energy landscape refinement job, each state is assigned a PES point character (MIN or TS) based on its vibrational frequencies before being included in the final database. States are only added if the PES point character after refinement remains unchanged. However, states are added without verifying if this option is `true`. Nonetheless, vibrational frequencies are calculated and stored for future analysis. This option is especially useful when using computationally demanding engines. Because in those cases, precision and computational effort must be balanced, resulting in significant vibrational frequencies inaccuracies.

RunInitialSinglePoints

Type Bool

Default value Yes

Description If it is `true`, just after loading the energy landscape to refine, the single energy point computations are disabled. Be aware that if you enable this, the output file's 'Initial Energy Landscape' section will display incorrect states' energy values. If the engine requires too much processing power, this option can help you save a small amount of time.

LoadEnergyLandscape

Type Block

Description Options related to the loading of an Energy Landscape from a previous calculation.

KeepOnly

Type Integer List

GUI name List of states to keep

Description Upon loading the Energy Landscape, only keep the states specified here. The states should be specified via a list of integers referring to the indices of the states you want to keep.

Path

Type String

GUI name Load energy landscape from

Description The path to load an energy landscape from. Accepts either AMS result folders, or `.con` files in the native EON format (only available through the text input file).

Remove

Type Integer List

GUI name List of states to remove

Description Upon loading the Energy Landscape, remove (i.e. do not load) the states specified here. The states should be specified via a list of integers referring to the indices of the states you want to remove (i.e. the states you don't want to load).

SeedStates

Type Integer List

GUI name List of seed states

Description By default when you start a new PES Exploration from a loaded Energy Landscape, expeditions can start from any of the loaded minima. By using this input option, you can instruct the program to only use some of the states as 'expedition starting point'. The states that serve as 'expedition starting points' should be specified via a list of integers referring to the indices of the states.

NegativeEigenvalueTolerance

Type Float

Default value -0.0005

Unit Hartree/Bohr²

Description The threshold in Hessian eigenvalue below which a mode is considered imaginary, i.e. indicating a transition state. This is a small negative number, as very small negative eigenvalues may be due to numerical noise on an essentially flat PES and do not indicate true transition states. We need a more flexible value for this parameter in PESExploration because the high computational cost of the task typically forces us to reduce the engine precision, which increases the noise in the vibrational frequencies evaluation. [PESPointCharacter%NegativeEigenvalueTolerance] is overridden by this parameter.

NudgedElasticBand

Type Block

Description Options for the Nudged Elastic Band (NEB) method.

ClimbingImageMethod

Type Bool

Default value Yes

Description Use the climbing image algorithm to drive the highest image to the transition state.

ConvergedForce

Type Float

Default value -1.0

Unit eV/Angstrom

Description Convergence threshold for nuclear gradients. Note: Special value of -1.0 means using the same convergence criterion as the PES explorer's geometry optimizer.

Images

Type Integer

Default value 5

Description Number of NEB images between the two endpoints.

MaxIterations

Type Integer

Default value 500

Description Maximum number of NEB iterations.

OldTangent

Type Bool

Default value No

Description Use the old central difference tangent.

Spring

Type Float

Default value 5.0

Unit eV/Ang²

Description Spring force constant.

NumExpeditions

Type Integer

Default value 1

Description Sets the number of subsequent expeditions our job will consist of. Larger values result in a more comprehensive exploration of the potential energy surface, but will take more computational time.

NumExplorers

Type Integer

Default value 1

Description Sets the number of independent PES explorers dispatched as part of each expedition. Larger values will result in a more comprehensive exploration of the potential energy surface, but will take more computational time. By default an appropriate number of explorers are executed in parallel.

OptTSMethod

Type Multiple Choice

Default value SaddleSearch

Options [SaddleSearch, NudgedElasticBand]

Description When the full set of states in the energy landscape are optimized (see PESExploration%Job = GeometryOptimization), transition states can be optimized using either SaddleSearch or NudgedElasticBand methods. SaddleSearch uses information only from the current geometry of the TS; contrary, NudgedElasticBand ignores the current geometry and runs a Nudged-Elastic-Band calculation trying to connect the associated reactants and products if they are available.

Optimizer

Type Block

Description Configures the details of the geometry optimizers used by the PES explorers.

ConvergedForce

Type Float

Default value 0.005

Unit eV/Angstrom

Description Convergence threshold for nuclear gradients.

MaxIterations

Type Integer

Default value 400

Description Maximum number of iterations allowed for optimizations.

Method

Type Multiple Choice

Default value CG

Options [CG, QM, LBFGS, FIRE, SD]

Description Select the method for geometry optimizations.

Parallel

Type Block

Description Options for double parallelization, which allows to split the available processor cores into groups working through all the available tasks in parallel, resulting in a better parallel performance. The keys in this block determine how to split the available processor cores into groups working in parallel.

nCoresPerGroup

Type Integer

GUI name Cores per group

Description Number of cores in each working group.

nGroups

Type Integer

GUI name Number of groups

Description Total number of processor groups. This is the number of tasks that will be executed in parallel.

nNodesPerGroup

Type Integer

GUI name Nodes per group

Description Number of nodes in each group. This option should only be used on homogeneous compute clusters, where all used compute nodes have the same number of processor cores.

ParallelReplica

Type Block

Description ???.

DephaseLoopMax

Type Integer

Default value 5

Description ???.

DephaseLoopStop

Type Bool

Default value No

Description ???.

DephaseTime

Type Float

Default value 1000.0

Description ???.

PostTransitionTime

Type Float

Default value 1000.0

Description ???.

RefineTransition

Type Bool

Default value Yes

Description ???.

StateCheckInterval

Type Float

Default value 1000.0

Description ???.

StateSaveInterval

Type Float

Default value -1.0

Description ???.

StopAfterTransition

Type Bool

Default value No

Description ???.

Prefactor

Type Block

Description ???.

Rate

Type Multiple Choice

Default value HTST

Options [HTST, QQHTST]

Description Calculates the pre-exponential factors of the Reaction Rates using either Harmonic Transition State Theory (HTST) or quasi-quantum HTST (QQHTST).

ProcessSearch

Type Block

Description Input options specific to the process search procedure.

MinimizationOffset

Type Float

Default value 0.2

Description After a saddle is found, images are placed on either side of the saddle along the mode and minimized to ensure that the saddle is connected to the original minimum and to locate the product state. MinimizationOffset is the distance those images are displaced from the saddle.

RandomSeed

Type Integer

Description Number used to initialize both the EON clients random number generators as well as the AMS global RNG. The latter is normally initialized with the RNGSeed keyword at the root level. Should be used by developers only. May or may not help to make more reproducible regression tests ...

SaddleSearch

Type Block

Description Configuration for the Saddle Search procedure (used in SaddleSearch and ProcessSearch Jobs).

ConvergedForce

Type Float

Default value -1.0

Unit eV/Angstrom

Description Convergence threshold for nuclear gradients. Note: Special value of -1.0 means using the same convergence criterion as the PES explorer's geometry optimizer.

DisplaceAtomsInRegion

Type String

Default value

Description A string corresponding to the name of a region. When performing the initial random displacement, only displace atoms in the specified region. This can help the Saddle Search procedure to start off in a desired region of the PES.

DisplaceMagnitude

Type Float

Default value 0.1

Unit Angstrom

Description The standard deviation of the Gaussian displacement in each degree of freedom for the selected atoms.

MaxEnergy

Type Float

Default value 20.0

Unit eV

Description The energy (relative to the starting point of the saddle search) at which a saddle search explorer considers the search bad and terminates it.

MaxIterations

Type Integer

Default value 400

Description Maximum number of iterations for each saddle search run.

MinEnergyBarrier

Type Float

Default value 0.001

Unit eV

Description Minimum energy barrier to accept a new transition state.

MinModeMethod

Type Multiple Choice

Default value dimer

Options [dimer, lanczos]

Description The minimum-mode following method to use.

StatesAlignment

Type Block

Description Configures details of how the energy landscape configurations are aligned respect to the main chemical system [System].

DistanceDifference

Type Float

Default value -1.0

Unit Angstrom

Description If the distance between two mapped atoms is larger than this threshold, the configuration is considered not aligned. If not specified, its value will set equal to [PESExploration%StructureComparison%DistanceDifference]

ReferenceRegion

Type String

Default value

Description Defines the region that is considered as the reference for alignments. Atoms outside this region are ignored in the alignments.

StructureComparison

Type Block

Description Settings for structure comparison.

CheckRotation

Type Bool

Description Rotates the system optimally before comparing structures. The default is to do this only for molecular systems when there are no fixed atom constraints.

CheckSymmetry

Type Bool

Default value No

Description Considers that two systems are equal if they are equivalent by symmetry.

DistanceDifference

Type Float

Default value 0.1

Unit Angstrom

Description If the distance between two mapped atoms is larger than this threshold, the two configurations are considered different structures.

EnergyDifference

Type Float

Default value 0.01

Unit eV

Description If the energy difference between two configurations is larger than this threshold, the two configurations are considered to be different structures.

IndistinguishableAtoms

Type Bool

Default value Yes

Description If yes, the order of the atoms does not affect the structural comparison. Atoms of the same element are then indistinguishable.

NeighborCutoff

Type Float

Default value 3.3

Unit Angstrom

Description Atoms within this distance of each other are considered neighbors.

RemoveTranslation

Type Bool

Description Translates the system optimally before comparing structures. The default is to do this only when there are no fixed atom constraints.

Temperature

Type Float

Default value 300.0

Unit Kelvin

Description The temperature that the job will run at. This may be used in different ways depending on the job, e.g. acceptance probabilities for Monte-Carlo based jobs, thermostating for dynamics based jobs, kinetic prefactors for jobs that find transition states. Some jobs may not use this temperature at all.

WriteHistory

Type Multiple Choice

Default value Converged

Options [None, Converged, All]

Description When to write the molecular geometry (and possibly other properties) to the history on the ams.rkf file. The default is to only write the converged geometries to the history. Can be changed to write no frames at all to the history, or write all frames (should only be used when testing because of the performance impact). Note that for parallel calculations, only the first group of processes writes to ams.rkf.

PESPointCharacter

Type Block

Description Options for the characterization of PES points.

Displacement

Type Float

Default value 0.04

Description Controls the size of the displacements used for numerical differentiation: The displaced geometries are calculated by taking the original coordinates and adding the mass-weighted mode times the reduced mass of the mode times the value of this keyword.

NegativeEigenvalueTolerance

Type Float

Default value -0.0001

Unit Hartree/Bohr²

Description The threshold in Hessian eigenvalue below which a mode is considered imaginary, i.e. indicating a transition state. This is a small negative number, as very small negative eigenvalues may be due to numerical noise on an essentially flat PES and do not indicate true transition states.

NumberOfModes

Type Integer

Default value 2

Description The number of (lowest) eigenvalues that should be checked.

Tolerance

Type Float

Default value 0.016

Description Convergence tolerance for residual in iterative Davidson diagonalization.

PESScan

Type Block

Description Configures the details of the potential energy surface scanning task.

CalcPropertiesAtPESPoints

Type Bool

Default value No

Description Whether to perform an additional calculation with properties on all the sampled points of the PES. If this option is enabled AMS will produce a separate engine output file for every sampled PES point.

FillUnconvergedGaps

Type Bool

Default value Yes

Description After the initial pass over the PES, restart the unconverged points from converged neighboring points.

ScanCoordinate

Type Block

Recurring True

Description Specifies a coordinate along which the potential energy surface is scanned. If this block contains multiple entries, these coordinates will be varied and scanned together as if they were one. Note that there can be only one ScanCoordinate containing a lattice scan in any PES scan job.

Angle

Type String

Recurring True

Description Scan the angle between three atoms. Three atom indices followed by two real numbers delimiting the transit range in degrees.

CellVolumeRange

Type Float List

Unit Angstrom³

Description Two numbers for the initial and final cell volume. The cell is scaled isotropically between these values. Can not be used together with any other coordinate within the same ScanCoordinate block.

CellVolumeScalingRange

Type Float List

Description Two scaling factors for the initial and final cell volume. A value of '0.9 1.1' would result in an isotropic scaling between 90% and 110% of the cell volume of the input system. Can not be used together with any other coordinate within the same ScanCoordinate block.

Coordinate

Type String

Recurring True

Description Scan a particular coordinate of an atom. Atom index followed by (xlylz) followed by two real numbers delimiting the transit range.

DifDist

Type String

Recurring True

Description Scan the difference distance between two pairs of atoms, R(12)-R(34). Four atom indices followed by two real numbers delimiting the transit range in Angstrom.

Dihedral

Type String

Recurring True

Description Scan the dihedral angle between four atoms. Four atom indices followed by two real numbers delimiting the transit angle in degrees.

Distance

Type String

Recurring True

Description Scan the distance between two atoms. Two atom indices followed by two real numbers delimiting the transit distance in Angstrom.

FromLattice

Type Non-standard block

Description Up to three lattice vectors to start the scan at. Has to be used in combination with the ToLattice keyword and no other coordinate within the same ScanCoordinate block. Unit can be specified in the header. Default unit is Angstrom.

FromStrainVoigt

Type Float List

Description The elements of the initial lattice strain in Voigt notation. One should specify 6 numbers for 3D periodic system (order: xx,yy,zz,yz,xz,xy), 3 numbers for 2D periodic systems (order: xx,yy,xy) or 1 number for 1D periodic systems. Has to be used in combination with the ToStrainVoigt keyword and no other coordinate within the same ScanCoordinate block.

LatticeARange

Type Float List

Unit Angstrom

Description Scans the length of the first lattice vector. Can be combined with the LatticeBRange and LatticeCRange keywords, but no other coordinates within the same ScanCoordinate.

LatticeBRange

Type Float List

Unit Angstrom

Description Scans the length of the second lattice vector. Can be combined with the LatticeARange and LatticeCRange keyword, but no other coordinates within the same ScanCoordinate..

LatticeCRange

Type Float List

Unit Angstrom

Description Scans the length of the third lattice vector. Can be combined with the LatticeARange and LatticeBRange keyword, but no other coordinates within the same ScanCoordinate..

SumDist

Type String

Recurring True

Description Scan the sum of distances between two pairs of atoms, R(12)+R(34). Four atom indices followed by two real numbers delimiting the transit range in Angstrom.

ToLattice

Type Non-standard block

Description Up to three lattice vectors to end the scan at. Unit can be specified in the header. Default unit is Angstrom.

ToStrainVoigt

Type Float List

Description The elements of the final lattice strain in Voigt notation. One should specify 6 numbers for 3D periodic system (order: xx,yy,zz,yz,xz,xy), 3 numbers for 2D periodic systems (order: xx,yy,xy) or 1 number for 1D periodic systems.

nPoints

Type Integer

Default value 10

Description The number of points along the scanned coordinate. Must be greater or equal 2.

Print

Type Block

Description This block controls the printing of additional information to stdout.

Timers

Type Multiple Choice

Default value None

Options [None, Normal, Detail, TooMuchDetail]

Description Printing timing details to see how much time is spend in which part of the code.

Properties

Type Block

Description Configures which AMS level properties to calculate for SinglePoint calculations or other important geometries (e.g. at the end of an optimization).

BondOrders

Type Bool

Default value No

Description Requests the engine to calculate bond orders.

For MM engines these might just be the defined bond orders that go into the force-field, while for QM engines, this might trigger a bond order analysis based on the electronic structure. For engines that do not have a bond order analysis method, a bond guessing algorithm will be used. See also the input options in the BondOrders block.

Charges

Type Bool

Default value No

Description Requests the engine to calculate the atomic charges.

DipoleGradients

Type Bool

Default value No

Description Requests the engine to calculate the nuclear gradients of the electric dipole moment of the molecule. This can only be requested for non-periodic systems.

DipoleMoment

Type Bool

Default value No

Description Requests the engine to calculate the electric dipole moment of the molecule. This can only be requested for non-periodic systems.

ElasticTensor

Type Bool

Default value No

Description Calculate the elastic tensor.

GSES

Type Bool

Default value No

Description Requests the engine to calculate the gradients of ground to excited state properties.

Gradients

Type Bool

Default value No

GUI name Nuclear gradients

Description Calculate the nuclear gradients.

Hessian

Type Bool

Default value No

Description Whether or not to calculate the Hessian.

Molecules

Type Bool

Default value No

Description Requests an analysis of the molecular components of a system, based on the bond orders calculated by the engine.

NormalModes

Type Bool

Default value No

GUI name Frequencies

Description Calculate the frequencies and normal modes of vibration, and for molecules also the corresponding IR intensities if the engine supports the calculation of dipole moments.

OrbitalsInfo

Type Bool

Default value No

Description Basic molecular orbitals information: orbital energies, occupations, HOMO, LUMO and HOMO-LUMO gap.

Other

Type Bool

Default value Yes

Description Other (engine specific) properties. Details are configured in the engine block.

PESPointCharacter

Type Bool

Default value No

GUI name Characterize PES point

Description Determine whether the sampled PES point is a minimum or saddle point. Note that for large systems this does not entail the calculation of the full Hessian and can therefore be used to quickly confirm the success of a geometry optimization or transition state search.

Phonons

Type Bool

Default value No

Description Calculate the phonons (for periodic systems).

Polarizability

Type Bool

Default value No

Description Requests the engine to calculate the polarizability tensor of the system.

Raman

Type Bool

Default value No

Description Requests calculation of Raman intensities for vibrational normal modes.

SelectedRegionForHessian

Type String

GUI name Hessian only for

Description Compute the Hessian matrix elements only for the atoms in a particular region. If not specified, the Hessian will be computed for all atoms.

StressTensor

Type Bool

Default value No

GUI name Stress tensor

Description Calculate the stress tensor.

VCD

Type Bool

Default value No

Description Requests calculation of VCD for vibrational normal modes.

VROA

Type Bool

Default value No

Description Requests calculation of VROA for vibrational normal modes.

Raman

Type Block

Description Configures details of the Raman or VROA calculation.

FreqRange

Type Float List

Unit cm-1

Recurring True

GUI name Frequency range

Description Specifies a frequency range within which all modes will be scanned. 2 numbers: an upper and a lower bound.

IncidentFrequency

Type Float

Default value 0.0

Unit eV

Description Frequency of incident light.

LifeTime

Type Float

Default value 0.0

Unit hartree

Description Specify the resonance peak width (damping) in Hartree units. Typically the lifetime of the excited states is approximated with a common phenomenological damping parameter. Values are best obtained by fitting absorption data for the molecule, however, the values do not vary a lot between similar molecules, so it is not hard to estimate values. A typical value is 0.004 Hartree.

Replay

Type Block

Description Configures the details of the Replay task.

File

Type String

GUI name Restart from

Description Provide an ams.rkf file (or a .results folder) from a previously run job to replay. The file needs to contain a History section.

Frames

Type Integer List

Description List of frames from the History section to recompute.

If not specified the recomputed frames are determined automatically based on the task of the job that is being replayed: PES scans and NEB calculations will only have the converged points replayed, while all other tasks will have all frames recomputed.

Specifying the frames to recompute in the input is probably only useful when replaying trajectories from MolecularDynamics calculations.

StoreAllResultFiles

Type Bool

Default value No

Description If this option is enabled AMS will produce a separate engine output file for every replayed frame.

While basic properties like energy, gradients, stress tensor, etc. are stored anyway on the History section in the AMS driver output file (if they were requested in the Properties block), engine specific properties (e.g. excitations energies from ADF) will only be available if the full result files are stored.

Restrains

Type Block

Description The Restrains block allows to add soft constraints to the system. A restraint is a potential energy function (a spring) attached to a certain coordinate, for example, an interatomic distance, with its minimum at the specified optimal value. A restraint is defined using one or two parameters: the ForceConstant and, for some types, the F(Inf) value. The ForceConstant parameter corresponds to second derivative of the restraint potential energy $d^2V(x)/dx^2$ for any x (harmonic restrains) or only at $x=0$ (other restrains). Here, x is a deviation from the restraint's optimal value.

Angle

Type String

Recurring True

Description Specify three atom indices $i j k$ followed by an angle in degrees and, optionally, by the ForceConstant (default is 0.3 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the i - j - k angle at the given value. For periodic systems this restraint follows the minimum image convention.

DifDist

Type String

Recurring True

Description Specify four atom indices $i j k l$ followed by the distance in Angstrom and, optionally, by the ForceConstant (default is 1.0 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the difference $R(ij)$ - $R(kl)$ at the given value. For periodic systems this restraint follows the minimum image convention.

Dihedral

Type String

Recurring True

Description Specify four atom indices $i j k l$ followed by an angle in degrees and, optionally, by the ForceConstant (default is 0.1 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the i - j - k - l dihedral angle at the given value. For periodic systems this restraint follows the minimum image convention.

Distance

Type String

Recurring True

Description Specify two atom indices followed by the distance in Angstrom and, optionally, by the ForceConstant (default is 1.0 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the distance between the two specified atoms at the given value. For periodic systems this restraint follows the minimum image convention.

FInfinity

Type Float

Default value 1.0

GUI name Default F(inf)

Description Specify the default asymptotic value for the restraint force for the Hyperbolic and Erf profiles, in Hartree/Bohr or Hartree/radian.

A per-restraint value can be specified after the profile type on the corresponding restraint line.

Profile

Type Multiple Choice

Default value Harmonic

Options [Harmonic, Hyperbolic, Erf, GaussianWell]

GUI name Default restraint profile

Description Select the default type of restraint profile.

The harmonic profile is most suitable for geometry optimizations but may result in very large forces that can be problematic in molecular dynamic.

For MD simulations the Hyperbolic or Erf may be more suitable because the restraint force is bounded by a user-defined value.

A per-restraint profile type can be specified after the ForceConstant value on the corresponding restraint line.

SumDist

Type String

Recurring True

Description Specify four atom indices i j k l followed by the distance in Angstrom and, optionally, by the ForceConstant (default is 1.0 in a.u.), profile type and F(Inf) (in a.u.). This restraint will try to keep the sum $R(ij)+R(kl)$ at the given value. For periodic systems this restraint follows the minimum image convention.

Units

Type Multiple Choice

Default value Default

Options [Default, MD]

GUI name Units

Description Change units for energy, force and force constant values from the default (atomic units) to those often used in the MD community (based on kcal/mol and Angstrom). Units for the optimal distances are not affected and are always Angstrom.

RigidMotions

Type Block

Description Specify which rigid motions of the total system are allowed. An external field is not considered part of the system. Normally the automatic option is doing what you want. However this feature can be used as a means of geometry constraint.

AllowRotations

Type Multiple Choice

Default value Auto

Options [Auto, None, All, X, Y, Z, XY, XZ, YZ]

Description Which overall rotations of the system are allowed

AllowTranslations

Type Multiple Choice

Default value Auto

Options [Auto, None, All, X, Y, Z, XY, XZ, YZ]

Description Which overall translations of the system are allowed

Tolerance

Type Float

Default value 1e-06

Description Tolerance for detecting linear molecules. A large value means larger deviation from linearity is permitted.

RNGSeed**Type** Integer List**Description** Initial seed for the (pseudo)random number generator. This should be omitted in most calculations to avoid introducing bias into the results. If this is unset, the generator will be seeded randomly from external sources of entropy. If you want to exactly reproduce an older calculation, set this to the numbers printed in its output.**SCMatrix****Type** Block**Description** Technical settings for programs using the AMT matrix system. Currently this is only used by DFTB**DistributedMatrix****Type** Block**Description** Technical settings for Distributed matrices**ColBlockSize****Type** Integer**Default value** 64**Description** See comment of RowBlockSize.**RowBlockSize****Type** Integer**Default value** 64**Description** The matrix is divided into blocks of size RowBlockSize x ColBlockSize. The smaller the blocks the better the distribution, but at the expense of increased communication overhead**Type****Type** Multiple Choice**Default value** Elpa**Options** [Auto, Reference, ScaLapack, Elpa]**Description** Determines which implementation is used to support the AbstractMatrixType.**Symmetry****Type** Block**Description** Specifying details about the details of symmetry detection and usage.**SymmetrizeTolerance****Type** Float**Default value** 0.05**Description** Tolerance used to detect symmetry in case symmetrize is requested.**Tolerance****Type** Float**Default value** 1e-07

Description Tolerance used to detect symmetry in the system.

System

Type Block

Recurring True

Description Specification of the chemical system. For some applications more than one system may be present in the input. In this case, all systems except one must have a non-empty string ID specified after the System keyword. The system without an ID is considered the main one.

AllowCloseAtoms

Type Bool

Default value No

Description If AllowCloseAtoms is set to False, the AMS driver will stop with an error if it detects almost-coinciding atomic coordinates. If set to True, the AMS driver will try to carry on with the calculation.

Atoms

Type Non-standard block

Description The atom types and coordinates. Unit can be specified in the header. Default unit is Angstrom.

BondOrders

Type Non-standard block

Description Defined bond orders. Each line should contain two atom indices, followed by the bond order (1, 1.5, 2, 3 for single, aromatic, double and triple bonds) and (optionally) the cell shifts for periodic systems. May be used by MM engines and for defining constraints. If the system is periodic and none of the bonds have the cell shift defined then AMS will attempt to determine them following the minimum image convention.

Charge

Type Float

Default value 0.0

GUI name Total charge

Description The system's total charge in atomic units.

ElectrostaticEmbedding

Type Block

Description Container for electrostatic embedding options, which can be combined.

ElectricField

Type Float List

Unit V/Angstrom

Description External homogeneous electric field with three Cartesian components: ex, ey, ez, the default unit being V/Å.

In atomic units: Hartree/(e bohr) = 14.39964 V/Angstrom; the relation to SI units is: 1 Hartree/(e bohr) = 5.14 ... e11 V/m.

Supported by the engines adf, band, dftb and mopac.

For periodic systems the field may only have nonzero components orthogonal to the direction(s) of periodicity (i.e. for 1D periodic system the x-component of the electric field should be zero, while for 2D periodic systems both the x and y components should be zero. This options cannot be used for 3D periodic systems.

MultipolePotential

Type Block

Description External point charges (and dipoles).

ChargeModel

Type Multiple Choice

Default value Point

Options [Point, Gaussian]

Description A multipole may be represented by a point (with a singular potential at its location) or by a spherical Gaussian distribution.

ChargeWidth

Type Float

Default value -1.0

Description The width parameter in a.u. in case a Gaussian charge model is chosen. A negative value means that the width will be chosen automatically.

Coordinates

Type Non-standard block

Description Positions and values of the multipoles, one per line. Each line has the following format:

x y z q, or x y z q μ_x μ_y μ_z .

Here x, y, z are the coordinates in Å, q is the charge (in atomic units of charge) and μ_x , μ_y , μ_z are the (optional) dipole moment components (in atomic units, i.e. $e \cdot \text{Bohr}$).

Periodic systems are not supported.

FractionalCoords

Type Bool

Default value No

Description Whether the atomic coordinates in the Atoms block are given in fractional coordinates of the lattice vectors. Requires the presence of the Lattice block.

GeometryFile

Type String

Description Read the geometry from a file (instead of from Atoms and Lattice blocks). Supported formats: .xyz

GuessBonds

Type Bool

Default value No

Description Whether or not UFF bonds should be guessed.

Lattice

Type Non-standard block

Description Up to three lattice vectors. Unit can be specified in the header. Default unit is Angstrom.

LatticeStrain

Type Float List

Description Deform the input system by the specified strain. The strain elements are in Voigt notation, so one should specify 6 numbers for 3D periodic system (order: xx,yy,zz,yz,xz,xy), 3 numbers for 2D periodic systems (order: xx,yy,xy) or 1 number for 1D periodic systems.

LoadForceFieldAtomTypes

Type Block

Description This is a mechanism to set the ForceField.Type attribute in the input. This information is currently only used by the ForceField engine.

File

Type String

Description Name of the (kf) file. It needs to be the result of a forcefield calculation.

LoadForceFieldCharges

Type Block

Recurring True

Description This is a mechanism to set the ForceField.Charge attribute in the input. This information is currently only used by the ForceField engine.

CheckGeometryRMSD

Type Bool

Default value No

Description Whether the geometry RMSD test should be performed, see MaxGeometryRMSD. Otherwise only basic tests are performed, such as number and atom types. Not doing the RMSD test allows you to load molecular charges in a periodic system.

File

Type String

Description Name of the (kf) file

MaxGeometryRMSD

Type Float

Default value 0.1

Unit Angstrom

Description The geometry of the charge producing calculation is compared to the one of the region, and need to be the same within this tolerance.

Region

Type String

Default value *

Description Region for which the charges should be loaded

Section

Type String

Default value AMSResults

Description Section name of the kf file

Variable

Type String

Default value Charges

Description Variable name of the kf file

MapAtomsToUnitCell

Type Bool

Default value No

Description For periodic systems the atoms will be moved to the central cell.

ModifyAlternativeElements

Type Bool

Default value No

Description When using alternative elements (using the nuclear_charge attribute) set the element to the nearest integer Z. If you specify an H atom with a nuclear_charge of 2.9 it is replaced by a Li atom with the same nuclear charge.

PerturbCoordinates

Type Float

Default value 0.0

Unit Angstrom

Description Perturb the atomic coordinates by adding random numbers between [-PerturbCoordinates,PerturbCoordinates] to each Cartesian component. This can be useful if you want to break the symmetry of your system (e.g. for a geometry optimization).

PerturbLattice

Type Float

Default value 0.0

Description Perturb the lattice vectors by applying random strain with matrix elements between [-PerturbLattice,PerturbLattice]. This can be useful if you want to deviate from an ideal symmetric geometry, for example if you look for a phase change due to high pressure.

RandomizeAtomOrder

Type Bool

Default value No

Description Whether or not the order of the atoms should be randomly changed. Intended for some technical testing purposes only. Does not work with bond information.

Region

Type Block

Recurring True

Description Properties for each region specified in the Atoms block.

Properties

Type Non-standard block

Description Properties for each region specified in the Atoms block.

ShiftCoordinates

Type Float List

Unit Bohr

Description Translate the atoms by the specified shift (three numbers).

SuperCell

Type Integer List

Description Create a supercell of the input system (only possible for periodic systems). The integer numbers represent the diagonal elements of the supercell transformation; you should specify as many numbers as lattice vectors (i.e. 1 number for 1D, 2 numbers for 2D and 3 numbers for 3D periodic systems).

SuperCellTrafo

Type Integer List

Description Create a supercell of the input system (only possible for periodic systems) $\vec{a}'_i = \sum_j T_{ij} \vec{a}_j$. The integer numbers represent the supercell transformation T_{ij} : 1 number for 1D PBC, 4 numbers for 2D PBC corresponding to a 2x2 matrix (order: (1,1),(1,2),(2,1),(2,2)) and 9 numbers for 3D PBC corresponding to a 3x3 matrix (order: (1,1),(1,2),(1,3),(2,1),(2,2),(2,3),(3,1),(3,2),(3,3)).

Symmetrize

Type Bool

Default value No

Description Whether to symmetrize the input structure. This might also rototranslate the structure into a standard orientation. This will symmetrize the atomic coordinates to machine precision. Useful if the system is almost symmetric or to rototranslate a symmetric molecule into a standard orientation.

Symmetry

Type Multiple Choice

Default value AUTO

Options [AUTO, NOSYM, C(LIN), D(LIN), C(I), C(S), C(2), C(3), C(4), C(5), C(6), C(7), C(8), C(2V), C(3V), C(4V), C(5V), C(6V), C(7V), C(8V), C(2H), C(3H), C(4H), C(5H), C(6H), C(7H), C(8H), D(2), D(3), D(4), D(5), D(6), D(7), D(8), D(2D), D(3D), D(4D), D(5D), D(6D), D(7D), D(8D), D(2H), D(3H), D(4H), D(5H), D(6H), D(7H), D(8H), I, I(H), O, O(H), T, T(D), T(H), S(4), S(6), S(8)]

Description Use (sub)symmetry with this Schoenflies symbol. Can only be used for molecules. Orientation should be correct for the (sub)symmetry. If used icw Symmetrize, the symmetrization will not reorient the molecule.

Task**Type** Multiple Choice**Options** [GCMC, GeometryOptimization, IRC, MolecularDynamics, NEB, PESExploration, PESS-can, Replay, SinglePoint, TransitionStateSearch, VibrationalAnalysis]**Description** Specify the computational task to perform:

- Single Point: keep geometry as is
- Geometry Optimization: optimize the geometry
- Transition State: search for the transition state
- IRC: intrinsic reaction coordinate
- PES Scan: scan the potential energy surface
- NEB: Nudged elastic band for reaction path optimization
- Vibrational Analysis: perform one of the analysis types selected on the options page
- Molecular Dynamics: perform MD simulation
- GCMC: Grand Canonical Monte Carlo simulation
- PES Exploration: automated potential energy surface exploration
- Replay: recompute frames from the trajectory of a previously run job

Thermo**Type** Block**Description** Options for thermodynamic properties (assuming an ideal gas). The properties are computed for all specified temperatures.**LowFrequencyCorrector****Type** Block**Description** Options for the dampener-powered free rotor interpolator that corrects thermodynamic quantities for low frequencies. See DOI:10.1021/jp509921r and DOI:10.1002/chem.201200497.**Alpha****Type** Float**Default value** 4.0**Description** The exponent term used in the dampener.**Frequency****Type** Float**Default value** 100.0**Unit** cm⁻¹**Description** The frequency around which the dampener interpolates between harmonic oscillator and free rotor quantities.**MomentOfInertia****Type** Float**Default value** 1e-44**Unit** kg m²**GUI name** Averaging Moment of Inertia**Description** The moment of inertia used to restrict entropy results for very small frequencies (generally around less than 1 cm⁻¹).**Pressure****Type** Float

Default value 1.0

Unit atm

Description The pressure at which the thermodynamic properties are computed.

Temperatures

Type Float List

Default value [298.15]

Unit Kelvin

Description List of temperatures at which the thermodynamic properties will be calculated.

TransitionStateSearch

Type Block

Description Configures some details of the transition state search.

ModeToFollow

Type Integer

Default value 1

Description In case of Transition State Search, here you can specify the index of the normal mode to follow (1 is the mode with the lowest frequency).

ReactionCoordinate

Type Block

Description Specify components of the transition state reaction coordinate (TSRC) as a linear combination of internal coordinates (distances or angles).

Angle

Type String

Recurring True

Description The TSRC contains the valence angle between the given atoms. Three atom indices followed by the weight.

Coordinate

Type String

Recurring True

Description The TSRC contains Cartesian displacement of an atom: atom index followed by [x|y|z] and the weight.

Dihedral

Type String

Recurring True

Description The TSRC contains the dihedral angle between the given atoms. Four atom indices followed by the weight.

Distance

Type String

Recurring True

Description The TSRC contains the distance between the given atoms. Two atom indices followed by the weight.

UseSymmetry

Type Bool

Default value Yes

Description Whether to use the system's symmetry in AMS. Symmetry is recognized within a tolerance as given in the Symmetry key.

VibrationalAnalysis

Type Block

Description Input data for all vibrational analysis utilities in the AMS driver.

AbsorptionSpectrum

Type Block

Description Settings related to the integration of the spectrum for vibronic tasks.

AbsorptionRange

Type Float List

Default value [-200.0, 4000.0]

Unit cm-1

Recurring True

Description Specifies frequency range of the vibronic absorption spectrum to compute. 2 numbers: an upper and a lower bound.

FrequencyGridPoints

Type Integer

Default value 400

Description Number of grid points to use for the spectrum

LineWidth

Type Float

Default value 200.0

Unit cm-1

Description Lorentzian line-width.

SpectrumOffset

Type Multiple Choice

Default value relative

Options [absolute, relative]

Description Specifies whether provided frequency range are absolute frequencies or frequencies relative to computed 0-0 excitation energy.

Displacement

Type Float

Unit Bohr

Description Step size for finite difference calculations.

ExcitationSettings

Type Block

Description Block that contains settings related to the excitation for vibronic tasks.

EnergyInline

Type Float

Unit hartree

Description Vertical excitation energy, used when [ExcitationInfo] = [Inline].

ExcitationFile

Type String

Description Path to a .rkf/.t21 file containing the excited state information (gradients, transition dipoles and energies).

ExcitationInputFormat

Type Multiple Choice

Default value File

Options [File, Inline]

Description Select how the application should retrieve the excited state information (energy, gradient).

GradientInline

Type Non-standard block

Description Excited state gradient at ground state equilibrium geometry, used when [ExcitationInfo] = [Inline].

Singlet

Type Non-standard block

Description Symmetry labels + integer indices of desired singlet transitions (VG-FC absorption spectra support only 1 at a time)

Triplet

Type Non-standard block

Description Symmetry labels + integer indices of desired triplet transitions (VG-FC absorption spectra support only 1 at a time)

ModeTracking

Type Block

Description Input data for Mode Tracking.

HessianGuess

Type Multiple Choice

Default value CalculateWithFastEngine

Options [Unit, File, CalculateWithFastEngine]

GUI name Guess Hessian

Description Sets how to obtain the guess for the Hessian used in the preconditioner (if one is to be used).

HessianInline

Type Non-standard block

Description Initial guess for the (non-mass-weighted) Hessian in a $3N \times 3N$ block, used when [HessianGuess] = [Inline].

HessianPath

Type String

Description Path to a .rkf file containing the initial guess for the Hessian, used when [HessianGuess] = [File]. It may also be the name of the results folder containing the engine file.

ToleranceForBasis

Type Float

Default value 0.0001

Description Convergence tolerance for the contribution of the newest basis vector to the tracked mode.

ToleranceForNorm

Type Float

Default value 0.0005

Description Convergence tolerance for residual RMS value.

ToleranceForResidual

Type Float

Default value 0.0005

Description Convergence tolerance for the maximum component of the residual vector.

ToleranceForSpectrum

Type Float

Default value 0.01

Description Convergence tolerance for the spectrum in Vibronic Structure Tracking.

TrackingMethod

Type Multiple Choice

Default value OverlapInitial

Options [OverlapInitial, DifferenceInitial, FreqInitial, IRInitial, OverlapPrevious, DifferencePrevious, FreqPrevious, IRPrevious, HighestFreq, HighestIR, LowestFreq, LowestResidual]

Description Set the tracking method that will be used. Vibronic Structure Tracking uses Largest Displacement.

UpdateMethod

Type Multiple Choice

Options [JD, D, I]

Description Chooses the method for expanding the Krylov subspace: (I) No preconditioner (VST default), (D) Davidson or (JD) vdVorst-Slejpen variant of Jacobi-Davidson (Mode tracking default).

NormalModes

Type Block

Description All input related to processing of normal modes. Not available for vibronic structure tracking (as no modes are required there).

MassWeightInlineMode

Type Bool

Default value Yes

Description MODE TRACKING ONLY: The supplied modes must be mass-weighted. This tells the program to mass-weight the supplied modes in case this has not yet been done. (True means the supplied modes will be mass-weighted by the program, e.g. the supplied modes are non-mass-weighted.)

ModeFile

Type String

Description Path to a .rkf or .t21 file containing the modes which are to be scanned. Which modes will be scanned is selected using the criteria from the [ModeSelect] block.) This key is optional for Resonance Raman and Vibronic Structure. These methods can also calculate the modes using the engine.

ModeInline

Type Non-standard block

Recurring True

Description MODE TRACKING ONLY: Coordinates of the mode which will be tracked in a $N \times 3$ block (same as for atoms), used when [ModeInputFormat] = [Inline]. Rows must be ordered in the same way as in the [System%Atoms] block. Mode Tracking only.

ModeInputFormat

Type Multiple Choice

Default value File

Options [File, Inline, Hessian]

GUI name Tracked mode source

Description Set how the initial guesses for the modes are supplied. Only mode tracking supports the Inline and Hessian options.

ModeSelect

Type Block

Description Pick which modes to read from file.

DisplacementBound

Type Float

Description Vibronic Structure (Refinement), Resonance Raman: Select all modes with a dimensionless oscillator displacement greater than the specified value.

FreqAndIRRange

Type Float List

Unit cm-1 and km/mol

Recurring True

Description Specifies a combined frequency and IR intensity range within which all modes will be selected. First 2 numbers are the frequency range, last 2 numbers are the IR intensity range.

FreqRange

Type Float List

Unit cm-1

Recurring True

Description Specifies a frequency range within which all modes will be selected. 2 numbers: an upper and a lower bound. Calculating all modes higher than some frequency can be achieved by making the upper bound very large.

Full

Type Bool

Default value No

GUI name All modes

Description Select all modes. This only make sense for Mode Scanning calculations.

HighFreq

Type Integer

GUI name # High frequencies

Description Select the N modes with the highest frequencies.

HighIR

Type Integer

GUI name # High IR

Description Select the N modes with the largest IR intensities.

IRRange

Type Float List

Unit km/mol

Recurring True

Description Specifies an IR intensity range within which all modes will be selected. 2 numbers: an upper and a lower bound.

ImFreq

Type Bool

Default value No

GUI name All imaginary frequencies

Description Select all modes with imaginary frequencies.

LargestDisplacement

Type Integer

Description Vibronic Structure (Refinement), Resonance Raman: Select the N modes with the largest VG-FC displacement.

LowFreq

Type Integer

GUI name # Low frequencies

Description Select the N modes with the lowest frequencies. Includes imaginary modes which are recorded with negative frequencies.

LowFreqNoIm

Type Integer

GUI name # Low positive frequencies

Description Select the N modes with the lowest non-negative frequencies. Imaginary modes have negative frequencies and are thus omitted here.

LowIR

Type Integer

GUI name # Low IR

Description Select the N modes with the smallest IR intensities.

ModeNumber

Type Integer List

GUI name Mode numbers

Description Indices of the modes to select.

ScanModes

Type Bool

Default value No

GUI name Scan after refining

Description Supported by: Mode Tracking, Mode Refinement, Vibronic Structure Refinement: If enabled an additional displacement will be performed along the new modes at the end of the calculation to obtain refined frequencies and IR intensities. Equivalent to running the output file of the mode tracking calculation through the AMS ModeScanning task.

ResonanceRaman

Type Block

Description Block that contains settings for the calculation of Resonance Raman calculations

IncidentFrequency

Type Float

Unit cm-1

Description Frequency of incident light. Also used to determine most important excitation in case more than one is provided.

LifeTime

Type Float

Default value 0.00045

Unit hartree

Description Lifetime of Raman excited state.

RamanOrder

Type Integer

Default value 2

Description Order up to which to compute Raman transitions

RamanRange

Type Float List

Default value [0.0, 2000.0]

Unit cm-1

Recurring True

Description Specifies frequency range of the Raman spectrum to compute. 2 numbers: an upper and a lower bound.

Type

Type Multiple Choice

Options [ModeScanning, ModeTracking, ModeRefinement, VibronicStructure, VibronicStructureTracking, VibronicStructureRefinement, ResonanceRaman]

Description Specifies the type of vibrational analysis that should be performed

VSTRestartFile

Type String

Description Path to a .rkf file containing restart information for VST.

16.1 What is the difference between AMS and the AMS driver?

Amsterdam Modeling Suite (AMS) refers to the whole suite which includes the AMS driver for complex potential energy surface tasks with any underlying engine. The AMS bundle further includes the integrated GUI and the compute engines ADF, BAND, DFTB, MOPAC, ReaxFF, UFF, COSMO-RS.

16.2 What is the AMS driver?

It's a driver for running molecular dynamics or exploring the potential energy surface (finding transition states etc.)

It can be used with different modules: ADF, BAND, DFTB, MOPAC, ReaxFF and external engines. And as such you can switch easily between them, e.g. to transfer a Hessian from a low-lying method.

16.3 What will AMS do when one point fails to converge?

With AMS2018.103 it will exit with an error.

Starting with r69000, AMS geometry optimizations try to continue even if engine fails to solve for a geometry.

This can happen if there are for example SCF convergence problems in the engine. The energy/gradients might then not be quite correct, but it is probably safe to continue the optimization and hope that things are fine again for the next step. Note that this fix also applies to PES scans, transition state searches, and any other applications that use geometry optimizations internally (e.g. elastic property calculations).

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