Solutions for exercise 03

GROMACS Simulation Set-up

Deadline: Please hand in your protocol in pdf format by Thursday, 2nd June, 10.15 a.m. to **saleksic@zedat.fu-berlin.de**. The proctol should contain GROMACS commands, Python code, plots, and comments if necessary.

1.1 Download PDB File and Visualize with VMD (10)

In this exercise you can practice how to download a pdb structure and visualize it wih VMD. Download from the Protein Data Bank (PDB) website the structure of Langerin:
`http://www.rcsb.org/pdb/explore/explore.do?structureId=3P5H`. Open downloaded pdb file in a text editor and extract the Langerin monomer A, by deleting other monomers, crystal water, and Ca^{2+} ions. (5)
Visualize Langerin structure in VMD (New Cartoon as view style) and highlight the α-helicies in red, β-sheets in blue, and loops and coils in silver. Set background color to white. Include a snapshot of the VMD representation in your report. (5)

1.2 Gromacs Set-up - Structure Minimization (30)

Dowloded Langerin pdb file convert into files suitable for GROMACS (**pdb2gmx** command). Minimize the structure in vacuum (for this minimization step use file **minim1.mdp**), and then solvate it. Are the counter ions needed? Why? (*use AMBERff99SB-ILDN as a force field and TIP3P water model. Use a dodecahedron box and place Langerin in the center of it, at least 1 nm from the box walls*). (12)

Check the size of the simulation box. How many water molecules are needed to solvate such a protein? How many atoms are in the solvated system? (Take a snapshot of the Linux screen with the necessary information, and include it into report). (2)

Check if the solvated system (for this step use file **minim.mdp** which should be in the next tasks modifed as described) is truly minimized by using the **g_energy** command of GROMACS and plotting the potential energy, the kinetic energy and the total energy. Write a Python script which loads output file of the **g_energy** command and plots the potential energy as a function of minimization time. Can you plot the kinetic energy at this stage the structure preparation? (6)

Change the number of minimization steps (try 2500, and 7500 steps) in minim.mdp file and check again the potential energy. Include the potential energy plots like in previous task, and discuss how the increased number of the minimization steps influenced the minimization process. (5)

Set back number of minimization stepst to 5000 and change the energy cutoff (try 50, 100, and 150). What happens at the different values of emtol? Include the potential energy plots like in the previous tasks. (5)

1.3 Gromacs Set-up - Equilibration in NVT Ensemble (25)

Use the *.gro file of the structure for which minimization was succesfull. Modify given nvt.mdp file so that, integration step is 2 fs, NVT equlibration lasts for 100 ps, trajectory is updated every 1 ps, equilibration temperature is 300K, and modified Berendsen thermostat is used. Include **modified nvt.mdp** file into your report. (10)

Run NVT equilibration, detect the time needed for NVT equilibration, and check total, potential, and kinetic energy of the system. Include a figure containing all three energies plotted as a function of the equilibration time. (15)

1.4 Gromacs Set-up - Equilibration in NPT Ensemble (25)

Modify given npt.mdp file so that, integration step is 2 fs, NPT equlibration lasts for 100 ps, trajectory is updated every 1 ps, Parrinello-Rahman barostat is used, and velocity generation is switched off. Include **modified npt.mdp** file into your report. (8)

Run NPT equilibration, detect the time needed for NPT equilibration, and check total, potential, and kinetic energy, as well as pressure. Include in your report a figure containing all three energies, and a separate figure in which pressure is plotted as a function of the equilibration time. What would you suggest on how to improve NPT equilibration? (8)

Generated *.gro file after NPT equilibration convert to new *.gro file without water molecules and with fixed pbc conditions (hint: use **trjconv** command). Newly generated *.gro file upload in VMD together with *.gro file generated with **pdb2gmx** command. Align both structures and color them differently (New Cartoon as view style). Background color should be set to white. Include the snapshot in your report. (9)

1.5 Gromacs Set-up - MD Run (10)

Modify given md.mdp file so that, integration step is 2 fs, MD run lasts for 100 ns, compressed trajectory is updated every 1 ps, while full trajectory, log,velocity, and energy files every 50 ns. Include **modified md.mdp** file into your report. (8)
Based on the **md.mdp** file conclude if MD simulation is about to be performed in the NVT, or in the NPT ensemble. (2)

Since MD simulation of a protein is computationally quite expensive, we will not run it now.

2 Files

`https://www.dropbox.com/sh/vmqi8vl0sxj6q2k/AAAuDrZi_gRZRY82xHyr6Ygta?dl=0`