

# Calculating Free Energy Differences from Molecular Simulation

## Hands-on notes for the exercises

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Version: January 23, 2023

## 1 Overview

In the computational exercises the dimerization of two united-atom methane molecules will be investigated using different types of equilibrium free energy calculations. The situation is depicted in the thermodynamic cycle in Figure 1. The simulations can be divided into those regarding the two methanes in an empty computational box ("vacuum simulations") and simulations conducted in a box of SPC water ("water simulations"). Two basic types of free energy calculations will be used: (1) *Umbrella Sampling* (US) representing the family of physical-path-based methods and (2) *Incremental Alchemical Decoupling* representing the family of alchemical perturbation methods. This tutorial will guide you through the individual steps for obtaining a *potential of mean force* (PMF) along a characteristic order parameter (in this case the methane-methane distance) using US as well as the determination of a hydration free enthalpy from alchemical decoupling. In addition to all the required input files and scripts, also the simulation output relevant for the analysis will be provided. Since it is assumed that you are familiar with the basic GROMACS features the instructions are represented as short as possible in a cook book-like recipe. Care was taken of writing the simulation parameter files (`.mdp`) clear and well commented and to establish an easy to understand automatized workflow using simple (rather than aesthetic) scripts. The exercises were designed with the purpose to gather freely available useful tools for the simulation setup and analysis distributed over the community which should be easy to apply to your own real world problem.

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should be straightforward. All the required files (topology, initial configuration, simulation parameter files) are located in:

`~/Simulations/day_1_2/US_CH4Dimer.Vacuum/`

distributed over different subfolders labeled with prefixes from 0 to 4 representing the chronological order of the workflow. GROMACS specific commands for each step can be looked up in the respective `command` file within each subdirectory. Simulation parameter files (`.mdp`) are located under `mdp_files`.

### 3.1 Starting Configuration and Topology

`0_coord` contains the initial coordinates `start.gro` for the two methane molecules oriented along the z-axis. The folder `0_topo` contains the topology files (system topology `topol.top` and molecular topology `2CH4.itp`) and a subfolder containing position restraint files (`posre_all.itp`, `posre_us1D.itp`, `posre_us3D.itp`). The force field parameters (located in `gromos54a7.ff`) are taken from the GROMOS 54a7 force field parameter set [5]. For practical reasons the Lennard-Jones-Energy parameter  $\epsilon$  for the  $\text{CH}_4\text{-CH}_4$  interaction was increased by a factor of 20 compared to the original GROMOS 54a7 force field parameter set to make the methane model more "sticky". Since we overwrite a given force field parameter a warning is issued. Moreover, recent versions of GROMACS issue a warning when the GROMOS force field is used which is related to the fact that the GROMOS force fields was parametrized using a twin-range cutoff scheme, in which longer ranged nonbonded forces and energies are updated less frequently than shorter ranged ones. The effect of this choice on thermodynamic, structural, and dynamic properties has been discussed recently [6]. In the realm of this exercise the two warnings can be ignored which is achieved by the usage of `-maxwarn 2` for every call of the GROMACS pre-processor `grompp`. However, if you want to use the GROMOS force field within the GROMACS software in your own research project it is recommended to check whether the standard settings in GROMACS regarding treatment of non-bonded interactions affect any relevant properties.

### 3.2 Defining the Simulation Box

Go to the subdirectory `1_box`. A rectangular box with an uniform length of 3.2 nm can be defined using `editconf`:

```
$ gmx editconf -f ../0_coord/start.gro -o box.gro -box 3.2
```

### 3.3 Energy Minimization

For removing clashes between the solute molecules, an energy minimization is conducted first. Go to the subdirectory `2_min_vac` and do:

```
$ gmx grompp -f ../mdp_files/em.mdp -c ../1_box/box.gro  
-p ../0_topo/topol.top -o min.tpr -maxwarn 2  
$ gmx mdrun -deffnm min
```

Note that performing a simulation in GROMACS is always composed of a two-stage process: first the GROMACS pre-processor **grompp** is called. The generated binary portable tpr-file which contains everything needed for the simulation (topology, parameters, coordinates and velocities) is then used by **mdrun**. Be aware of the usage of the **maxwarn** flag during the call of **grompp** to ignore (i) the reported warning due to the conflict of the original CH4-atomtype, taken from the included GROMOS 54a7 parameter set (in **topol.top**) and the re-defined one from the include topology file (**2CH4.itp**), and (ii) the warning about the GROMOS force field in general.

### 3.4 NVT Equilibration

Go to the subdirectory **3\_eq\_nvt**. For assigning particle velocities according to the temperature of interest a short NVT equilibration is performed (even though one can not expect to get instantaneous or even averaged temperature values from the simulation which are close to the target value for only two particles). The stochastic dynamics integrator is used for thermostatisation with  $T_{ref} = 300$  K and  $\tau_T = 0.1$  ps (see simulation parameters file **eq\_nvt.mdp**). The equilibration can be performed by:

```
$ gmx grompp -f ../mdp_files/eq_nvt.mdp -c ../2_min/min.gro
-p ../0_topo/topol.top -o nvt_eq.tpr -n ../index.ndx
-maxwarn 2
$ gmx mdrun -deffnm nvt_eq -plumed ../plumed.dat
```

In the simulation parameters file (**nvt.mdp**), two non-standard energy groups (CH4\_1, CH4\_2) are referenced, corresponding to the two individual molecules in order to evaluate the interactions between them. These two groups have to be provided by the index file **index.ndx**. The PLUMED input file **plumed.dat** required for writing out collective variables such as the intermolecular distance is read in via the flag **-plumed**. Explanation about the PLUMED syntax is given in the next section.

### 3.5 US Setup

For doing the actual Umbrella Sampling (US) simulations go to the subdirectory **4\_US** which contains two bash scripts for setting up and starting the simulations (**prepare\_sim.sh**, **run\_sim.sh**). An additional script can be used for extending the simulation time of every window (**extend\_sim.sh**). First a short equilibration run is performed such that the system has time to adjust the actual value of the order parameter to the desired equilibrium value of this particular window (as specified by the applied bias potential). The output data as used for the analysis are sampled within a subsequent production phase. The relevant **mdp**-files (**us\_eq.mdp**, **us\_prod.mdp**) for the equilibration and production phase are located under **mdp\_files**. The whole US specification (definition of the order parameter, equilibrium value, type and force constant of the bias potential) is done via PLUMED in the form of a quite simple input file which will be automatically generated by **prepare\_sim.sh**:

```
$ bash prepare_sim.sh
```

It will generate a number of folders named **w.XY** each one containing a PLUMED input file **plumed.dat** where XY stands for the equilibrium value of the distance restraining bias potential. The number and the spacing of the umbrella windows can be controlled by the bash script:

```
window=$(LC_NUMERIC="C" awk 'BEGIN{ for (i=0.35; i < 1.20; i+=0.05) printf("%.2f\n", i); }'))
length=${#window[@]}
```

Using the script as it is will generate 17 equidistant windows with reference values for the order parameter ranging from 0.35 to 1.15 nm with an uniform spacing of 0.05 nm. The generated PLUMED files all have the same structure and only differ in the equilibrium value (**AT**) of the distance restraining potential:

```
#PLUMED INPUT FOR UMBRELLA SAMPLING
#Definition of Groups
CH41: GROUP ATOMS=1
CH42: GROUP ATOMS=2
#Definition of Collective Variables
Dist_CH41_CH42: DISTANCE ATOMS=CH41,CH42
Dist_CH41_CH42_comp: DISTANCE ATOMS=CH41,CH42 COMPONENTS
#Definition of Restraints
#Force Constant KAPPA, Equilibrium Value AT
disrest: RESTRAINT ARG=Dist_CH41_CH42 KAPPA=500.0 AT=0.35
#Write to File
PRINT ARG=Dist_CH41_CH42,Dist_CH41_CH42_comp.x,Dist_CH41_CH42_comp.y,Dist_CH41_CH42_comp.z,
disrest.bias STRIDE=250 FILE=COLVAR.0.35
ENDPLUMED
```

Note that PLUMED specific keywords like **GROUP**, **ATOMS**, **DISTANCE**, **COMPONENTS**, **RESTRAINT**, **PRINT** etc., called "actions", are written in capitals. In the third and fourth line, both methanes are called by their ID's and assigned to the variable names **CH41** and **CH42**. Next PLUMED calculates the radial distance between the defined groups together with the three Cartesian components of the separation vector. Each component can be addressed by the point operator like **Dist\_CH41\_CH42\_comp.z** for instance. The 10th line defines a harmonic restraint acting on the radial distance (order parameter!) with a force constant **KAPPA** of 500 kJ mol<sup>-1</sup> nm<sup>-2</sup> and an equilibrium value **AT** of 0.35 nm. The quantities of interest (radial distance, three Cartesian components, value of the bias potential) are written to a file named **COLVAR.0.35** every 250'th step with the **PRINT** command. For the analysis of the US runs only the time series of the order parameter together with the applied force constant and the equilibrium value for every umbrella window is needed. Note that one could also use the GROMACS built-in Pull Code for Umbrella Sampling. However PLUMED offers you more flexibility in the definition of order parameters and the PLUMED syntax is in our opinion more intuitive.

For starting the simulations just run the second bash script **start\_sim.sh**:

```
$ bash start_sim.sh
```

If you have a look at the script you will see that every window is simulated sequentially after the other. After a short equilibration run (**us\_eq.mdp**) during which the system has time to adjust the actual value of the order parameter to the desired equilibrium value of this particular window the real production

run (`us_prod.mdp`) is performed. The whole simulation with the given settings should take up to a couple of minutes on a dual core machine. Note that all of the windows can be simulated independently which means that if you have access to a computer cluster they can be run in parallel. Using a cluster should require only minor modifications of the job and running script for which templates can be found in the subfolder `scripts_cluster`.

One could also imagine performing a (quasi) one-dimensional setup in which the two methanes are pulled apart on a linear path (e.g. z-axis). This can be realized for instance by using harmonic position restraints in all three directions acting on the first methane making it immobile. On the second methane only two orthogonal position restraints (x,y) are applied. The position restraints can be activated in the mdp-file by the line:

```
define      = -DPOSRES_US1D
```

The respective force constants ( $2.5 \cdot 10^4 \text{ kJ mol}^{-1} \text{ nm}^{-2}$ ) are read from `0_topo/posres_files/posre_us1D.itp`. In GROMACS, the reference values for the position restraints are taken from the initial coordinate file (in our case `3_eq_nvt/nvt_eq.gro`). In this 1D-setup the Cartesian z-component of the vector pointing from the first to the second methane (`Dist_CH41_CH42_comp.z`) would be used as the order parameter rather than the radial distance itself.

### 3.6 Potential of Mean Force (PMF)

To obtain a PMF from the generated collective variable timeseries (`w_XY/`  
`COLVAR_XY`) we use three different estimators: MBAR, UI and WHAM. Even though these methods are related to each other they use different informations from the sampled data and error estimates. It is always good practice to check if the different estimators yield the same PMF. Theoretical background informations can be found in the lecture slides and the aforementioned key publications. The prepared scripts are located in `4_US/ana`.

The usage of the UI Python implementation (requires `umbrella_integration.py` !) requires some transformation of the COLVAR files to the specified format: time  $t_i$  — value of order parameter at  $t_i$  — reference value of current window — respective force constant. The subfolder UI contains the script `prepare_UI_python.py` which will do the job for you. Before using it, one should check that the path to the folder containing all the COLVAR files is set correctly. The values for the applied force constant (`forceconst_DR`) as well as the array containing the reference values for the distance restraining (`refpos`), which should match the values and the format of the respective subfolders `w_XY` for every umbrella window, are hard-coded. Calling

```
$ python prepare_UI.py
```

will produce the inputfiles `UI_XY.out` in the specified format required for `umbrella_integration.py`. Now the UI code can be executed via:

```
$ python ~/Programs/umbrella_integration-master/  
umbrella_integration.py -t 300 -i UI.*out -n 100 -o pmf_UI.dat  
-pp pmf_UI.eps -pd derivatives.eps -ph histos.eps
```

The flags `-t`, `-n` and `-m` define the simulated temperature, the number of bins and the borders for the binning respectively. All available options can be displayed by calling `umbrella_integration.py` with `-h`. A plot of the PMF along with error estimates (`pmf_UI.dat`, `pmf_UI.eps`) will be produced together with a histogram plot (`histos.eps`).

The procedure for using WHAM (GROMACS implementation `gmx wham`) is quite similar. First the COLVAR files are transformed to a specified format:

```
$ python prepare_gmx_wham.py
```

Make sure that the paths to the folders containing the COLVAR files are set correctly together with the hard-coded values for the applied force constant and array of reference positions for the biasing potential. This will generate the set of modified timeseries (`pullx_umbrella_XY.pdo`) as well as a list containing the corresponding file names (`pdo-files.dat`). Now we can call `gmx wham`:

```
$ gmx wham -ip pdo-files.dat -o pmf_WHAM.xvg -min 0.39  
-max 1.15
```

which will produce the PMF (`pmf_WHAM.xvg`) as well as the histograms (`histo.xvg`). Error estimates can be performed using the implemented bootstrapping techniques for example. More details on this can be found in the program description (`gmx wham -h`) or in the literature [7].

The script (`umbrella_sampling_MBAR.py`) which calls the Python implementation of the MBAR estimator (`alchemlyb` has to be installed via `pip install alchemlyb`) is located in the subfolder `MBAR`. It should be checked that the path to the COLVAR files is set correctly. Values for temperature, force constant, number of bins and the equilibrium values of the umbrella windows are hard-coded in the script. Calling it via:

```
$ python umbrella_sampling_MBAR.py
```

yields the resulting PMF (`pmf_mbar_histo.out`) along with error estimates as well as the PMF (`pmf_mbar_kde.out`) employing a kernel density approximation. The details on the use of MBAR to calculate free energy surfaces are discussed by Shirts and Ferguson [8].

Comparison between the PMF profiles calculated by the different approaches is shown in Figure 2. It can be seen that the three analysis methods yield the same PMF within error bars. Now calculate the PMF for two methane molecules solvated in water. The procedure is very similar but contains some additional steps. Note that before starting the US simulations you have to generate an index file.

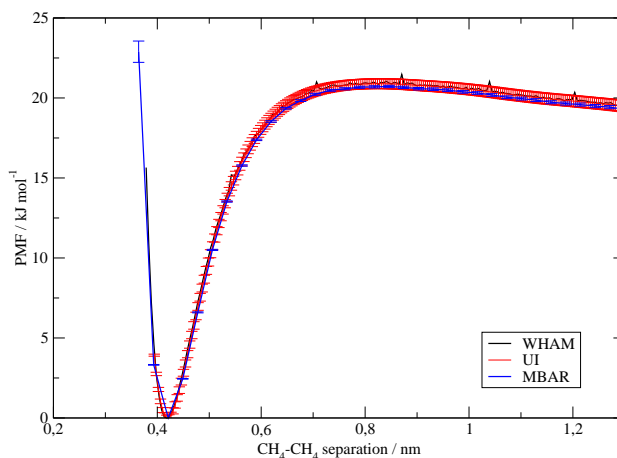


Figure 2: Comparison of calculated PMF's for two methanes in vacuum from different estimators (WHAM, UI, MBAR). Each window was simulated for 10 ns at 300 K.

## 4 Alchemical Decoupling

This section describes the workflow how to obtain the hydration free enthalpy for the example of a single methane molecule using incremental alchemical decoupling. All the required files are located in:

~/Simulations/day\_3/Solvation\_1CH4/

The other decoupling simulations, delivering the remaining free energy contributions of the thermodynamic cycle in Figure 1 (hydration free enthalpy for the dimerized methane complex, decoupling of one methane within the complex), are prepared in an identical way and the transfer should be straightforward.

### 4.1 Preparing the Simulation

The topology files and starting coordinates are located in the subfolders `0_topo` and `0_coord` respectively. Simulation parameter files (`.mdp`) together with the GROMACS specific command files for solvation, energy minimization, NVT- and NpT-equilibration (steps 2 to 5) are contained in the corresponding subfolders and should be self-explaining for MD-experienced users.

### 4.2 Performing Decoupling

We will perform the decoupling within 9  $\lambda$ -points by perturbing the solvated methane molecule (initial state A) into an ideal gas particle (end state B). The folder `6_Decoupling` contains a Perl script `write_sh.pl` for the automated generation of a set of job scripts (`job_0.sh`, ..., `job_8.sh`), each for every  $\lambda$ -point based upon the template `job.sh`:

```
$ perl write_sh.pl job.sh
```



Note that in principal you should only have to adapt the paths to the binaries (PLUMED, GROMACS) in `job.sh`:

```
#!/bin/bash
source $HOME/Programs/plumed-2.7.1/sourceme.sh
source $HOME/Programs/gromacs-2021.2_plumed-2.7.1_INSTALL/bin/GMXRC
```

If you have a look at the job script you will notice that after generating a new directory `Lambda_XY` for every  $\lambda$ -point it will perform again a short energy minimization, followed by two equilibrations (NVT, NpT) before the real production starts. The two additional post-processing scripts `run_BAR.sh` and `collect_dhdl.sh` are for the analysis of the results using the GROMACS implementation of the BAR method as well as various estimators implemented in the alchemlyb library. The folder `mdp_files` contains the simulation parameter files for each stage (EM, NVT, NPT, Production\_MD) for every of the 9  $\lambda$ -points. Since we are doing free energy calculations, the mdp-files contain an additional free energy calculation block which is important to have a look at. For example `mdp_files/Production_MD/md_3.mdp`:

```
; Free energy control stuff
free-energy                = yes
init_lambda_state          = 0
delta_lambda              = 0
calc_lambda_neighbors      = -1 ; Calculate Potential Energy Differences between ALL neighbors
; Vectors of lambda specified here
; init_lambda_state        0      1      2      3      4      5      6      7      8
vdw_lambdas                = 0.00 0.20 0.38 0.48 0.55 0.62 0.70 0.85 1.00
coul_lambdas               = 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
; Options for the decoupling
sc-alpha                   = 0.5
sc-coul                    = no ; linear interpolation of Coulomb
sc-power                   = 1
sc-sigma                   = 0.3
couple-moltype              = CH4 ; name of moleculetype to decouple
couple-lambda0              = vdw ; state A: only van der Waals interactions
couple-lambda1              = none ; state B: turn off everything
couple-intramol             = no
nstddhdl                   = 500
```

For detailed explanations of each option one should look at the GROMACS user manual or at the mdp-options of the online User Guide<sup>5</sup>. Just to comment a few: the lambdas (Van-Der-Waals (VDW)-interactions, electrostatics, restraints, ...) have to be written as an array starting from 0.0 and ending at 1.0 with arbitrary spacing which does not have to be equidistant as it is the case above. Here only the VDW-interactions are perturbed since there are no charges on the methane and the mass stays the same over all lambdas. The assigned value to `init_lambda_state` stands for the index of the lambda array and thus defines which  $\lambda$  state we are simulating. In this case it is 3 (the corresponding mdp-file is designated appropriately as `md_3.mdp`) and corresponds to `lambda[3] = 0.48`. `init_lambda_state = 0` means the initial state A (fully interacting methane). Since MBAR requires the potential energy differences between all states (not only neighboring ones as for BAR) for input, one have to set `calc_lambda_neighbors = -1 (!)`. `couple-moltype` is the name of the [moleculetype] looked up in the topology file to be decoupled. `couple-lambda0` and `couple-lambda1` define the activated non-bonded interactions for both of the end states. Here only VDW-interactions are present in the initial state ( $\lambda = 0$ ) whereas in the fully decoupled state ( $\lambda = 1$ ) all the interactions with the surrounding are switched off. `nstddhdl` sets the frequency for writing out  $\partial U/\partial \lambda$  and  $\Delta U$  ( $U$  stands for the system's potential energy) to the outputfile `dhdl.xvg`. These `dhdl.xvg` files are needed as input for the analysis with BAR and MBAR.

<sup>5</sup><http://manual.gromacs.org/documentation/2021.2/user-guide/mdp-options.html>

After generating the job files for every  $\lambda$ -point as described above one can run the simulations via:

```
$ bash start_sim.sh
```

Each  $\lambda$ -point will be simulated sequentially after the other. However, like in the US simulations, the  $\lambda$ -points can be run in parallel on a computer cluster since they are independent.

### 4.3 Analysis of the Results

After finishing the simulation of each  $\lambda$ -point all the analysis for obtaining the hydration free enthalpy  $\Delta G_{\text{hyd}}$  is performed in the current folder `6_Decoupling` via the two bash scripts `run_BAR.sh` and `run_Pymbar.sh`. The first one calls the built-in GROMACS implementation of BAR `gmx bar` and hence only needs GROMACS to be installed. The latter one calls the tool `alchemical-analysis.py` [9] (located and installed in the `Programs` folder) which also requires the `pymbar` module to be installed (also located in `Programs`). Both programs need the respective `dhdl` files located in `Lambda_XY/Production_MD/` as input. Running `gmx bar` can be done via:

```
$ gmx bar -f Lambda*/Production_MD/dhdl.xvg -o -oi -oh
```

or by simply executing the prepared bash script:

```
$ bash run_BAR.sh
```

For the MBAR analysis we will use a Jupyter notebook that uses the `alchemlyb` library. The notebook expects the input files `dhdl.xvg` to be stored in a central directory. Therefore, before executing the notebook run the prepared bash script:

```
$ bash collect_dhdl.sh
```

For a simulation of 10 ns per  $\lambda$ -point `gmx bar` shall give you a value around  $8.49 \pm 0.02 \text{ kJ mol}^{-1}$  for  $\Delta G_{\text{hyd}}$  quite close to the experimental value of  $8.4 \text{ kJ mol}^{-1}$  at 298 K [10]. Note that this is the negative (!) of the direct output since a decoupling was performed in our case above (the transfer from the liquid into the gas phase rather than the other way around). `gmx bar` will produce three additional output files (`.xvg`): `bar.xvg` which contains relative free enthalpy differences for each  $\lambda$ -interval, `barint.xvg` containing the cumulative  $\Delta G$  as a function of  $\lambda$  and `histogram.xvg` with the histograms converted from the time series of  $\partial U / \partial \lambda$  taken from the `dhdl` files. Within the notebook for the MBAR analysis several graphical representations of the results are generated `0_MBAR.pdf` contains the overlap matrix (Figure 3 (a)), `dhdl_TI.pdf` shows the average of the slope  $\partial U / \partial \lambda$  versus  $\lambda$  (Figure 3 (b)) and `dF_state.pdf` is a bar plot for the free energy differences between neighboring  $\lambda$  points calculated

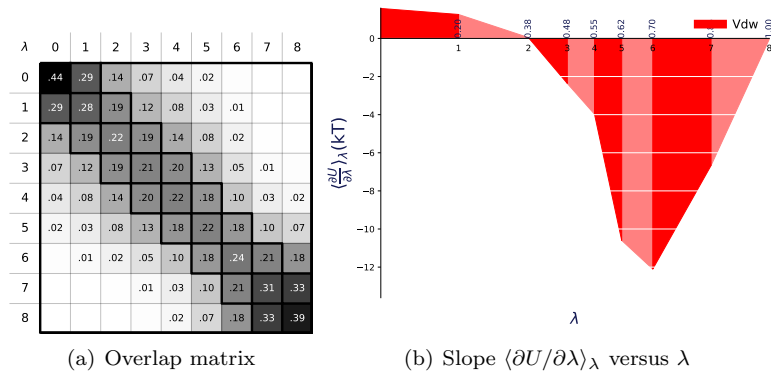


Figure 3: Generated graphical output from `alchemlyb`. Each  $\lambda$ -point was simulated for 10 ns at 300 K.

with different estimators (Figure 4). Finally, `dF_t.pdf` shows the convergence of the forward and reverse free energy change with the simulation time Figure 5.

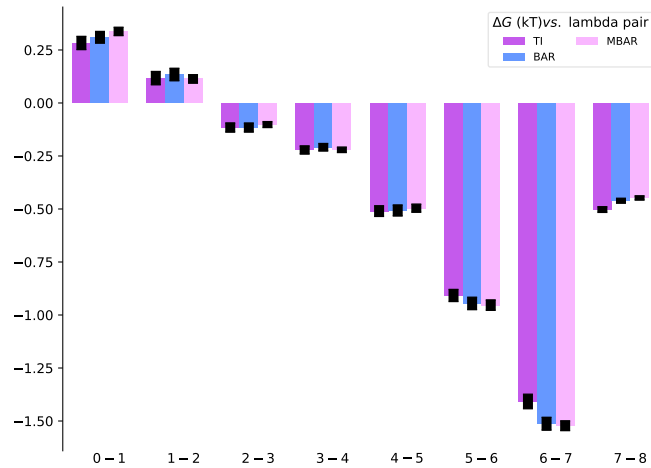


Figure 4: Generated graphical output from `alchemlyb`. Each  $\lambda$ -point was simulated for 10 ns at 300 K.

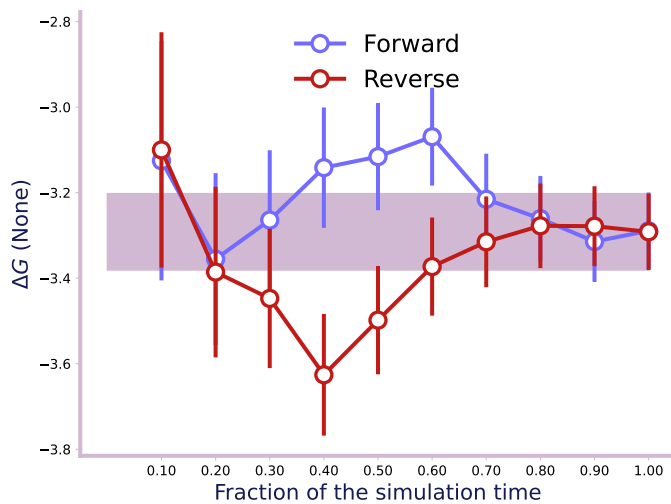


Figure 5: Generated graphical output from `alchemlyb`. Each  $\lambda$ -point was simulated for 10 ns at 300 K.

## 4.4 Cycle Closure [TO BE REVISED]

Attaching the distance restraint to the methane dimer in vacuum,  $\Delta G_{\text{attach rest}}^{\text{D}_2}$ , is calculated numerically by a free energy perturbation approach (FEP) derived from the Zwanzig-formula [11]:

$$\Delta G_{\text{attach rest}}^{\text{D}_2} = RT \ln \langle e^{V_r/RT} \rangle_{V_r} = -RT \ln \langle e^{-V_r/RT} \rangle \quad (1)$$

where  $\langle \dots \rangle$  and  $\langle \dots \rangle_{V_r}$  denote an ensemble average for which the restraining potential  $V_r$  is switched off and on respectively. From the above formula it follows that one basically has to calculate the exponential average of the time series of the bias potential which can be calculated from the sampled order parameter in the COLVAR file. Since we are regarding sticky methane, the free energy penalty of the applied distance restraint is quite low in the bound state and both identities of the FEP formula should yield almost the same (low) value. The contribution for releasing the distance restraint  $\Delta G_{\text{detach rest}}^{\text{DM}}$  between one (fully interacting) methane and a dummy can be calculated via:

$$\Delta G_{\text{detach rest}}^{\text{DM}} = -RT \ln \frac{V^\circ}{V_{\text{eff}}} \quad (2)$$

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