MedeA VOTCA: Generating Coarse-Grained Potentials from Atomistic Simulations

Contents

1 Introduction

Coarse-grained potential can be generated with *MedeA* using the interface to the Versatile Object-oriented Toolkit for Coarse-graining Applications (VOTCA) [1] available as a flowchart stage. *VOTCA* usesi trajectories from atomistic molecular dynamics simulations to derive potentials for coarse-grained simulations. A number of methods are implemented in *VOTCA*:

- Iterative Boltzmann inversion
- Force matching

and can be accessed through the *VOTCA* flowchart stage.

The theory behind these methods is discussed in detail in the section on the Theory of Coarse-Graining.

2 Working with the *VOTCA* interface

The generation and optimization of coarse-grained potentials typically proceeds in three steps. First, an atomistic trajectory is generated by a molecular dynamics simulation of the system of interest using a classical forcefield or MLP. Second, a coarse-grained potential is derived by VOTCA. Finally, the coarse-grained potential is validated by predicting selected properties for the system of interest and comparison with the results of the atomistic simulation.

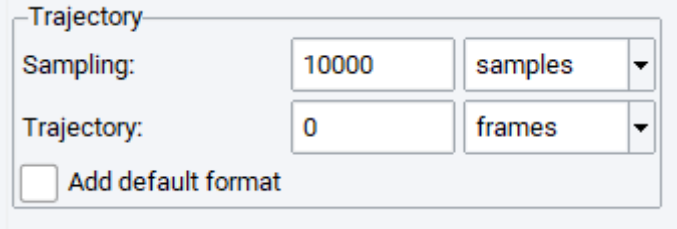
3 Creation of Training Data

Training data for a coarse-grained potential can be any atomistic trajectory from a molecular dynamics simulation using classical forcefields supported by *MedeA* and *LAMMPS*. VOTCA can handle trajectories created by LAMMPS, therefore a LAMMPS simulation needs to be run before a coarse-grained potential can be obtained.

The atomistic simulation should be of appropriate length. Tens of nanoseconds are typically being used in the literature. These simulations are usually performed in the NPT ensemble to make it possible to use the coarse-grained potential to study changes to the cell.

[1] V. Rühle, C. Junghans, A. Lukyanov, K. Kremer and D. Andrienko, *Versatile Object-Oriented Toolkit for Coarse-Graining Applications*, J. Chem. Theory Comput. **5(12)**, 3211-3223 (2009) (DOI)

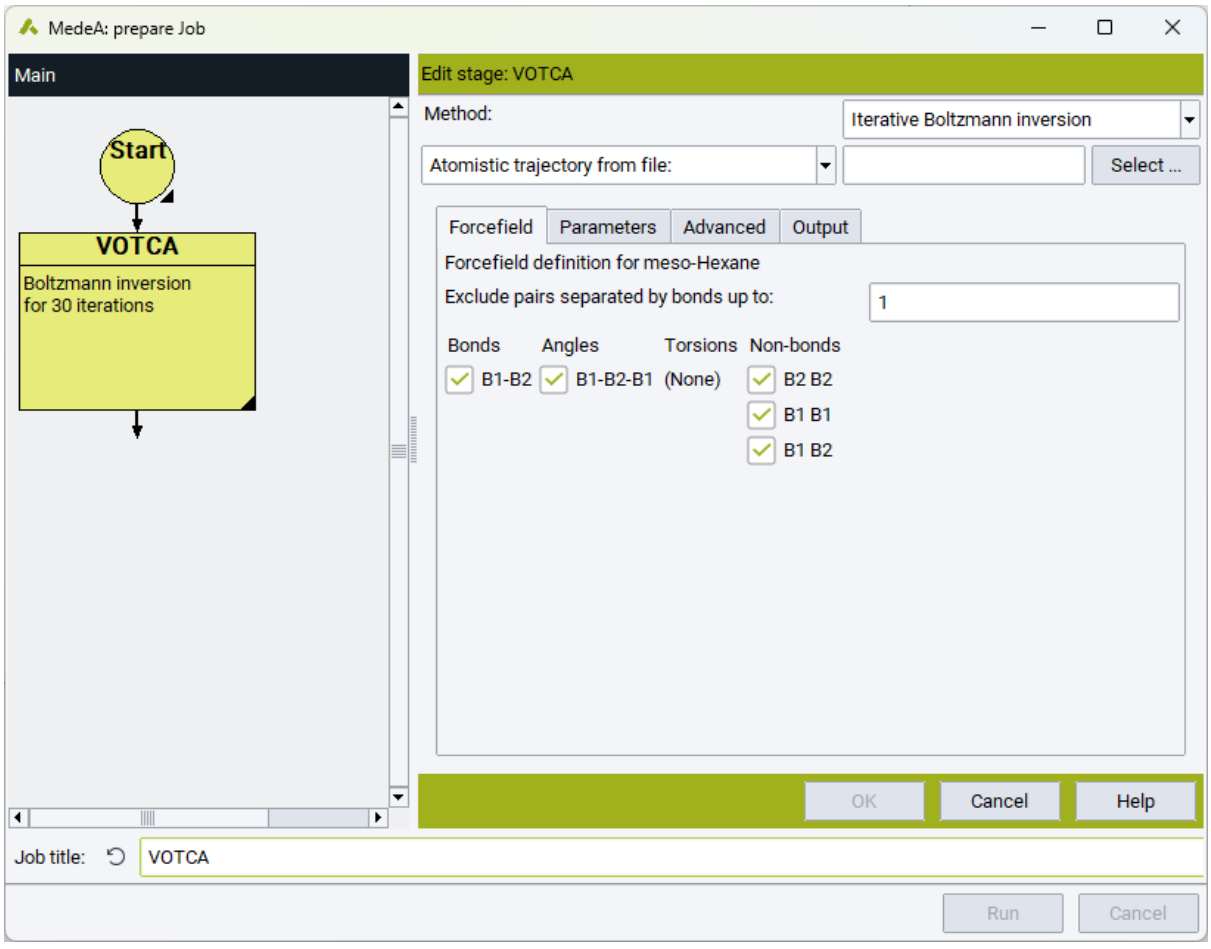
The trajectory has to be written in the default LAMMPS format by checking the Add default format checkbox for the corresponding *LAMMPS* stage.



4 Setting up and Generating a Coarse-Grained Potential

The *VOTCA* stage is accessed within the *MedeA* flowchart paradigm. This can be done by opening the flowchart interface with Jobs >> New Job... and adding a **VOTCA** stage to the empty flowchart.

Configure *VOTCA* by double-clicking on the **VOTCA** stage. A variety of options are offered.



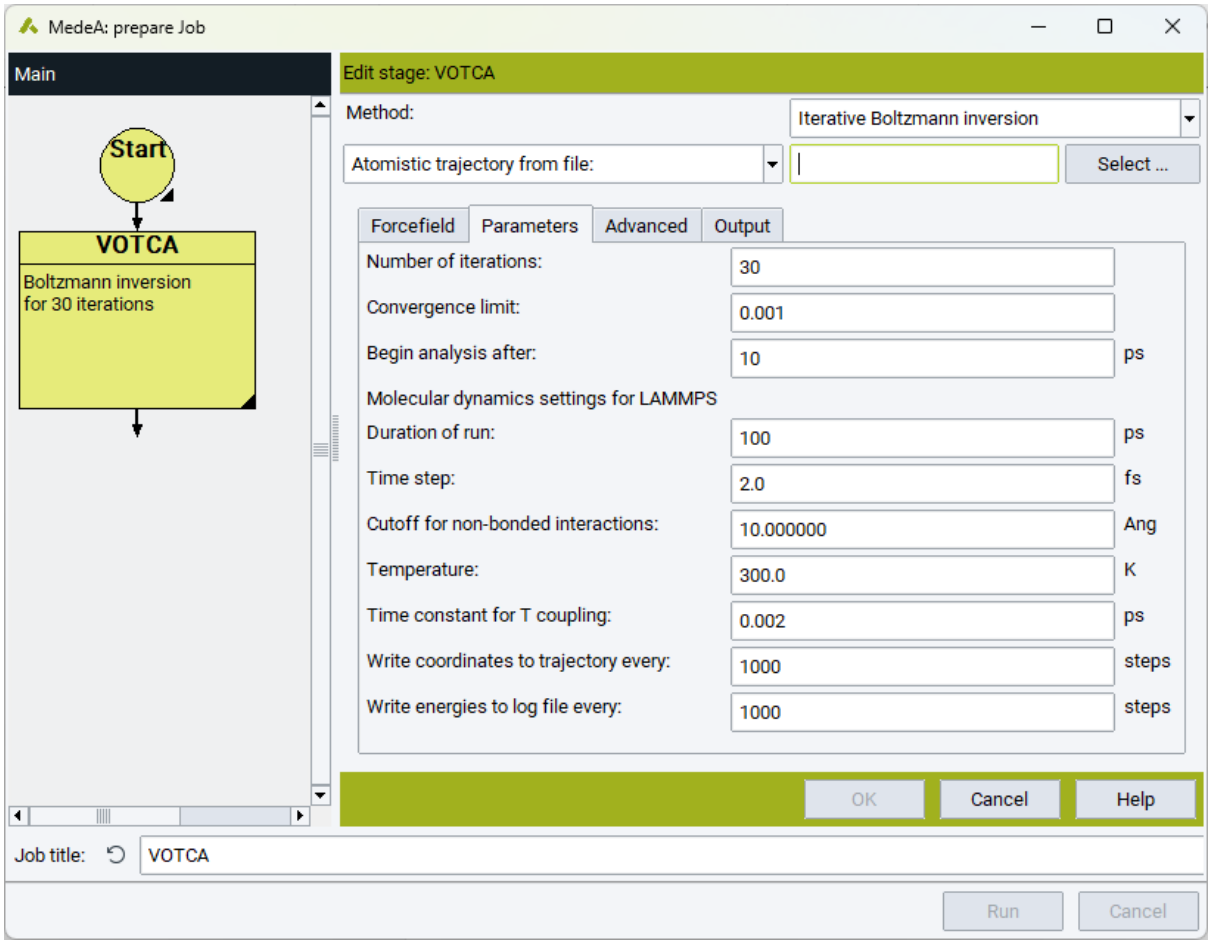
The first step consists of selecting the method for coarse-graining. The combobox Method offers *Iterative Boltzmann inversion* and *Force matching*. In the next row the atomistic trajectory can be specified. By default, *Atomistic trajectory from file* is selected which allows to use a trajectory from any file in the file system. Trajectory files can be rather large. To avoid copying large files over a network connection it is also possible to use a trajectory which is already stored on the job server where the VOTCA job should be submitted to. In this case the combobox should be set to *Atomistic trajectory of job from job server*. Use the Select button to open a job selection dialog and select either the trajectory file or the job which contains the trajectory (if multiple trajectories exist for a job, the one from the stage with the highest number is used).

At the bottom of the stage editor a number of tabs can be found. The Forcefield tab offers a selection of various terms of the coarse-grained potential to be created. The data corresponds to the active system in *MedeA*. If there is no active mesoscale system the message No mesoscale system found will be displayed.

At the top of the tab the text entry box Exclude pairs separated by bonds up to makes it possible to exclude non-bond interactions between beads up to a certain distance. E. g., it is quite common to exclude non-bond interactions between beads which share a common bond or are bonded to the same bead. Using the value *n* will exclude all interactions up to and including 1-n. The remainder of the tab contains checkboxes to select the individual interactions of the active mesoscale system.

On the Parameters tab various settings can be configured depending on the method chosen at the top of the editor.

4.1 Iterative Boltzmann inversion



The iterative Boltzmann inversion is controlled by the following parameters:

Number of iterations : Can be used to control the maximum number of iterations for the *Iterative Boltzmann inversion*. The calculation stops when either the number of iterations or the convergence limit is reached.

Convergence limit : Specifies the convergence limit. The calculation stops when either this limit or the number of iterations is reached.

Begin analysis after : Specify the time after which the analysis of the trajectory will start. The trajectory up to this point in time point is considered not to be equilibrated.

Duration of run : The duration of the coarse-grained LAMMPS simulation performed in each iteration.

Time step : The time step for the coarse-grained LAMMPS simulations.

Cutoff for non-bonded interactions : The cutoff for the non-bonded interactions in the coarse-grained LAMMPS simulations. The value given here will be automatically adjusted if it is larger than half the size of the simulation box. It is also used as upper bound of the interval for the potential table in which calculations are performed for both bonded and non-bonded potentials.

Temperature : The temperature at which to perform the coarse-grained LAMMPS simulations.

Time constant for T coupling : The time constant for the temperature coupling in the coarse-grained LAMMPS simulations.

Write coordinates to trajectory every : Specify the frequency for writing coordinates to the trajectory of the coarse-grained LAMMPS simulations.

Write energies to log file every : Specify the frequency of writing energies to the log file of the coarse-grained LAMMPS simulations.

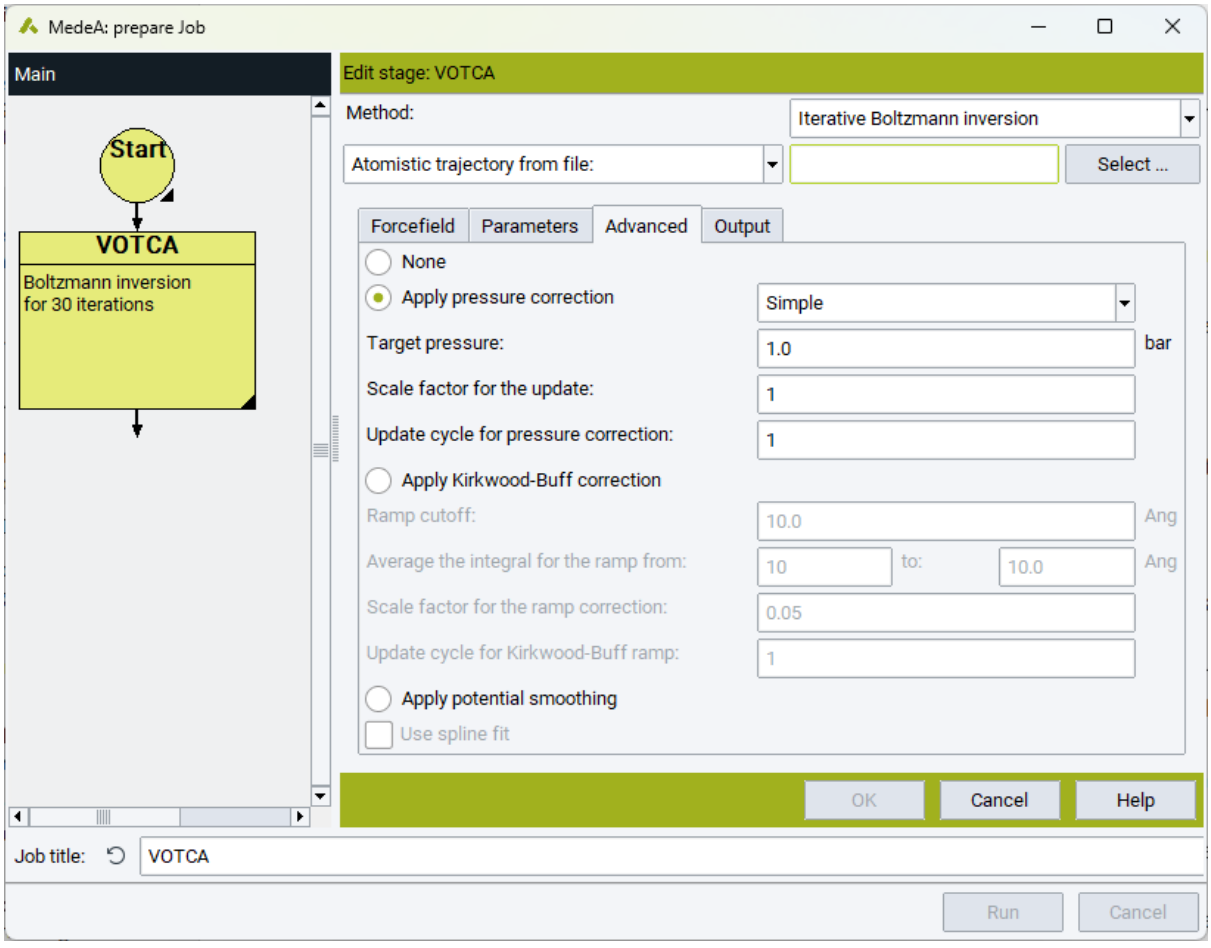
4.2 Force matching

Upper bound for non-bonded interactions : The upper bound of the interval for the potential table in which calculations are performed for both bonded and non-bonded potentials.

Number of frames for block averaging : The number of frames being used for block averaging. The atomistic trajectory is divided into blocks and the force matching equations are solved separately for each block. The coarse-grained forcefield is averaged over those blocks.

Accuracy for evaluating the difference in bead positions : Specify the accuracy for evaluating the difference in bead positions.

The Advanced tab is only active when *Iterative Boltzmann inversion* has been selected as method.



On this tab various corrections can be applied to the iterative Boltzmann inversion. By default, no corrections are applied. Use one of the radio buttons to enable a correction.

Apply pressure correction : Check to apply a pressure correction in order to match the pressure of the atomistic system. The pressure of the coarse-grained system usually does not match the pressure of the full atomistic system, since the iterative Boltzmann inversion only targets structural properties but not thermodynamic properties. Choose the type of pressure correction in the combobox, either *Simple* [3] or *Advanced* [5].

Target pressure : Specify the target pressure.

Scale factor for the update : Specify the scale factor for the update.

Update cycle for pressure correction : Specify update cycle for pressure correction (1 do, 0 do not). To do correction every third step specify “0 0 1”.

Apply Kirkwood-Buff correction : Check to apply the Kirkwood-Buff correction. The Kirkwood-Buff integrals are calculated from the radial distribution functions. In order to reproduce the exact Kirkwood-Buff integrals, a correction term is added to the coarse-grained potential [7].

Ramp cutoff : Specify the cutoff for the ramp.

Average the integral for the ramp : Specify start and end point for averaging the Kirkwood-Buff integral for the ramp.

Scale factor for the ramp correction : Specify the scaling factor for the ramp correction.

Update cycle for Kirkwood-Buff ramp : Specify update cycle for Kirkwood-Buff ramp correction (1 do, 0 do not). To do correction every third step specify “0 0 1”.

Apply potential smoothing : Check to smooth the potential update. It is better to smooth the potential update instead of the radial distribution function or the potential itself. A simple triangular smoothing (DU(i) =0.25DU(i1) + 0.5DU(i) + 0.25DU(i+1)) is used.

Use spline fit : Check to use a spline fit instead of the triangular smoothing.

The Output tab can be used to control the output of the coarse-grained potential.

Bin for bond potentials : Specify the bin size for bond potentials.

Bin for angle potentials : Specify the bin size for angle and torsion potentials.

Bin for non-bonded potentials : Specify the bin size for non-bonded potentials.

4.3 Assessing the Fit Obtained by *VOTCA*

The *Job.out* file of *VOTCA* provides information about the quality of the fit. For the iterative Boltzmann inversion the convergences for the last iteration per potential term is shown. In addition to the statistical information contained in Job.out, graphical output is also provided by the files:

- **convergence.png** shows the convergence as a function of the iteration step
- **X-Y.png**, **X-Y-Z.png**, **W-X-Y-Z.png** and **X_Y.png** show the distribution functions of the corresponding bond, angle, torsion or non-bond interaction as calculated from the atomistic trajectory and as obtained from a calculation with the coarse-grained potential. They should match.
- **X-Y_pot.png**, **X-Y-Z_pot.png**, **W-X-Y-Z_pot.png** and **X_Y_pot.png** show the bond, angle, torsion and non-bond potentials, respectively, derived for the coarse-grained system.

[3] D. Reith, M. Pütz and F. Müller-Plathe, *Deriving effective mesoscale potentials from atomistic simulations*, J. Comp. Chem. **24(13)**, 1624–1636 (2003) (DOI)
[5] H. Wang, C. Junghans and K. Kremer, *Comparative atomistic and coarse-grained study of water: What do we lose by coarse-graining?*, Eur. Phys. J. E **28(2)**, 221–229 (2009) (DOI)
[7] P. Ganguly, D. Mukherji, C. Junghans and N. F. A. van der Vegt, *Kirkwood-Buff coarse-grained force fields for aqueous solutions*, J. Chem. Theor. Comp. **8(5)**, 1802-1807 (2012) (DOI)

4.4 Using the Potential Created by *VOTCA*

If *VOTCA* achieved satisfactory agreement with the atomistic simulation the coarse-grained potential can be used in production calculations with *MedeA* LAMMPS. Each run of *VOTCA* creates an *frc* file with the parameters of the coarse-grained potential. This file can be found in the folder of the corresponding flowchart stage. Its exact name is given in the Job.out file. Save this file on your machine in *MD/data/Forcefields/custom* and read it in with Forcefields >> Read ... . When running calculations on an external JobServer this forcefield file is automatically transferred with all other data of the job.

Note: In any publication of results generated with *MedeA VOTCA* Ref. [1] should be cited.