Assignment 2: modeling of a protein

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Introduction

In this report the molecular dynamics simulation results are presented for 1RJU protein. The 1RJU pdb code corresponds to a crystal structure of a truncated form of yeast copper thionein which was obtained using X-Ray diffraction. The sequence is the following:

HIS GLU CYS GLN CYS GLN CYS GLY SER CYS LYS ASN ASN GLU GLN CYS GLN LYS SER CYS SER CYS PRO THR GLY CYS ASN SER ASP ASP LYS CYS PRO CYS GLY ASN

It consists of one chain with no alternative locations, has a length of 36 and no disulfide bridges are present.

Computational remarks

The simulation was performed by firstly preparing the structure: everything beside the peptide chain and crystallographic water was removed, the histidine residue was protonated along with the second residue – GLU. The guesscoord command was used for guessing the missing coordinates. Furtherly the rectangular box of water was created with thickness of 7 Å, ions of Na+ and Cl− were added to neutralize the system and to bring 0.5M salt concentration. The obtained net charge was: $3.8e^{-7}$e – desired numerically zero. The appropriate periodic boundary conditions were applied. The applied cutoff value was 12Å and the smooth switching over 1Å was used.

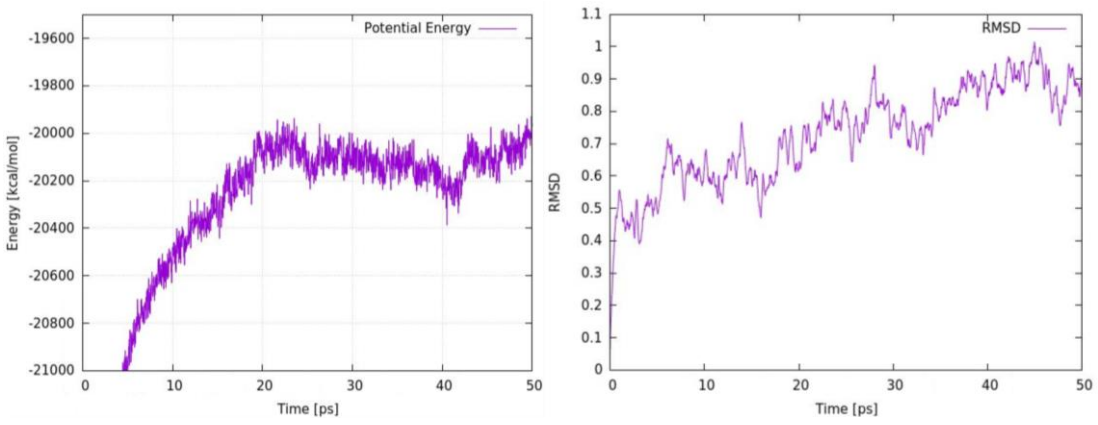
The molecular dynamics simulation was done in NPT ensemble with T=300 K and P=1 bar. The simulation lasted 50 ps (50 000 steps) and beforehand the minimization 2000 steps. The coordinates were saved every 20 steps. The results were saved into appropriate files and the necessary plots were created.

All the steps were performed using VMD and appropriate packages and plugins and Gnuplot and Python were used for plotting and average calculation.

Results

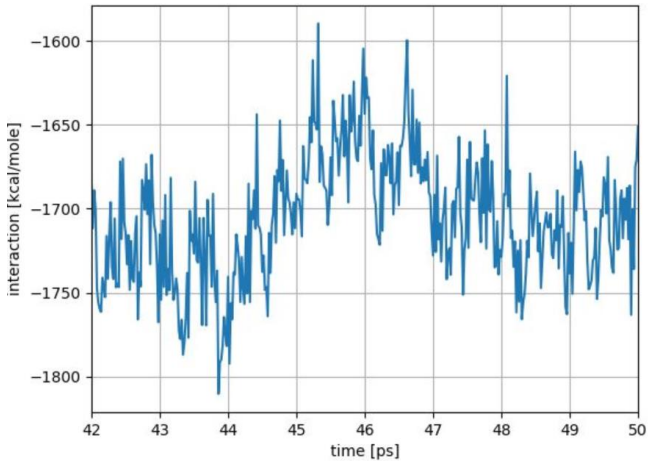
- Equilibration

  To properly state whether the system equilibrated both RMSD of the backbone in time as well as the potential energy in time should be plotted what is shown below.



When looking at the potential energy plot, at the first sight it seems that the system equilibrated after 20 ps. After 40 ps some slightly higher fluctuations appear but seem not to resemble the significantly different pattern. Regarding the RMSD plot, no overall increasing pattern is observed after 38 ps. However, within this period 38-50 ps the small jump is present in the potential energy (hard to state whether it is significant or not – all in all some pattern is a little bit broken), therefore I believe that the safest option would be to assume that after 42 ps the system has equilibrated – not increasing RMSD and rather stabilized potential energy. Nevertheless, I would strongly recommend performing a longer simulation to observe longer the behaviour especially of the potential energy.

- Energy of interaction between the protein and the solvent (period 42-50ps)
  The plot of the energy of the interaction energy in time (within the taken period when the system is assumed to be equilibrated) is shown below.



Average value: -1705.59 [kcal/mole]

Conclusion

After the performed analysis it is clear that for the short simulations like this one stating with a high degree of certainty whether the system has equilibrated or not is a hard task. The plots interpretation is challenging especially with regards to concluding whether some single jumps appearance in the plots of potential energy or RMSD is just another fluctuations a little bit but insignificantly stronger or maybe it is an indication that there's still lack of equilibration. Without no doubt the longer simulation periods would be helpful for more adequate and less uncertain analysis.

Path to files: bioinf8/Desktop/Molecular/Molecular_ass2/results