

BT4110 – Computational Biology Lab

Practical 2

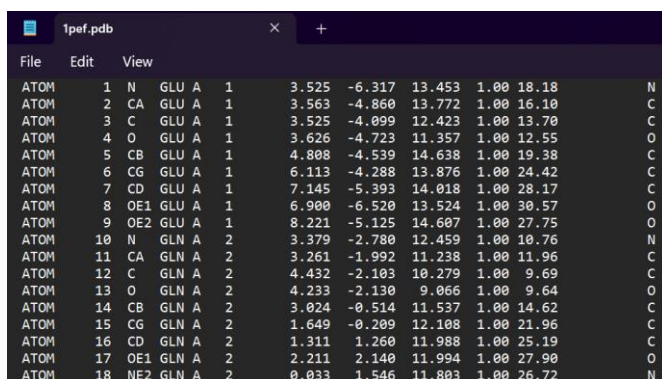
Task 1

Steps followed

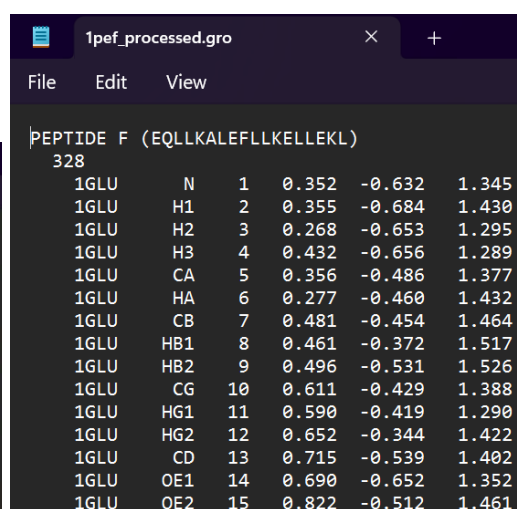
- The .pdb file for 1PEF was downloaded from the Protein Data Bank.
- Water molecules were removed from the .pdb file using a grep command.
- A .gro file was created using pdb2gmx. CHARMM27 was used as the force field and TIP3P was chosen as the water model.

Question 1a

- The .gro file produced by pdb2gmx is much more compact than the input .pdb file.
- All the remarks given in the .pdb file are erased and only the atomic coordinates are retained.
- The .pdb file may or may not have hydrogen coordinates but the .gro file includes hydrogen coordinates.
- The .gro file complies with a user-defined force field.
- The coordinates in .pdb are in angstrom units while those in the .gro file are in nanometre units.



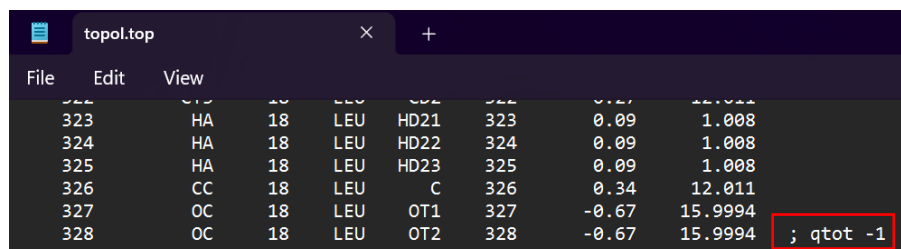
File	Edit	View
ATOM	1	N GLU A 1 3.525 -6.317 13.453 1.00 18.18 N
ATOM	2	CA GLU A 1 3.563 -4.860 13.772 1.00 16.10 C
ATOM	3	C GLU A 1 3.525 -4.099 12.423 1.00 13.70 C
ATOM	4	O GLU A 1 3.626 -4.723 11.357 1.00 12.55 O
ATOM	5	CB GLU A 1 4.808 -4.539 14.638 1.00 19.38 C
ATOM	6	CG GLU A 1 6.113 -4.288 13.876 1.00 24.42 C
ATOM	7	CD GLU A 1 7.145 -5.393 14.018 1.00 28.17 C
ATOM	8	OE1 GLU A 1 6.900 -6.520 13.524 1.00 30.57 O
ATOM	9	OE2 GLU A 1 8.221 -5.125 14.607 1.00 27.75 O
ATOM	10	N GLN A 2 3.379 -2.780 12.459 1.00 10.76 N
ATOM	11	CA GLN A 2 3.261 -1.992 11.238 1.00 11.96 C
ATOM	12	C GLN A 2 4.432 -2.103 10.279 1.00 9.69 C
ATOM	13	O GLN A 2 4.233 -2.130 9.066 1.00 9.64 O
ATOM	14	CB GLN A 2 3.024 -0.514 11.537 1.00 14.62 C
ATOM	15	CG GLN A 2 1.649 -0.209 12.108 1.00 21.96 C
ATOM	16	CD GLN A 2 1.311 1.260 11.988 1.00 25.19 C
ATOM	17	OE1 GLN A 2 2.211 2.140 11.994 1.00 27.90 O
ATOM	18	NE2 GLN A 2 0.033 1.546 11.803 1.00 26.72 N



PEPTIDE F (EQLLKALEFLKELLEKL)						
328						
1GLU	N	1	0.352	-0.632	1.345	
1GLU	H1	2	0.355	-0.684	1.430	
1GLU	H2	3	0.268	-0.653	1.295	
1GLU	H3	4	0.432	-0.656	1.289	
1GLU	CA	5	0.356	-0.486	1.377	
1GLU	HA	6	0.277	-0.460	1.432	
1GLU	CB	7	0.481	-0.454	1.464	
1GLU	HB1	8	0.461	-0.372	1.517	
1GLU	HB2	9	0.496	-0.531	1.526	
1GLU	CG	10	0.611	-0.429	1.388	
1GLU	HG1	11	0.590	-0.419	1.290	
1GLU	HG2	12	0.652	-0.344	1.422	
1GLU	CD	13	0.715	-0.539	1.402	
1GLU	OE1	14	0.690	-0.652	1.352	
1GLU	OE2	15	0.822	-0.512	1.461	

Question 1b

According to the topol.top file, the protein currently has a net charge of -1 .



Atom	Type	Count	Charge
323	HA	18	LEU
324	HA	18	LEU
325	HA	18	LEU
326	CC	18	LEU
327	OC	18	LEU
328	OC	18	LEU

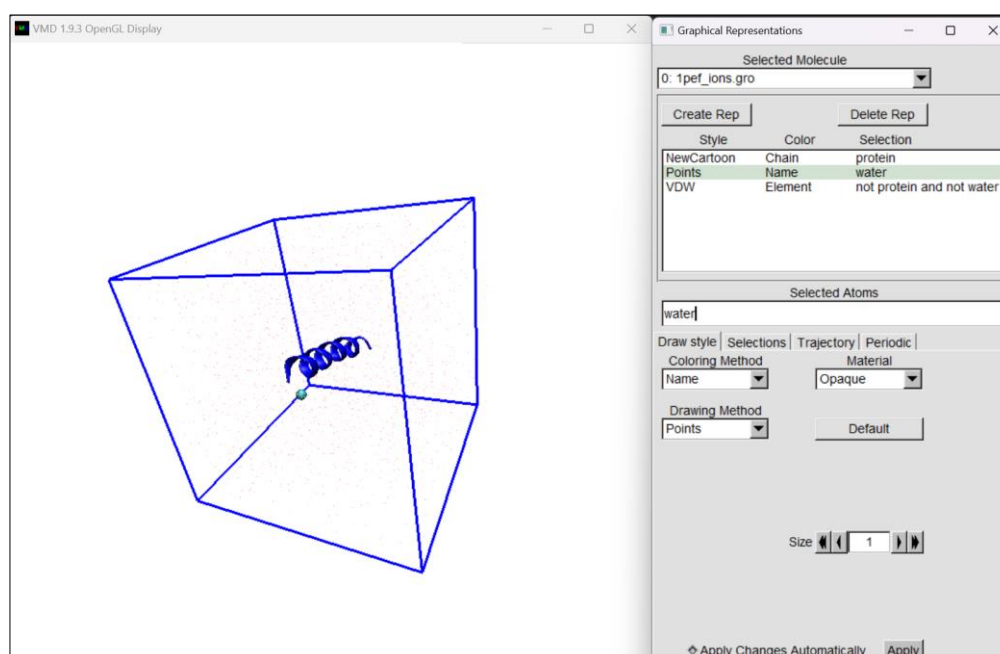
; qtot -1

Task 2

Steps followed

- A cubic box was created using `editconf` with the protein at the centre and a padding distance of 1 nm.
- The box was solvated using `solvate`.
- Ions were added using `grompp` and `genion`. 1 Na^+ ion was added since the net charge was -1

Question 2a



We can visualise the solvated box with the protein in VMD. To do so, we have to first load the solvated and neutralized .gro file in VMD. We can represent the protein with NewCartoon, the solvent with Points, and the ion with VDW as the Drawing Method. Then, in the Tk Console , we can run the command

```
draw pbcbox
```

Question 2b

The volume of the cubic box is 131.692 nm³.

4175 water molecules were added during solvation.

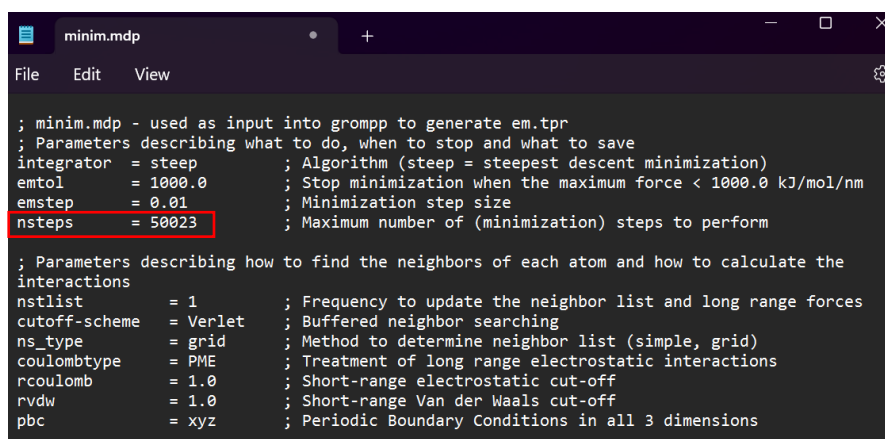
```
Output configuration contains 12853 atoms in 4193 residues
Volume                :      131.692 (nm^3)
Density                :      977.915 (g/l)
Number of solvent molecules:    4175
```

Task 3

Steps followed

- The minim.mdp file was modified as required.
- Energy minimisation was performed using grompp and mdrun.
- The potential energy as a function of time was obtained using energy.

Question 3a

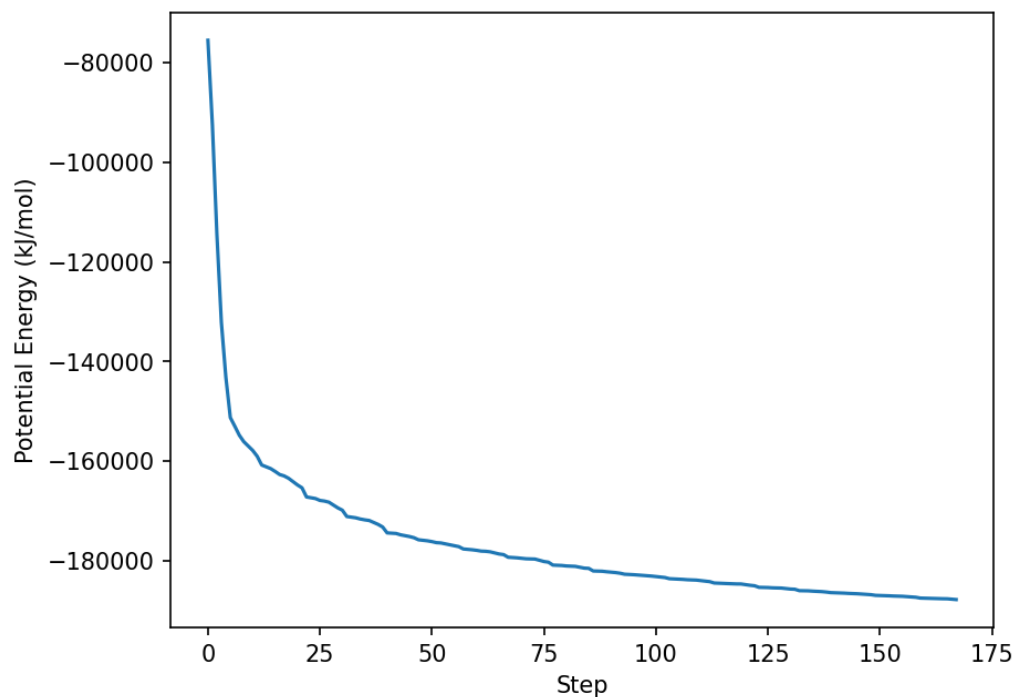


```
minim.mdp
File Edit View

; minim.mdp - used as input into grompp to generate em.tpr
; Parameters describing what to do, when to stop and what to save
integrator = steep          ; Algorithm (steep = steepest descent minimization)
emtol      = 1000.0         ; Stop minimization when the maximum force < 1000.0 kJ/mol/nm
emstep     = 0.01           ; Minimization step size
nsteps     = 50023          ; Maximum number of (minimization) steps to perform

; Parameters describing how to find the neighbors of each atom and how to calculate the
interactions
nstlist    = 1              ; Frequency to update the neighbor list and long range forces
cutoff-scheme = Verlet      ; Buffered neighbor searching
ns_type    = grid           ; Method to determine neighbor list (simple, grid)
coulombtype = PME           ; Treatment of long range electrostatic interactions
rcoulomb    = 1.0           ; Short-range electrostatic cut-off
rvdw        = 1.0           ; Short-range Van der Waals cut-off
pbc         = xyz           ; Periodic Boundary Conditions in all 3 dimensions
```

Question 3b



This was plotted using the following Python code:

```
import numpy as np
import matplotlib.pyplot as plt

x,y=np.loadtxt("potential.svg",comments=["#","@"],unpack=True)
plt.figure(dpi=150)
plt.plot(x,y)
plt.xlabel("Step")
plt.ylabel("Potential Energy (kJ/mol)")
plt.show()
```

The system converged to its minimum energy state in 168 steps.

```
Steepest Descents converged to Fmax < 1000 in 168 steps
Potential Energy = -1.8783233e+05
Maximum force    = 9.8512854e+02 on atom 28
Norm of force     = 5.2512326e+01
```

Task 4

Steps followed

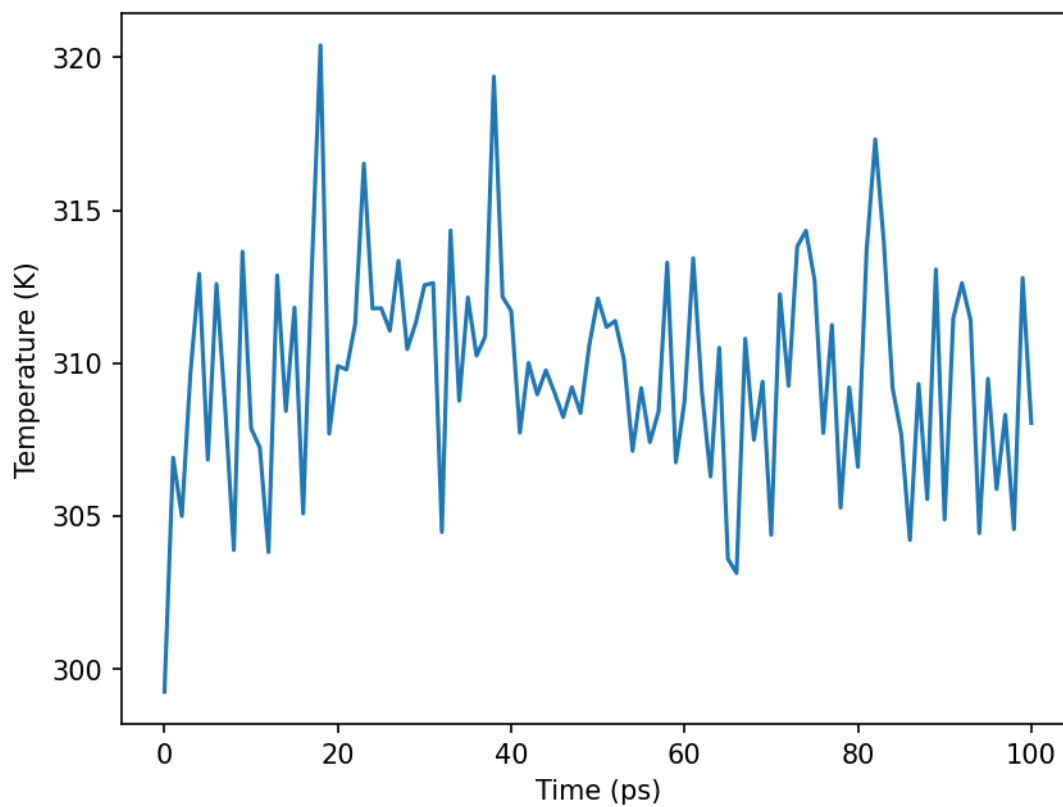
- The nvt.mdp file was modified to perform equilibration at 310 K.
- NVT equilibration was performed using `grompp` and `mdrun`.
- The temperature as a function of time was obtained using `energy`.

Question 4a

The average temperature at the end of the NVT run was 309.788 K.

Energy	Average	Err.Est.	RMSD	Tot-Drift
Temperature	309.788	0.32	3.56599	0.540081 (K)

Question 4b



This was plotted using the following Python code:

```
import numpy as np
import matplotlib.pyplot as plt
x,y=np.loadtxt("temperature.xvg",comments=["#","@"],unpack=True)
plt.figure(dpi=150)
plt.plot(x,y)
plt.xlabel("Time (ps)")
plt.ylabel("Temperature (K)")
plt.show()
```

Task 5

Steps followed

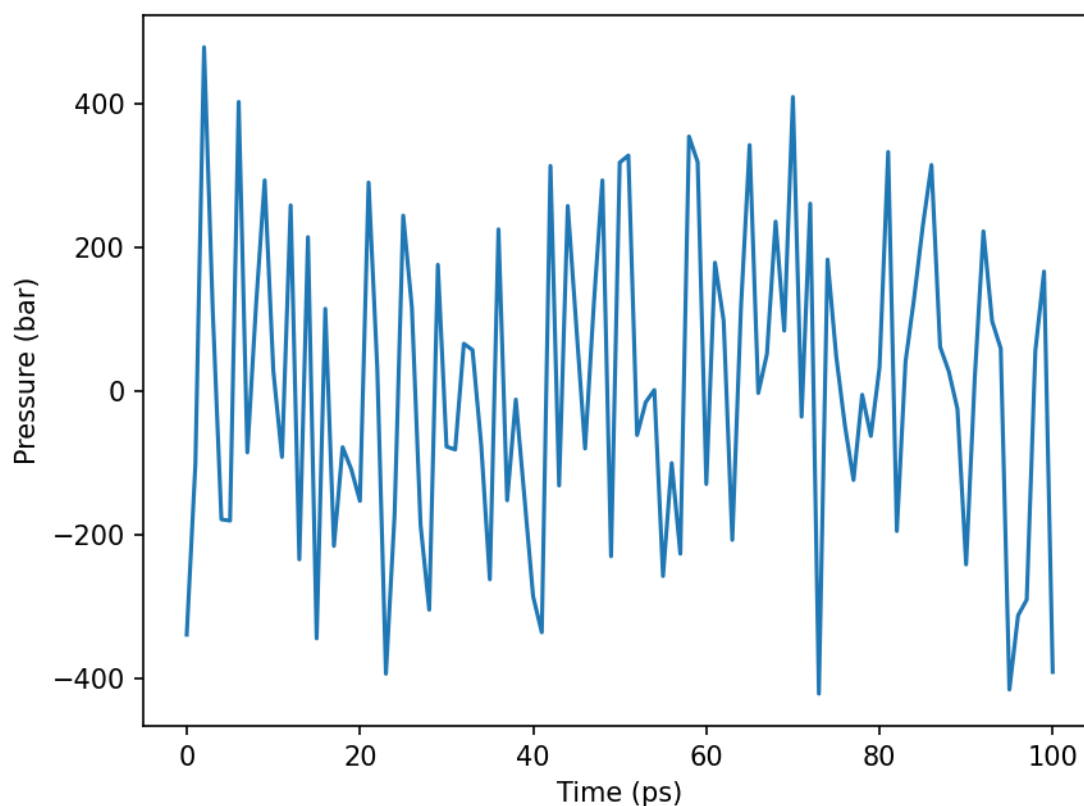
- The npt.mdp file was modified to perform equilibration at 310 K and 1 bar.
- NPT equilibration was performed using grompp and mdrun.
- The pressure as a function of time was obtained using energy.

Question 5a

The average temperature at the end of the NPT run was 0.0602295 bar.

Energy	Average	Err.Est.	RMSD	Tot-Drift
Pressure	0.0602295	3	220.301	-14.007 (bar)

Question 5b



This was plotted using the following Python code:

```
import numpy as np
import matplotlib.pyplot as plt
x,y=np.loadtxt("pressure.xvg",comments=["#","@"],unpack=True)
plt.figure(dpi=150)
plt.plot(x,y)
plt.xlabel("Time (ps)")
plt.ylabel("Pressure (bar)")
plt.show()
```

After this, the md.mdp file was modified to perform a 500,000 step (1 ns) simulation at 310 K and 1 bar, and a production MD run was carried out using grompp and mdrun.