- 1. Switch to new software stack: \$ env2lmod
- 2. \$ module load gcc/9.3.0
- 3. \$ module load cmake/3.26.3
- 4. \$ module load python/3.7.4
- 5. (you are in your home directory on Euler) \$ mkdir programs
- 6. \$ cd programs
- 7. Now get plumed from github: git clone https://github.com/plumed/plumed2.git
- 8. \$ cd plumed2
- 9. \$ ./configure --prefix=/cluster/home/hansenni/programs/plumed2\_INSTALL
- 10. \$ make -j4
- 11. \$ make install
- 12. \$ source sourceme.sh
- 13. Now download Gromacs 2023.2 from https://manual.gromacs.org/2023.2/download.html Move the tar ball into the programs directory, change into the programs directory and unpack it there.
- 14. \$ cd gromacs-2023.2
- 15. \$ plumed patch -p the best matching code/version in our case is gromacs-2023.2
- 16. \$ mkdir build
- 17. \$ cd build
- 18. \$ cmake .. -DGMX\_BUILD\_OWN\_FFTW=ON -DCMAKE\_INSTALL\_PREFIX=/cluster/home/hansenni/programs/gromacs-2023.2\_plumed2\_INSTALL
- 19. \$ make -j4
- 20. \$ make install
- 21. \$ source /cluster/home/hansenni/programs/gromacs-2023.2\_plumed2\_INSTALL/bin/GMXRC.bash
- 22. Now you are ready to start for using GROMACS in conjunction with PLUMED. If you type \$ gmx mdrun -h
  - in the terminal the option -plumed should be listed under the available options.
- 23. Enter the lines:
  - source /cluster/home/hansenni/programs/plumed2/sourceme.sh source /cluster/home/hansenni/programs/gromacs-2023.2\_plumed2\_INSTALL/bin/GMXRC.bash at the end of your .bashrc
- 24. Now obtain the umbrella integration program from github: \$ pip install --user git+https://github.com/M-R-Schaefer/umbrella\_integration
- 25. Get exercise files from github: git clone https://github.com/hansenniels/freeenergy\_tutorial.git
- 26. The umbrella sampling simulation in water can now be started with sbatch < start\_sim\_euler\_slurm.sh

- 1. Switch to new software stack: \$ env2lmod
- 2. **WHAM** (we use an older (pre-installed) version of GROMACS which can still read pdo-files):
  - \$ module load python/3.7.4
  - \$ module load gcc/8.2.0
  - \$ module load openmpi/4.0.2
  - \$ module load gromacs/2021.2
  - \$ python prepare\_gmx\_wham.py
  - \$ gmx\_mpi wham -ip pdo-files.dat -o pmf\_WHAM.xvg -min 0.39 -max 1.15

to display the PMF use xmgrace

\$ module load xmgrace

3. **UI**: \$ module load gcc/11.4.0

\$ module load python/3.11.6

\$ python prepare\_UI.py

\$./command\_UI\_python

The package will be installed in a local repository at \$HOME/.local. Since this is the default path for user-installed python packages, there should be no need to adjust PYTHONPATH.

**4. MBAR**: requires the package pymbar version 4 which comes with the alchemlyb package. For installing the required packages on Euler locally perform the following steps:

```
$ pip install --user alchemlyb
$ python umbrella_sampling_MBAR.py
```

The package will be installed in a local repository at \$HOME/.local. Since this is the default path for user-installed python packages, there is no need to adjust PYTHONPATH.