1.1 Introduction

ReaxFF is a program for modeling chemical reactions with atomistic potentials based on the reactive force field approach developed by Prof. Adri van Duin and coworkers. SCM has modernized, parallelized and greatly optimized the original Reax program but kept it input- and output-compatible with the original, with some extensions.

1.2 Release 2016

In comparison to ADF-ReaxFF 2014, the 2016 release offers the following new functionality:

- Performance improvements for very narrow and long unit cells
- Support for the ACKS2 charge equilibration method (page 15) (given a suitable force-field)
- Automated Discovery of Reaction Pathways, Rate Constants, and Reaction Networks with the Chemical Trajectory Analyzer ChemTraYzer developed by the Leonhard group (http://www.ltt.rwth-aachen.de/forschung/molekulare_thermodynamik/molekulare_thermodynamik/project/ChemTraYzer_Modellierung_chemi/) at Aachen University.

1.3 ReaxFF-GUI

The graphical user interface ReaxFF-GUI enables users to set up complicated calculations with a few mouse clicks, and provides graphical representations of calculated data fields, see the ReaxFF-GUI tutorials.
CHAPTER TWO

MCFFOPTEIMIZER: MONTE CARLO FORCE-FIELD PARAMETER OPTIMIZER

The MCFFOptimizer uses a Monte Carlo approach to finding the best-fit force-field for the given training set. It is based on the paper by E. Iype et. al. (http://dx.doi.org/10.1002/jcc.23246) In the following sections, the input and output of the MCFFOptimizer are described.

2.1 Input files

In order to optimize a ReaxFF forcefield, the files listed below must be present in the directory where the reaxff program is executed.

- **i opt** – file containing a single text line with 4 on it, written in the (i3) format. This will instruct reaxff to perform a Monte-Carlo force-field optimization.
- **ffield** – the initial force-field file.
- **ffield_min** – minimum values for each force-field value (this file has the same format as **ffield**).
- **ffield_max** – maximum values for each force-field value (this file has the same format as **ffield**).
- **ffield_bool** – contains 1.0 or 0.0 as a flag whether the corresponding value is to be optimized or not (this file has the same format as **ffield**).
- **trainset.in** – file with test values, the same as in the original reaxff force-field optimization, see page 27 of the ReaxFF User Manual.
- **geo** – file with test geometries in the BGF format, the same as in the original reaxff force-field optimization. Geometries of different molecules in this file must be concatenated.
- **control** – in addition to general ReaxFF control parameters it also contains the MCFFOptimizer-related ones explained below.

The mcffopt_water example in the examples/reaxff directory demonstrates the use of the MCFFOptimizer. Note however that this example is not physically meaningful. For example, many atomic force-field parameters are allowed to vary in a very broad range, which is the same for all elements. In practice, you will want to set the range for each element separately.

2.2 Control parameters

The following control parameters are related to MCFFOptimizer. The default value for each parameter is given in parentheses.
• mcffit – number of MC iterations (10000). Since the Monte-Carlo method does not have any notion of convergence the optimization is stopped after mcffit iterations.

• mcbeta – initial MC beta parameter in the acceptance probability calculation \( P = \exp(-\beta \Delta E) \) (1.0). Here, \( \Delta E \) is a difference in the error function between the current and the best step so far. If the current step is the best, it is always accepted. Otherwise, the acceptance probability is calculated using the formula above and it is calculated with a random number from the (0,1) range. The optimal value of beta depends on values of the error function.

• mcdbet – simulated annealing: increase the beta parameter by this value at each step (0.0). A positive mcdbet value means that the probability to take a step that increases the error function will decrease over time. This has the same effect as decreasing the temperature in the classical molecular Monte-Carlo method.

• mcbsca – simulated annealing: divide the beta parameter by this value at each step (1.0). A value of mcbsca 1.0 has an effect similar to positive mcdbet.

• mcacpf – probability to vary a variable at each step (0.2). To avoid taking very large steps only some of the variables are varied at each step (selected randomly).

• mcrxdd – number of steps to divide the parameter range between ffield_min and ffield_max into (100).

• mcstep – initial max step size in units of range/mcrxdd, where range = difference between ffield_max and ffield_min values (1.0).

• mcmxst – maximum allowed value of max step size (100);

• mcscps – factor to scale max step size to satisfy acceptance tolerance (1.1);

• mctart – target acceptance rate, percent (30.0);

• mcmax – max acceptance rate, percent (70.0);

• mcmini – if not 0, minimize the best force-field parameter set after so many iterations (0). The optimization is performed only if the best set has changed since the previous minimization. The minimization employed here is gradient-free and relatively slow so it should not be used too frequently.

• replic – number of replicas to try at each step (1). At each step, replic Monte-Carlo steps are done and the one with the lowest error is selected for the next iteration.

Relation between mcrxdd, mcstep, mcmxst, and mcscps. The allowed range for each parameter is divided into mcrxdd steps. At each optimization step, a number of force-field parameters is changed by the \( \Delta x = \text{mcstep}(X_{\text{max}} - X_{\text{min}})/\text{mcrxdd} \), where \( X_{\text{max}} \) and \( X_{\text{min}} \) are values of this parameter from ffield_max and ffield_min, respectively. When performing optimization, the program keeps track of the average acceptance rate and adjusts mcstep up or down by the mcscps factor to keep the acceptance rate close to mctart. If the acceptance rate is too low the step size is decreased to allow searching for a smaller parameter space. The mcstep value can never be larger than mcmxst.

It should be noted that the value of the MC step size (and thus all the parameters discussed in this section) applies to all force-field parameters to the same extent, which means that it is very important to select the min and max parameter values very carefully. The rule of thumb here is that the range should be as small as possible covering only the physically meaningful values.

2.3 Results

Main results of the MCFFOptimizer are saved in the following files:

• ffield_best - force-field file corresponding to the lowest error value

• ffield_last - the most recent accepted force-field
• MCFFOptimizer.log - summary of iterations including the error function value, number of changed and bounded force-field parameters, cumulative number of accepted and rejected steps at each step. Also the current MC parameters such as the $\beta$ value and the acceptance rate, are shown, as well as the elapsed time in seconds.
• fort.99 - the error function breakdown for the latest step

2.4 Run-time control

The progress of the force-field optimization can be controlled by changing parameters in the istop file present in the calculation directory. The file is read every 10 iterations. The parameters are explained below:

• StopKey - replace 0 with 1 to stop the calculation
• Beta - the current $\beta$ value corresponding to the mcbeta control parameter
• Command - one of: NONE, WALK, JUMPWALK, MINIMIZE, JUMPMINI:
  • NONE - no change in the procedure
  • WALK - switch to Monte-Carlo steps (the default);
  • MINIMIZE - switch to gradient-free minimization of the latest accepted force-field;
  • JUMPWALK - take the best force-field so far and start the Monte-Carlo procedure from there;
  • JUMPMINI - take the best force-field so far and minimize it.
• ScaleFactor - change the current step size corresponding to the mcstep control parameter
• ActiveParameterFraction - set the fraction of force-field parameters changed at each step (mcacpf)
• deltaBeta - change the current value of the mcdbet control parameter
• BetaScaling - change the current value of the mcbsca control parameter
• ScaleParSpace - change the current value of the mcscps control parameter
3.1 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

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 Reaxff GCMC code

The GCMC code for reaxff was originally developed by Thomas Senftle, working as a Graduate Student at Penn State University under the supervision of Dr. Adri van Duin. 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.

A rewrite of the code, made by Hans van Schoot (SCM) in close collaboration with Thomas Senftle, is now available in the ADF package. The rewrite directly integrates into the ADF-ReaxFF code, solving performance issues of the original code by removing the calling overhead of the reaxff executable and the relatively slow file management. It also merged several modifications of the original code to support the usage of whole molecules for Monte Carlo moves, and supports the usage of multiple atom/molecule types during the simulation. Other improvements were made on the input options, the accessible volume calculation, the MC acceptance prefactor calculation and the writing of logfiles.

The relevant papers are:


Thomas P. Senftle, Adri C.T. van Duin, Michael J. Janik, Determining in situ phases of a nanoparticle catalyst via grand canonical Monte Carlo simulations with the ReaxFF potential, Catalysis Communications volume 52, 5 July 2014, Pages 72–77 (http://dx.doi.org/10.1016/j.catcom.2013.12.001)

3.2 Input

Overview
The GCMC code in ADF-ReaxFF needs the following input files to run:

- **control_MC**: The GCMC control file, which holds MC settings and the atoms/molecules to insert/move/delete
- **control**: A reaxff control file, in which only a small number of parameters is of interest
- **ffield**: A standard reaxff forcefield file
- **geo**: A geometry file, preferably in biograph format (code not yet tested with xyz)
- **iopt**: Text file that should only contain a “5” (without the quotes)
- **insertData_MC**: (optional file) Table used when restarting GCMC simulations

Also, the current version of the GCMC code can only run in serial, so please set the NSCM environment variable to 1 (type “export NSCM=1” (without quotes) in the shell before starting a GCMC reaxff run).

**the control_MC file**

Lines in the control_MC file that start with ! or # will be ignored, so those can be used for comments. Empty lines are also ignored, so feel free to leave some in the file. Lines with keywords should have their value in the first 8 columns, followed by a couple of spaces (at least 1), followed by the 6-character keyword. The order is free, except for the **nmols** keyword, which should be the last one. The **nmols** keyword signals the parser that the next section of control_MC will define X new MC Molecule Types.

This is an example for the control_MC file:

```plaintext
! GCMC control file example
0 iensmb !select MC ensemble (0=Mu-NVT with fixed volume, 1=Mu-NPT with variable volume)
5000 niter !number of MC iterations to do this simulation
0 nstart !start the iteration counter with an offset, usefull for restarts to avoid double files
300.0 mctemp !Temperature of the simulation, affects acceptance rate for steps that increase the energy
0.0 mcpres !NPT pressure in GPa (set to zero for incompressible solid systems unless at very high pressure)
3.0 rmaxpl !Max radius for atom placement on insert/displace move
1.2 rminpl !Min radius for atom placement on insert/displace move
2000 nmctry !Maximum number of trials allowed when inserting or moving a molecule. If the
! ! rmaxpl and rminpl variables are very strict, this number needs to be large
1 igcfac !include GC prefactor in probabilities? 0 = no 1 = yes
0 ivol !select MC volume calculation technique:
! ! 0: vvacu needed! volume = total volume - occupied volume - specified vacuum volume
! ! 1: volume = total cell volume
! ! 2: vacc needed! volume = specified accessible volume (vacc)
! ! 3: volume = total cell volume - occupied volume
! ! 4: vacc needed! volume = specified accessible volume (vacc) - occupied volume
435.0 vacc !if ivol=2 or ivol=4, specify Vacc in angstroms^3
0.0 vvacu !if ivol=0 specify non-accessible (vacuum) volume Vvacu in angstroms^3
0.25 ivlim !volume change limit (value between between 0 and 1, Vnew = (1+ivlim)*V1)
1 resopt !write restart files: 0=no, 1=yes
1 resfrq !frequency of writing restart files (MC code only writes files if the MC move is accepted)
0 debug !print debug output if set to 1, print even more debug output when set to 2
5 nmols !Number of MC molecule types, must match the number of molecule blocks that follow!

! Molecule Specific Data: C2H2 example
! This part is fixed format!
! We need cmpot on line 1,
! possibly followed by the noinsr on line two,
! and forced to be ended with nmatom on line 2 or 3, followed by nmatom lines of coordinates.
! the coordinates are FIXED FORMAT! (24d.15,1x,A2) x,y,z (24 wide, 15 after decimal), 1 space, 2chars symbol
-75.00 cmpot !chemical potential of molecule
12.00 nmatom !number of atoms in molecule
4
12.1804800000000 0.42169600000000 1.316689000000000 C
13.12473100000000 0.37690200000000 0.568360000000000 C
```

Chapter 3. Grand Canonical Monte Carlo (GCMC)
!Molecule Specific Data: C2H4 example
-75.00 cmpot !chemical potential of molecule
6 nmatom !number of atoms in molecule
13.989222000000000 0.405391000000000 1.000150000000000 C
13.316784000000000 0.399646000000000 0.885795000000000 C
11.494513000000000 0.461837000000000 1.970612000000000 H
11.335219000000000 0.353577000000000 0.129581000000000 H
13.811701000000000 0.340224000000000 -0.084000000000000 H
13.970561000000000 0.453325000000000 1.756236000000000 H

!Molecule Specific Data: H2O Example
-75.00 cmpot !chemical potential of molecule
3 nmatom !number of atoms in molecule
39.996720000000000 40.747660000000000 40.512210000000000 H
40.000210000000000 39.999520000000000 39.934730000000000 O
40.000030000000000 39.259880000000000 40.523700000000000 H

!Molecule Specific Data: H2 Example
-75.00 cmpot !chemical potential of molecule
2 nmatom !number of atoms in molecule
5.025812000000000 0.000000000000000 0.000000000000000 H
5.774188000000000 0.000000000000000 0.000000000000000 H

!Molecule Specific Data: Single atom example
-75.00 cmpot !chemical potential of molecule
1 nmatom !number of atoms in molecule
0.000000000000000 0.000000000000000 0.000000000000000 H

The Molecule Specific Data blocks define the molecules (or atoms) that can be inserted/moved/deleted with the MC code. The atoms named here should of course be in the forcefield files, and 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 the molecule stays inside the boundaries of the box, the code only checks that the rmaxpl/rminpl values are satisfied. If you plan on inserting large molecules, make sure there is enough room in the rmaxpl value, otherwise the code will stop with an error message.

The chemical potential (cmpot) keyword

The cmpot keyword sets the chemical potential of the molecule (or atom) reservoir, and is employed 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:

\[
\text{cmpot} = \text{Mu}_O(T,P) = 1/2 * \text{Mu}_O2(T,P) = 1/2 * \left[ \text{Mu}_{\text{ref}}(T,P_{\text{ref}}) + kT \log \left( \frac{P}{P_{\text{ref}}} \right) - E_{\text{diss}} \right]
\]

where the reference chemical potential \( \text{Mu}_{\text{ref}}(T,P_{\text{ref}}) \) is the experimentally determined chemical potential of O2 at T and Pref, \( kT \log \left( \frac{P}{P_{\text{ref}}} \right) \) is the pressure correction to the free energy, and \( E_{\text{diss}} \) is the dissociation energy of the O2 molecule.

The no insert (noinsr) keyword

The noinsr keyword tells 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 (if the iensmb keyword is set to 1).
the control file

The control file is a regular reaxff control file and it influences the minimization step after an MC trial move. Because of this, only a small number of the reaxff keywords are used during the GCMC simulation.

An example of the control file:

```plaintext
# some of the parameters that influence the minimization step in the GCMC code
1 icentr Put the center of mass at the center of the cube
1 igeofo 0:xyz-input geometry 1: Biograf input geometry 2: xmol-input geometry
2.50000 endmm End point criterium for MM energy minimisation
500 imaxit Maximum number of iterations
0 icelop Optimize cell parameters 0=no 1=yes
1.00050 celopt Cell parameter change
0 imaxmo In this case: 0: POLAK_RIBIERE Conj.Grad method, 1: Limited-memory BFGS method
```

The code has been tested with various imaxit and endmm values, the other options have not been fully tested. Other reaxff keywords might also influence the minimization procedure, but those are best left to their default settings.

the ffield file

The ffield file should be a normal reaxff forcefield file, as described in the reaxff documentation by A. van Duin (visit the documentation section on the SCM website to obtain this document).

the geo file

The GCMC code has been tested with biograph input files, but other input formats might work. The details of this file are also described in the original reaxff documentation by van Duin.

the iopt file

The iopt file is a text file with a single digit inside that selects the execution mode of the reaxff code. To run the GCMC code, this file should contain a “5” (without the quotes).

the insertData_MC file

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 of 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 (keep in mind that they can move around during the minimization step). The insertData_MC file can be used to tell the GCMC code what atoms in the geo file belong to which molecule.

An example of the insertData_MC file:

```plaintext
# atomNumber MCInsMolType MCInsertNmbr
30 1 1
40 2 1
46 2 1
47 1 2
48 1 3
```

This example specifies 4 molecules/atoms that are modifiable by the GCMC code, belonging to 2 different GCMC molecules/atoms that are defined in the control_MC file. The first “molecule” in the control_MC file should thus consist of a single atom (if this doesn’t match, the code will most likely crash!). It was inserted three times (atom 30, 47 and 48) The second molecule has two atoms, and was inserted once.

The atoms do not have a fixed order, and not all atoms have to be defined. If an atom is not appointed to a certain MCInsMolType and MCInsertNmbr, if will simply not be modified during the MC moves. The insertData_MCXXXXXX files generated by the restart option of the code can be directly used as valid insertData_MC files, just remove the digits from the filename and replace the geo file with the corresponding geo_MCXXXXXX file.
3.3 Output

Overview

The GCMC code writes a couple of output files, each described in this section. It also produces a number of reaxff output files, and some of these are described in the original reaxff documentation by van Duin. Keep in mind that these files might not provide a complete or correct picture of the simulation, as they could also contain data originating from rejected MC trial moves.

geo_MCXXXXXX

This file is generated every X accepted MC moves and contains the current geometry of the system in biograph format (X is set with the resfrq keyword in the control_MC file).

insertData_MCXXXXXX

This file contains a table of all the atoms in the system with their MC Molecule Type and MC Insert Number. This data can be used to map atoms to an inserted molecule, and is needed if you want to restart your calculation from an accepted MC step. The table contains -1 values for atoms that were in the original input and did not get a manually assigned MCInsert Molecule Type and MC Insert Number, the GCMC code will not modify these atoms during the MC steps.

Also see the section on insertData_MC file.

MCstats

The MCstats file is a logfile that contains the statistics of the MC simulation. The GCMC code writes a single line to it after every MC step, containing the number of: Tried MC moves (tried), Accepted MC moves (accept), Rejected MC moves (reject), Accepted Insertion/Deletion/Moving/Volume change MC moves (addAcc/delAcc/mvAcc/volAcc), Rejected Insertion/Deletion/Moving/Volume change MC moves (addRej/delRej/mvRej/volRej)

An example of the MCstats file:

<table>
<thead>
<tr>
<th>tried</th>
<th>accept</th>
<th>reject</th>
<th>addAcc</th>
<th>delAcc</th>
<th>mvAcc</th>
<th>volAcc</th>
<th>addRej</th>
<th>delRej</th>
<th>mvRej</th>
<th>volRej</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>4</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>5</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>6</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>1</td>
<td>7</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>3</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>8</td>
<td>1</td>
<td>8</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>3</td>
<td>4</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>9</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>4</td>
<td>4</td>
<td>0</td>
</tr>
<tr>
<td>10</td>
<td>1</td>
<td>10</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>4</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>11</td>
<td>2</td>
<td>10</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>4</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>12</td>
<td>3</td>
<td>10</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>4</td>
<td>5</td>
<td>0</td>
</tr>
</tbody>
</table>

Elog

The Elog file contains the Volume and energies of the accepted MC steps. The energies in this logfile are the pure ReaxFF energy of the system (RxFFEnergy) and the MC corrected energy, which is used in determining if the step should be accepted or not (see the section on calculating energies for details).

An example of the Elog file:

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Naccepted</th>
<th>Volume</th>
<th>MC Energy</th>
<th>RxFFEnergy</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
<td>15625.00</td>
<td>-3098.88</td>
<td>-3179.88</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>15625.00</td>
<td>-3107.92</td>
<td>-3269.92</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>15625.00</td>
<td>-3130.13</td>
<td>-3373.13</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>15625.00</td>
<td>-3160.05</td>
<td>-3484.05</td>
</tr>
</tbody>
</table>
3.4 Code Details

Overview

The GCMC code will perform niter (control_MC file option) Grand Canonical Monte Carlo trial moves, and accept or reject them based on the Energy produced by the ReaxFF minimization step of the trial geometry. 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 code works.

MC Moves (Insert/Delete/Move/Volume)

The GCMC code currently supports 4 types of MC Moves: Insert, Delete, Move (displace), Volume change. The first three moves always change a whole “molecule” of the system, as defined in the control_MC file (a molecule can of course contain only a single atom). Every MC iteration selects one MC Molecule Type from the defined molecules in control_MC at random, followed by a random MC Move (unless there are no molecules of the type in the system, in that case it will do an insert move).

The Insert and Displace (move) MC Moves will generate a random rotation and position for the molecule, and then check if the random positions are within the “RminPl” and “RmaxPl” boundaries (this means no atom in the molecule can be closer to any atom currently in the system than “RminPl”, and it should be within “RmaxPl” distance to an atom in the system). If the conditions are not satisfied, a new set of coordinates is generated and the code checks again. This is repeated a maximum number of “nmctry” times before stopping with an error.

The volume change is controlled by the “ivlim” variable in control_MC. The ivlim sets the volume change limit, and it should be a value between between 0 and 1. The new volume will be calculated like this: Vnew = (1+ivlim)*Vold.

Calculating energies

Because the GCMC simulation adds and deletes atoms or molecules during the runtime, it cannot directly compare the ReaxFF 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 balance this out, the GCMC code calculates a “corrected” MC energy to compare the trial reaxFF energy with, consisting of the previously accepted ReaxFF energy + the chemical potential (cmpot in control)MC) for the inserted molecule, or the ReaxFF energy - the chemical potential for the deleted molecule. The volume change energy is also corrected, using the following formula:

E_MC_Corr = E_reaxff_last_accept - (Pressure * 0.1439 * (newV-oldV)) + ((1.0/beta) * nInsertedMols * log(newVavail/oldVavail))

where newVavail and oldVavail are calculated from the MC available volume (see the section calculating volumes).

Calculating volumes

The GCMC code can calculate the available volume in a couple of different ways, depending on the ivol setting in control_MC:

- ivol = 0: volume = total volume - occupied volume - specified vacuum volume (vvacu)
- ivol = 1: volume = total cell volume
- ivol = 2: volume = specified accessible volume (vacc)
• $ivol = 3$: volume = total cell volume - occupied volume
• $ivol = 4$: volume = specified accessible volume ($vacc$) - occupied volume

Where the occupied volume is calculated by summing up the volumes of the atoms in the geo file that are not specified to be part of an MC type molecule. The volume of an atom is calculated using the average of the covalent atomic radius and the vd Waals radius of the atom, which are found in the reaxff forcefield file (ffield).

The $vacc$ and $vvacu$ options can be specified in the control_MC file to get a more accurate available volume.

**Acceptance criteria**

An MC move is always accepted if the reaxff 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 bigger than:

$prob = \text{preFactor} \times \exp(-\text{Beta}\times\delta\text{E})$

Where 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.
NEW FEATURES AND FIXES

4.1 ACKS2: Atom-condensed Kohn-Sham DFT approximated to second order

The ACKS2 charge equilibration scheme has been implemented following the original paper “ACKS2: Atom-condensed Kohn-Sham DFT approximated to second order” by T. Verstraelen et al. J. Chem. Phys. 138 (2013) 074108.

Using the ACKS2 scheme requires a suitable force-field, which is recognized by “[ acks2 ]” at the start of the first line of force field file (note: the spaces around “acks2” are important!). Besides, the icharg parameter in the control file must be set to 7. In addition to the general EEM parameters the ACKS2 scheme needs the general force-field parameter #35 (“Xamp”) and the atomic cut-off parameter #23 (“softcut”).

4.2 Correction for torsion angles asymptotics

There is a discontinuity problem for small bond orders in the expression for torsion angles and conjugation contributions f(BO). These terms correspond to expressions for f_{10} (eq. 10b) and f_{12} (eq. 11b) in the original ReaxFF paper “ReaxFF: A Reactive Force Field for Hydrocarbons”, J. Phys. Chem. A 2001, 105, 9396-9409. The new expression for each term in f_{10} is [1 - \exp(-2 * \lambda_{23} * BO**2)] and in f_{12} it is \sin(BO*pi/3)**4. The new expressions ensure correct asymptotic behavior for the dE/dBO for BO \rightarrow 0. Using this makes geometry optimizations more stable and improves conservation of energy during MD.

The correction can be enabled by setting the tors13 flag in the control file to 1.

4.3 LG dispersion


The LG dispersion correction is turned on when using a suitable forcefield, which is recognized by the “[ lgDispersion=1 ]” key in the file header.

4.4 ChemTraYzer

The ChemTraYzer scripts, developed in the Leonhard group (http://www.ltt.rwth-aachen.de/forschung/molekulare_thermodynamik/molekulare_thermodynamik/project/ChemTraYzer_Modellierung_chemi/)
at Aachen University, provide a methodology for deducing quantitative reaction models from reactive molecular
dynamics simulations by identifying, quantifying, and evaluating elementary reactions of ReaxFF trajectories.

For usage with ADF’s ReaxFF the scripts have been slightly modified and use
RDKit instead of the openbabel-bindings. A GUI-tutorial is available here
(http://acc.scm.com/documentation/Tutorials/ReaxFF/Burning_methane/#step-5-analyze-it-create-a-reaction-
network). 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).
INCLUDED FORCEFIELDS

See also *Included Forcefields (development version)* (page 27).

Description of ReaxFF force fields

Disclaimer: Using these forcefields for systems they have not been explicitly trained against may produce unrealistic results. Please see the full manuscripts for more detailed information.

The force field files used by the SCM version of ReaxFF are compatible with those used by the original ReaxFF code. So if you have the force field information from somewhere else you can just use it (save it in a text file, and select it in ADFinput via the Other... option).


- QM data were generated describing the single and (if relevant) double and triple bond dissociation for all B/N/O/H combinations. These data were used to derive initial ReaxFF bond parameters, and all calculations were performed using DFT with the B3LYP functional and the Pople 6-311G** basis set.
- The training set was then extended with QM data describing angular distortions in a set of small AB-related (AB H3N-BH3) molecules. These data were used to derive the initial ReaxFF angular parameters.
- The training set was extended with reaction barriers for key reaction steps such as H2 release from AB, dimerization of H2B-NH2 and reaction energies associated with H2 release from AB and with AB oxidation.


- The original Au-Au parameters were extended by three publications:
- The forcefield does not include Au/N parameters

- To obtain the H/C/O compound data required to extend the hydrocarbon-training set, DFT calculations were performed on the following systems: (a) dissociation energies for various bonds containing carbon, oxygen, and hydrogen. The ground state structure was obtained through full geometry optimization. Dissociation curves were calculated by constraining only the bond length of interest and re-optimization of the remaining internuclear coordinates. Optimization was also performed for the various angles and torsions associated with C/H/O interactions.


- The parameters in this forcefield were extended/improved by two other publications:

- The C/H/O parameters are the same as in the CHO forcefield, with added S/C, S/H and S/O descriptions. This force field was used in Castro et al, Combustion and Flame 2011
- The Boron and Nitrogen parameters are based on (but not identical to) the parameters used in Weismiller et al, JPC-A 2010.


- This forcefield is an extension of: A.C.T. van Duin, V.S. Bryantsev, M.S. Diallo, W.A. Goddard, O. Rahaman, D.J. Doren, D. Raymand, and K. Hermansson Development and validation of a ReaxFF reactive force field for Cu cation/water interactions and copper metal/metal oxide/metal hydroxide condensed phases Journal of Physical Chemistry A 2010, 114, 9507-9514 http://dx.doi.org/10.1021/jp102272z


- The initial force field parameters for the Fe-Fe parameters were taken from an earlier force field development project on bulk-iron metal, based on DFT-calculations on antiferromagnetic BCC and FCC. The ReaxFF parameters have not been published yet, however the DFT data can be found in ref 31 of the above mentioned manuscript. The O/H parameters were taken from the ReaxFF bulk water description. The Fe/Fe and O/H parameters were kept fixed to these initial values, whereas the Fe/O parameters were reoptimized against the quantum mechanical results presented in the above mentioned manuscript.
- Detailed information on the force field parameters is given in the supporting information of the above mentioned manuscript.

Part of this forcefield is also published in: L.Z. Zhang, S.V. Zybin, A.C.T. van Duin, S. Dasgupta, W.A. Goddard, and E.M. Kober Carbon Cluster Formation during Thermal Decomposition of Octahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine and 1,3,5-Triamino-2,4,6-trinitrobenzene High Explosives from ReaxFF Reactive Molecular Dynamics Simulations Journal of Physical Chemistry A (2009) 113, 10619-10640 http://dx.doi.org/10.1021/jp901353a

The parameters of the nitramine ReaxFF are based on a large number of ab initio QM calculations. Over 40 reactions and over 1600 equilibrated molecules have been used; they are designed to characterize the atomic interactions under various environments likely and unlikely high energy each atom can encounter. The training set contains bond breaking and compression curves for all possible bonds, angle and torsion bending data for all possible cases, as well as crystal data.

The included forcefield is based on the Newsome reference, with slightly improved parameters by van Duin et al.


This forcefield originally had a typo, defining the H-Na-Na angle twice. The same typo is in table 4 of the publication, but the text clearly mentions that the second line should define Na-H-Na instead.


This force field was trained to model the interaction of water at the SiO2 surface, with specific emphasis on proton-transfer reactions. Updated parameters were fitted for all Si/O/H bond, angle, and torsion interactions as well, in addition to the dissociation of a water molecule from a single Si(OH)4 molecule and reaction energies for the polymerization of Si(OH)4


The included forcefield is based on the Newsome reference, with slightly improved parameters by van Duin et al.


The ReaxFF force field parameters have been fit to a large quantum mechanics (QM) training set containing over 700 structures and energetics related to bond dissociations, angle and dihedral distortions, and reactions between hydrocarbons and vanadium oxide clusters. In addition, the training set contains charge distributions for small vanadium oxide clusters and the stabilities of condensed-phase systems including V2O5, VO2, and V2O3 in addition to metallic V (V0).

ZnOH.ff: (Zn/O/H) D.Raymand, A.C.T. van Duin, M. Baudin, K. Hermansson A reactive force field (ReaxFF) for zinc oxide Surface Science 2008, 602, 1020-1031 (http://dx.doi.org/10.1016/j.susc.2007.12.023)


Based on QM calculations for Zn(s), ZnO(s), and Zn hydroxide clusters [Zn(OH)2 and O(ZnOH)2],

ZnOH.ff: (Zn/O/H)
ReaxFF parameters were generated for Zn-O and Zn-Zn bond energies and for Zn-O-Zn, O-Zn-O, O-Zn-Zn and Zn-O-H valence angle energies.

- QM calculations were performed for the four crystal polymorphs of the wurtzite, zincblende, rocksalt and caesium chloride structures (the structures are also referred to as h-ZnS, c-ZnS, NaCl and CsCl, respectively).


CaSiAIo.ff: (C/H/O/Fe/Cl/Si/Al/Ca) M.C. Pitman and A.C.T. van Duin Dynamics of Confined Reactive Water in Smectite Clay–Zeolite Composites J. Am. Chem. Soc., 2012, 134 (6), 3042–3053 (http://dx.doi.org/10.1021/ja208894m)


- This forcefield adds London dispersion correction terms to reaxFF, and is optimized for the energetic materials RDX, PETN, TATB, and NM plus graphite, polyethylene, solid carbon dioxide, and solid N2, using the low temperature crystal structures to determine the lg correction parameters.

CHOFeAlNiCuS.ff: (C/H/O/Fe/Al/Ni/Cu/S) O.Rahaman, A.C.T. van Duin, W.A. Goddard III and D.J. Doren Development of a ReaxFF reactive force field for glycine and application to solvent effect and tautomerization Journal of Physical Chemistry B 115 (2011), 249-261. (http://dx.doi.org/10.1021/jp201496x)


- Not all cross-terms between the two forcefield files are defined, which might cause problems if the system has (for example) C-Cu interactions.


AuSCH_2013.ff: (Au/S/C/H) Gyun-Tack Bae and Christine M. Aikens Improved ReaxFF Force Field Parameters for Au–S–C–H Systems Journal of Physical Chemistry A 2013 117 (40), 10438-10446 (http://dx.doi.org/10.1021/jp405992m)


- yields improvements for bond bending potential energy surfaces

- aims to agree with DFT geometries of small clusters and gold–thiolate nanoparticles


- Specialized forcefield, designed to “investigate the failure of the poly(dimethylsiloxane) polymer (PDMS) at high temperatures and pressures and in the presence of various additives”

TiOCHNCl.ff: (C/H/O/N/S/Mg/P/Na/Ti/Cl/F) S.Y. Kim, A.C.T. van Duin, and J.D. Kubicki Molecular dynamics simulations of the interactions between TiO2 nanoparticles and water with Na+ and Cl-, methanol, and formic acid using a reactive force field Journal of Materials Research / Volume 28 / Issue 03 / 2013, pp 513-520 (http://dx.doi.org/10.1557/jmr.2012.367)
• used for simulating TiO2 (both rutile and anatase) nanoparticles with water, methanol, and formic acid
• The force field was validated by comparing water dissociative adsorption percentage and bond length between Na-O with density functional theory (DFT) and experimental results


• Aimed at oxygen interactions with realistic silica surfaces

CHOFe.ff: (C/H/O/Fe/Cl/Si/Al) Chenyu Zou, A.C.T. Van Duin Investigation of Complex Iron Surface Catalytic Chemistry Using the ReaxFF Reactive Force Field Method JOM, December 2012, Volume 64, Issue 12, pp 1426-1437 (http://dx.doi.org/10.1007/s11837-012-0463-5)

• only the parameters for Fe (and crossterms) differ from the CHOAlSi.ff forcefield

CHOAlSi.ff: (C/H/O/Fe/Cl/Si/Al) F.Castro-Marcanoa, A.C.T. van Duin Comparison of thermal and catalytic cracking of 1-heptene from ReaxFF reactive molecular dynamics simulations Combustion and Flame, Volume 160, Issue 4, April 2013, Pages 766–775 (http://dx.doi.org/10.1016/j.combustflame.2012.12.007)

• only the parameters for Fe (and crossterms) differ from the CHOFe.ff forcefield

CHOLi.ff: (C/H/O/N/S/Mg/P/Na/Li) D.Bedrov, G.D. Smith, A.C.T. van Duin Reactions of Singly-Reduced Ethylene Carbonate in Lithium Battery Electrolytes: A Molecular Dynamics Simulation Study Using the ReaxFF Journal of Physical Chemistry A, 2012, 116 (11), pp 2978–2985 (http://dx.doi.org/10.1021/jp210345b)

• specifically generated for simulating Lithium battery electrolytes
• must be used in combination with the MOLCHARGE keyword to set a charge restraint on Li and CO3!

SiOAIIi.ff: (H/O/Si/Al/Li) B.Narayanan, A.C.T. van Duin, B.B. Kappes, I.E. Reimanis and C.V. Ciobanu A reactive force field for lithium–aluminum silicates with applications to eucryptite phases Modelling and Simulation in Materials Science and Engineering 2012 20 015002 (http://dx.doi.org/10.1088/0965-0393/20/1/015002)

- used for studying Oxidation states of Pd nanoparticles, surfaces and bulk configurations with a GCMC method


- used in combination with a GCMC method


- forcefield was generated using a recently developed Monte Carlo algorithm with simulated annealing.

**CHONSMgPNaCuCl.ff**: (C/H/O/N/S/Mg/P/Na/Cu/Cl)  Susanna Monti, Cui Li, and Vincenzo Caravetta *Reactive Dynamics Simulation of Monolayer and Multilayer Adsorption of Glycine on Cu(110)* J. Phys. Chem. C, 2013, 117 (10), pp 5221–5228 (http://dx.doi.org/10.1021/jp312828d)

- Reactive MD-force field for amino acids on copper

**CHOSMoNiLiBFPN.ff**: (C/H/O/S/Mo/Ni/Li/B/F/P/N)  Md M. Islam, V.S. Bryantsev, A.C.T. van Duin *ReaxFF Reactive Force Field Simulations on the Influence of Teflon on Electrolyte Decomposition during Li/SWCNT Anode Discharge in Lithium-Sulfur Batteries* J. Electrochem. Soc. 2014 volume 161, issue 8, E3009-E3014 (http://dx.doi.org/10.1149/2.005408jes)

- forcefield for Electrochemistry in Li-S batteries


- comments in the forcefield file: interactions with water and Na+ Fogarty et al. JCP-2010 ; with glycine + C/H/F parameters; Si-F bond/offdiag/angle parameters; Si-S dummy parameters + S-O-Hparameters(Yun 2012 Oct8) + H-F bond/offdiag (Jan14 2013 Joon) Jan31: added Zr/O/H/C

**TiClOH.ff**: (C/H/O/N/S/Mg/P/Ti/C/F)  Sung-Yup Kim and A.C.T. van Duin *Simulation of Titanium Metal/Titanium Dioxide Etching with Chlorine and Hydrogen Chloride Gases Using the ReaxFF Reactive Force Field* J. Phys. Chem. A, 2013, 117 (27), pp 5655–5663 (http://dx.doi.org/10.1021/jp3031943)

- adaptation/evolution of the TiOCHNCl.ff forcefield by Kim, S.-Y. et al.

**CHONSSiAl.ff**: (C/H/O/N/S/Si/Na/Al)  C.Bai, L. Liu, and H. Sun *Molecular Dynamics Simulations of Methanol to Olefin Reactions in HZSM-5 Zeolite Using a ReaxFF Force Field* J. Phys. Chem. C, 2012, 116 (12), pp 7029–7039 (http://dx.doi.org/10.1021/jp300221j)

- used to simulate methanol to olefin (MTO) reactions in H-ZSM-5 zeolite

**undocumented/NiCH.ff**: (Ni/C/H/O/N/S/F/Pt/Cl)  Unknown *No Name Not published* (http://)

- This forcefield is from april 2009, and is not published


- Developed for and used to study Sulfur cathode behaviour in Li battery cells


- Force field was developed by combining the YSZ and Ni/C/H descriptions
From the summary: “The products obtained in our simulations are the same as those in experiment, which indicates that the developed ReaxFF potential properly describes complex physicochemical processes, such as the oxide-ion diffusion, fuel conversion, water formation reaction, coking, and delamination, occurring at the TPB and can be recommended for further computational studies of the fuel/electrode/electrolyte interfaces in a SOFC.”

The Aa atom type is a rename of the Zr atom type, which was defined twice.


- The forcefield file mentions “Gly with dummy N-P parameters”
- It was developed for studying Carbon dioxide interactions with the ionic liquid tetrabutylphosphonium glycinate, both physical and chemical absorption.

CHOLi_2.ff: (C/H/O/Li) M.Raju, P. Ganesh, P.R.C. Kent, and A.C.T. van Duin Reactive Force Field Study of Li/C Systems for Electrical Energy Storage J. Chem. Theory Comput., not yet printed, publication date (web) April 2nd, 2015 (http://dx.doi.org/10.1021/ct501027v)

- Used for studying Li/C systems with GCMC and MD
- Also contains parameters for “Vi” and “Gl”, but these virtual elements are not mentioned in the paper

CHONSSiCaCsKSrNaMgAlCu.ff: (C/H/O/N/S/Si/Ca/Cs/K/Sr/Na/Mg/Al/Cu) G.M. Psosfogiannakis, J.F. McCleerey, E. Jaramillo and A.C.T. van Duin ReaxFF Reactive Molecular Dynamics Simulation of the Hydration of Cu-SSZ-13 Zeolite and the Formation of Cu Dimers J. Phys. Chem. C, 2015, 119 (12), pp 6678–6686 (http://dx.doi.org/10.1021/acs.jpc.c5b00699)

- This Cu/Si/Al/O/H forcefield was developed for and used in MD simulations of the hydration of Cu-exchanged SSZ-13 catalyst.
- The force field was developed by merging and expanding previously tested and published ReaxFF force fields for Si/Al/O/H systems and Cu/O/H systems (citations 19-26 of the publication)
- This forcefield is an extension of K.L. Joshi et al 2014, http://dx.doi.org/10.1039/C4CP02612H, all non-Cu parameters are the same.


- This forcefield is optimized with a metropolis Monte-Carlo algorithm with simulated annealing to search for the optimum parameters for the ReaxFF force field in a high- dimensional parameter space.
- The optimization is done against a set of quantum chemical data for MgSO4 hydrates.

CHONSMgPNaCuCl_v2.ff: (C/H/O/N/S/Mg/P/Na/Cu/Cl) S.Monti, A. Corozzi, P. Fristrup, K.L. Joshi, Yun Kyung Shin, P. Oelschlaeger, A.C.T. van Duin and V. Baronee Exploring the conformational and reactive dynamics of biomolecules in solution using an extended version of the glycine reactive force field Phys. Chem. Chem. Phys., 2013, 15, 15062-15077 (http://dx.doi.org/10.1039/C3CP51931G)

- This forcefield is an extension of CHONSMgPNaCuCl.ff by S. Monti et al., J. Phys. Chem. C, 2013, 117 (10), pp 5221–5228, http://dx.doi.org/10.1021/jp312828d
- Developed for peptide and protein simulations


- Pt-Pt parameters for bulk platinum phases, low & high-index platinum surfaces and nanoclusters.
• O-Pt parameters for bulk platinum oxides, as well as oxygen adsorption and oxide formation on Pt(111) terraces and the {111} and {100} steps connecting them.

**CHONSMgPNaTiClF.ff**: (C/H/O/N/S/Mg/P/Na/Ti/Cl/F)
Stijn Huygh, Annemie Bogaerts, Adri C.T. van Duin and Erik C. Neyts
*Development of a ReaxFF reactive force field for intrinsic point defects in titanium dioxide*
Computational Materials Science, Volume 95, December 2014, Pages 579-591, ISSN 0927-0256 (http://dx.doi.org/10.1016/j.commatsci.2014.07.056)

• Forcefield developed for studying the influence of intrinsic point defects on the chemistry with TiO2 condensed phases.
• Forcefield seems to be based on TiOCHNCl.ff, http://dx.doi.org/10.1557/jmr.2012.367

**LiSi.ff**: (Li/Si)
*Stress effects on the initial lithiation of crystalline silicon nanowires: reactive molecular dynamics simulations using ReaxFF*

**CHOFeAlNiCuSCr.ff**: (C/H/O/Fe/Al/Ni/Cu/S/Cr)
*Development of a ReaxFF Reactive Force Field for Fe/Cr/O/S and Application to Oxidation of Butane over a Pyrite-Covered Cr2O3 Catalyst*
ACS Catalysis, 2015, 5 (12), pp 7226–7236 (http://dx.doi.org/10.1021/acscatal.5b01766)

• Forcefield optimized for Fe/Cr/O/S

**CHOFeAlNiCuSCr_v2.ff**: (C/H/O/Fe/Al/Ni/Cu/S/Cr) Ni-O-vacancy
C. Zou et al.
*Molecular dynamics simulations of the effects of vacancies on nickel self-diffusion, oxygen diffusion and oxidation initiation in nickel, using the ReaxFF reactive force field*

• Forcefield optimized for Ni/O, trained with a QM data on Ni, NiO and vacancies
• The non-carbon parameters are the same as in CHOFeAlNiCuSCr_v3.ff

**CHOFeAlNiCuSCr_v3.ff**: (C/H/O/Fe/Al/Ni/Cu/S/Cr) Ni-O-vacancy
F. Tavazza, T.P. Senftle, C. Zou, C.A. Becker and A.C.T. van Duin
*Molecular Dynamics Investigation of the Effects of Tip–Substrate Interactions during Nanoindentation*

• Combination of the C.ff (condensed carbon) forcefield with Ni/C/O/H parameters
• The non-carbon parameters are the same as in CHOFeAlNiCuSCr_v2.ff

**C.ff**: (C) C-2013
S.G. Srinivasan, A.C.T. van Duin and P. Ganesh
*Development of a ReaxFF Potential for Carbon Condensed Phases and Its Application to the Thermal Fragmentation of a Large Fullerene*

• Forcefield designed for modeling Carbon condensed phases

**CHONSSiGe.ff**: (C/H/O/N/S/Si/Ge)
G. Psogogiannakis and A.C.T. van Duin
*Development of a ReaxFF reactive force field for Si/Ge/H systems and application to atomic hydrogen bombardment of Si, Ge, and SiGe (100) surfaces*
Surface Science 2016, Vol. 646, pp 253–260 (http://dx.doi.org/10.1016/j.susc.2015.08.019)

• Forcefield designed for bombardment of Si, Ge and SiGe surfaces with atomic hydrogen

**CHONSSPtClNi.ff**: (C/H/O/N/S/Pt/Cl/Ni) Water-Pt-Ni-Nafion
D. Fantauzzi, J.E. Mueller, L. Sabo, A.C.T. van Duin and T. Jacob
*Surface Buckling and Subsurface Oxygen: Atomistic Insights into the Surface Oxidation of Pt(111)*

• Extension of the OPt.ff forcefield parameters

**CHONSSPtZrNiCuCoHeNeArKrXe.ff**: (C/H/O/N/S/Pt/Zr/Ni/Cu/Co/He/Ne/Ar/Kr/Xe) A.M. Kamat, A.C.T. van Duin and A. Yakovlev
*Molecular Dynamics Simulations of Laser-Induced Incandescence of Soot Using an Extended ReaxFF Reactive Force Field*
- forcefield designed for the study of Laser-induced incandescence of soot


- forcefield designed for studying the combustion of the high-energy material a-HMX
INCLUDED FORCEFIELDS (DEVELOPMENT)

This is a list of forcefields included in the development distribution! See also Included Forcefields (adf2016) (page 17).

Description of ReaxFF force fields

Disclaimer: Using these forcefields for systems they have not been explicitly trained against may produce unrealistic results. Please see the full manuscripts for more detailed information.

The force field files used by the SCM version of ReaxFF are compatible with those used by the original ReaxFF code. So if you have the force field information from somewhere else you can just use it (save it in a text file, and select it in AD FINput via the Other... option).

**AB.ff:** (H/O/N/B) Ammonia Borane


- QM data were generated describing the single and (if relevant) double and triple bond dissociation for all B/N/O/H combinations. These data were used to derive initial ReaxFF bond parameters, and all calculations were performed using DFT with the B3LYP functional and the Pople 6-311G** basis set.
- The training set was then extended with QM data describing angular distortions in a set of small AB-related (AB H3N-BH3) molecules. These data were used to derive the initial ReaxFF angular parameters.
- The training set was extended with reaction barriers for key reaction steps such as H2 release from AB, dimerization of H2B-NH2 and reaction energies associated with H2 release from AB and with AB oxidation.

**AuCSOH.ff:** (Au/C/S/O/H)


- The original Au-Au parameters were extended by three publications:
- The forcefield does not include Au/N parameters

• To obtain the H/C/O compound data required to extend the hydrocarbon-training set, DFT calculations were performed on the following systems: (a) dissociation energies for various bonds containing carbon, oxygen, and hydrogen. The ground state structure was obtained through full geometry optimization. Dissociation curves were calculated by constraining only the bond length of interest and re-optimization of the remaining internal coordinates. Optimization was also performed for the various angles and torsions associated with C/H/O interactions.


• The parameters in this forcefield were extended/improved by two other publications:
  • A.M. Kamat, A.C.T. van Duin, and A. Yakovlev Molecular Dynamics Simulations of Laser-Induced Incandescence of Soot Using an Extended ReaxFF Reactive Force Field. Journal of Physical Chemistry A (2010), 114, 12561-1257 http://dx.doi.org/10.1021/jp1080302

• The C/H/O parameters are the same as in the CHO forcefield, with added S/C, S/H and S/O descriptions. This force field was used in Castro et al, Combustion and Flame 2011

• The Boron and Nitrogen parameters are based on (but not identical to) the parameters used in Weismiller et al, JPC-A 2010.


• This forcefield is an extension of: A.C.T. van Duin, V.S. Bryantsev, M.S. Diallo, W.A. Goddard, O. Rahaman, D.J. Doren, D. Raymand, and K. Hermansson Development and validation of a ReaxFF reactive force field for Cu cation/water interactions and copper metal/metal oxide/metal hydroxide condensed phases Journal of Physical Chemistry A 2010, 114, 9507-9514 http://dx.doi.org/10.1021/jp102272z


• The initial force field parameters for the Fe-Fe parameters were taken from an earlier force field development project on bulk-iron metal, based on DFT-calculations on antiferromagnetic BCC and FCC. The ReaxFF parameters have not been published yet, however the DFT data can be found in ref 31 of the above mentioned manuscript. The O/H parameters were taken from the ReaxFF bulk water description. The Fe/Fe and O/H parameters were kept fixed to these initial values, whereas the Fe/O parameters were reoptimized against the quantum mechanical results presented in the above mentioned manuscript.

• Detailed information on the force field parameters is given in the supporting information of the above mentioned manuscript.

• Part of this forcefield is also published in: L.Z. Zhang, S.V. Zybin, A.C.T. van Duin, S. Dasgupta, W.A. Goddard, and E.M. Kober Carbon Cluster Formation during Thermal Decomposition of Octahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine and 1,3,5-Triamino-2,4,6-trinitrobenzene High Explosives from ReaxFF Reactive Molecular Dynamics Simulations Journal of Physical Chemistry A (2009) 113, 10619-10640 http://dx.doi.org/10.1021/jp901353a

• The parameters of the nitramine ReaxFF are based on a large number of ab initio QM calculations. Over 40 reactions and over 1600 equilibrated molecules have been used; they are designed to characterize the atomic interactions under various environments likely and unlikely high energy each atom can encounter. The training set contains bond breaking and compression curves for all possible bonds, angle and torsion bending data for all possible cases, as well as crystal data.

• Please see the supplemental material from Phys. Rev. Lett. 2003, 91, 098301 for a detailed description of the parameterization of this force field.


• This forcefield originally had a typo, defining the H-Na-Na angle twice. The same typo is in table 4 of the publication, but the text clearly mentions that the second line should define Na-H-Na instead.


• This force field was trained to model the interaction of water at the SiO2 surface, with specific emphasis on proton-transfer reactions. Updated parameters were fitted for all Si/O/H bond, angle, and torsion interactions as well, in addition to the dissociation of a water molecule from a single Si(OH)4 molecule and reaction energies for the polymerization of Si(OH)4


• The included forcefield is based on the Newsome reference, with slightly improved parameters by van Duin et al.


• The ReaxFF force field parameters have been fit to a large quantum mechanics (QM) training set containing over 700 structures and energetics related to bond dissociations, angle and dihedral distortions, and reactions between hydrocarbons and vanadium oxide clusters. In addition, the training set contains charge distributions for small vanadium oxide clusters and the stabilities of condensed-phase systems including V2O5, VO2, and V2O3 in addition to metallic V (V0).

ZnOH.ff: (Zn/O/H) D.Raymand, A.C.T. van Duin, M. Baudin, K. Hermansson A reactive force field (ReaxFF) for zinc oxide Surface Science 2008, 602, 1020-1031 (http://dx.doi.org/10.1016/j.susc.2007.12.023)


• Based on QM calculations for Zn(s), ZnO(s), and Zn hydroxide clusters [Zn(OH)2 and O(ZnOH)2],
ReaxFF parameters were generated for Zn-O and Zn-Zn bond energies and for Zn-O-Zn, O-Zn-O, O-Zn-Zn and Zn-O-H valence angle energies.

- QM calculations were performed for the four crystal polymorphs of the wurtzite, zincblende, rocksalt and caesium chloride structures (the structures are also referred to as h-ZnS, c-ZnS, NaCl and CsCl, respectively).


**CaSiAlO.ff**: (C/H/O/Fe/Cl/Si/Al/Ca)  M.C. Pitman and A.C.T. van Duin *Dynamics of Confined Reactive Water in Smectite Clay–Zeolite Composites* J. Am. Chem. Soc., 2012, 134 (6), 3042–3053 (http://dx.doi.org/10.1021/ja208894m)


  - This forcefield adds London dispersion correction terms to reaxFF, and is optimized for the energetic materials RDX, PETN, TATB, and NM plus graphite, polyethylene, solid carbon dioxide, and solid N2, using the low temperature crystal structures to determine the lg correction parameters.

**CHOFeAlNiCuS.ff**: (C/H/O/Fe/Al/Ni/Cu/S)  O. Rahaman, A.C.T. van Duin, W.A. Goddard III, and D.J. Doren *Development of a ReaxFF reactive force field for glycine and application to solvent effect and tautomerization* Journal of Physical Chemistry B 115 (2011), 249-261. (http://dx.doi.org/10.1021/jp204894m)


  - Not all cross-terms between the two forcefield files are defined, which might cause problems if the system has (for example) C-Cu interactions.


**AuSCH_2013.ff**: (Au/S/C/H)  Gyun-Tack Bae and Christine M. Aikens *Improved ReaxFF Force Field Parameters for Au–S–C–H Systems* Journal of Physical Chemistry A 2013 117 (40), 10438-10446 (http://dx.doi.org/10.1021/jp405992m)


  - yields improvements for bond bending potential energy surfaces

  - aims to agree with DFT geometries of small clusters and gold–thiolate nanoparticles


  - Specialized forcefield, designed to “investigate the failure of the poly(dimethylsiloxane) polymer (PDMS) at high temperatures and pressures and in the presence of various additives”

**TiOCHNCl.ff**: (C/H/O/N/S/Mg/P/Na/Ti/Cl/F)  S.Y. Kim, A.C.T. van Duin, and J.D. Kubicki *Molecular dynamics simulations of the interactions between TiO2 nanoparticles and water with Na+ and Cl-, methanol, and formic acid using a reactive force field* Journal of Materials Research / Volume 28 / Issue 03 / 2013, pp 513-520 (http://dx.doi.org/10.1557/jmr.2012.367)
• used for simulating TiO2 (both rutile and anatase) nanoparticles with water, methanol, and formic acid
• The force field was validated by comparing water dissociative adsorption percentage and bond length between Na-O with density functional theory (DFT) and experimental results


• Aimed at oxygen interactions with realistic silica surfaces


• only the parameters for Fe (and crossterms) differ from the CHOAlSi.ff forcefield


• only the parameters for Fe (and crossterms) differ from the CHOFef.ff forcefield

CHOFe.ff: (C/H/O/Fe/Cl/Si/Al) F.Castro-Marcanoa, A.C.T. van Duin *Comparison of thermal and catalytic cracking of 1-heptene from ReaxFF reactive molecular dynamics simulations Combustion and Flame*, Volume 160, Issue 4, April 2013, Pages 766–775 (http://dx.doi.org/10.1016/j.combustflame.2012.12.007)

• only the parameters for Fe (and crossterms) differ from the CHOFef.ff forcefield

CHOFe.ff: (C/H/O/Fe/Cl/Si/Al) F.Castro-Marcanoa, A.C.T. van Duin *Comparison of thermal and catalytic cracking of 1-heptene from ReaxFF reactive molecular dynamics simulations Combustion and Flame*, Volume 160, Issue 4, April 2013, Pages 766–775 (http://dx.doi.org/10.1016/j.combustflame.2012.12.007)

• only the parameters for Fe (and crossterms) differ from the CHOFef.ff forcefield

CHOFe.ff: (C/H/O/Fe/Cl/Si/Al) F.Castro-Marcanoa, A.C.T. van Duin *Comparison of thermal and catalytic cracking of 1-heptene from ReaxFF reactive molecular dynamics simulations Combustion and Flame*, Volume 160, Issue 4, April 2013, Pages 766–775 (http://dx.doi.org/10.1016/j.combustflame.2012.12.007)

• only the parameters for Fe (and crossterms) differ from the CHOFef.ff forcefield

CHOLi.ff: (C/H/O/N/S/Mg/P/Na/Li) D.Bedrov, G.D. Smith, A.C.T. van Duin *Reactions of Singly-Reduced Ethylene Carbonate in Lithium Battery Electrolytes: A Molecular Dynamics Simulation Study Using the ReaxFF Journal of Physical Chemistry A*, 2012, 116 (11), pp 2978–2985 (http://dx.doi.org/10.1021/jp210345b)

• specifically generated for simulating Lithium battery electrolytes

• must be used in combination with the MOLCHARGE keyword to set a charge restraint on Li and CO3!

SiOAIff.ff: (H/O/Si/Al/Li) B.Narayanan, A.C.T. van Duin, B.B. Kappes, I.E. Reimanis and C.V. Ciobanu *A reactive force field for lithium–aluminum silicates with applications to eucryptite phases* Modelling and Simulation in Materials Science and Engineering 2012 20 015002 (http://dx.doi.org/10.1088/0965-0393/20/1/015002)

• used for studying Oxidation states of Pd nanoparticles, surfaces and bulk configurations with a GCMC method


• used in combination with a GCMC method


• forcefield was generated using a recently developed Monte Carlo algorithm with simulated annealing.

CHONSMgPNaCuCl.ff: (C/H/O/N/S/Mg/P/Na/Cu/Cl) Susanna Monti, Cui Li, and Vincenzo Carravetta *Reactive Dynamics Simulation of Monolayer and Multilayer Adsorption of Glycine on Cu(110)* J. Phys. Chem. C, 2013, 117 (10), pp 5221–5228 (http://dx.doi.org/10.1021/jp312828d)

• Reactive MD-force field for amino acids on copper

CHOSMoNiLiBFPN.ff: (C/H/O/S/Mo/Ni/Li/B/F/P/N) Md M. Islam, V.S. Bryantsev, A.C.T. van Duin *ReaxFF Reactive Force Field Simulations on the Influence of Teflon on Electrolyte Decomposition during Li/SWCNT Anode Discharge in Lithium-Sulfur Batteries* J. Electrochem. Soc. 2014 volume 161, issue 8, E3009-E3014 (http://dx.doi.org/10.1149/2.005408jes)

• forcefield for Electrochemistry in Li-S batteries

TiClOH.ff: (C/H/O/N/S/Mg/P/Na/Ti/Cl/F) Sung-Yup Kim and A.C.T. van Duin *Simulation of Titanium Metal/Titanium Dioxide Etching with Chlorine and Hydrogen Chloride Gases Using the ReaxFF Reactive Force Field* J. Phys. Chem. A, 2013, 117 (27), pp 5655–5663 (http://dx.doi.org/10.1021/jp3031943)

• adaptation/evolution of the TiOCHNCl.ff forcefield by Kim, S.-Y. et al.


• Force field was developed by combining the YSZ and Ni/C/H descriptions
• From the summary: “The products obtained in our simulations are the same as those in experiment, which indicates that the developed ReaxFF potential properly describes complex physicochemical processes, such as the oxide-ion diffusion, fuel conversion, water formation reaction, coking, and delamination, occurring at the TPB and can be recommended for further computational studies of the fuel/electrode/electrolyte interfaces in a SOFC.”

• The Aa atom type is a rename of the Zr atom type, which was defined twice.


- The forcefield file mentions “Gly with dummy N-P parameters”
- It was developed for studying Carbon dioxide interactions with the ionic liquid tetrabutylphosphonium glycinate, both physical and chemical absorption.

**CHOLi_2.ff: (C/H/O/Li)** M.Raju, P. Ganesh, P.R.C. Kent, and A.C.T. van Duin *Reactive Force Field Study of Li/C Systems for Electrical Energy Storage* J. Chem. Theory Comput., not yet printed, publication date (web) April 2nd, 2015 (http://dx.doi.org/10.1021/ct501027v)

- Used for studying Li/C systems with GCMC and MD
- Also contains parameters for “Vi” and “Gl”, but these virtual elements are not mentioned in the paper

**CHONSSiCaKSrNaMgAlCu.ff: (C/H/O/N/Si/Ca/K/Sr/Na/Mg/Al/Cu)** G.M. Pssofogiannakis, J.F. McCleerey, E. Jaramillo and A.C.T. van Duin *ReaxFF Reactive Molecular Dynamics Simulation of the Hydration of Cu-SSZ-13 Zeolite and the Formation of Cu Dimers* J. Phys. Chem. C, 2015, 119 (12), pp 6678–6686 (http://dx.doi.org/10.1021/jp500699)

- This Cu/Si/Al/O/H forcefield was developed for and used in MD simulations of the hydration of Cu-exchanged SSZ-13 catalyst.
- The force field was developed by merging and expanding previously tested and published ReaxFF force fields for Si/Al/O/H systems and Cu/O/H systems (citations 19-26 of the publication)
- This forcefield is an extension of K.L. Joshi et al 2014, http://dx.doi.org/10.1039/C4CP02612H, all non-Cu parameters are the same.


- This forcefield is optimized with a metropolis Monte-Carlo algorithm with simulated annealing to search for the optimum parameters for the ReaxFF force field in a high- dimensional parameter space.
- The optimization is done against a set of quantum chemical data for MgSO4 hydrates.

**CHONSMgPNaCuCl_v2.ff: (C/H/O/N/S/Mg/P/Na/Cu/Cl)** S.Monti, A. Corozzi, P. Fristrup, K.L. Joshi, Yun Kyung Shin, P. Oelschlaegler, A.C.T. van Duin and V. Baronee *Exploring the conformational and reactive dynamics of biomolecules in solution using an extended version of the glycine reactive force field* Phys. Chem. Chem. Phys., 2013,15, 15062-15077 (http://dx.doi.org/10.1039/C3CP51931G)

- This forcefield is an extension of CHONSMgPNaCuCl.ff by S. Monti et al., J. Phys. Chem. C, 2013, 117 (10), pp 5221–5228, http://dx.doi.org/10.1021/jp312828d
- Developed for peptide and protein simulations


- Pt-Pt parameters for bulk platinum phases, low & high-index platinum surfaces and nanoclusters.
• O-Pt parameters for bulk platinum oxides, as well as oxygen adsorption and oxide formation on Pt(111) terraces and the {111} and {100} steps connecting them.

CHONSMgPNaTiClF.ff: (C/H/O/N/S/Mg/P/Na/Ti/Cl/F) Stijn Huygh, Annemie Bogaerts, Adri C.T. van Duin and Erik C. Neyts Development of a ReaxFF reactive force field for intrinsic point defects in titanium dioxide Computational Materials Science, Volume 95, December 2014, Pages 579-591, ISSN 0927-0256 (http://dx.doi.org/10.1016/j.commatsci.2014.07.056)

• Forcefield developed for studying the influence of intrinsic point defects on the chemistry with TiO2 condensed phases.

• Forcefield seems to be based on TiOCHNCl.ff, http://dx.doi.org/10.1016/j.commatsci.2014.07.056


• Forcefield developed for Fe/Cr/O/S


• Forcefield optimized for Fe/Cr/O/S

• The non-carbon parameters are the same as in CHOFeAlNiCuSCr_v3.ff


• Combination of the C.ff (condensed carbon) forcefield with Ni/C/O/H parameters

• The non-carbon parameters are the same as in CHOFeAlNiCuSCr_v2.ff


• Forcefield designed for modeling Carbon condensed phases

CHONSSiGe.ff: (C/H/O/N/S/Si/Ge) G.Psofogiannakis and A.C.T. van Duin Development of a ReaxFF reactive force field for Si/Ge/H systems and application to atomic hydrogen bombardment of Si, Ge, and SiGe (100) surfaces Surface Science 2016, Vol. 646, pp 253–260 (http://dx.doi.org/10.1016/j.susc.2015.08.019)

• Forcefield designed for bombardment of Si, Ge and SiGe surfaces with atomic hydrogen


• extension of the OPt.ff forcefield parameters

CHONSSPtZrNiCuCHeNeArKrXe.ff: (C/H/O/N/S/Pt/Zr/Ni/Cu/Co/He/Ne/Ar/Kr/Xe) A.M. Kamat, A.C.T. van Duin and A. Yakovlev Molecular Dynamics Simulations of Laser-Induced Incandescence of Soot Using an Extended ReaxFF Reactive Force Field J. Phys. Chem. A, 2010, 114 (48), pp 12561–12572 (http://dx.doi.org/10.1021/jp1080302)
• forcefield designed for the study of Laser-induced incandescence of soot


• forcefield designed for studying the combustion of the high-energy material a-HMX
When you publish results in the scientific literature that were obtained with programs of the ADF package, you are required to include references to the program package with the appropriate release number, and a few key publications. In addition to these general references, references to special features are mandatory, in case you have used them.

### 7.1 General References

The ReaxFF software that SCM makes available is based on the ReaxFF program developed by Adri van Duin. For calculations with ReaxFF:


The ReaxFF GUI (ReaxFFinput and ADFmovie) has been developed within SCM (with O. Visser as primary developer).

The ReaxFF program has been parallelized, optimized, and extended by SCM (with A.L. Yakovlev as primary developer).

If you use one of the included force fields you must also add the proper reference for it (page 17).

Many examples of ReaxFF applications can be found on Prof. van Duin’s publication list (http://www.engr.psu.edu/adri/Publications.aspx).

### 7.2 Features References

When you have used force fields or special features, you should include the reference(s) to the implementation.


**ReaxFF Force Field References** When you publish results in the scientific literature that were obtained with one of the included force fields for ReaxFF, including the proper reference for the force field used is mandatory.

- Forcefields included in the development snapshots (http://www.scm.com/ReaxFF/forcefields-trunk.html)


### 7.3 External programs and Libraries

Click here for the list of programs and/or libraries used in the ADF package. On some platforms optimized libraries have been used and/or vendor specific MPI implementations.