Lab 01: Small molecule parameterization and optimization

Aim:

- Create a new residue in GROMACS, optimize its structure, and calculate and visualize its normal modes of vibration with the visualization program VMD.

Objectives:

- Familiarize with NoMachine and working remotely on MSI computers.
- Familiarize with the Linux OS and its basic commands.
- Familiarize with the "vim" editor to create and edit files within Linux.
- Familiarize with the "VMD" visualization program.
- Understand the structure of the main force field files for the GROMACS software package.
- Learn how to run a GROMACS job, and analyze its output.

Description:

In this lab module you will create a new residue for the molecule *1-propanol* for the CHARMM36 force field working with the GROMACS 5.0 simulation software. You will choose appropriate atom types and charges to transfer to the new residue from existing ones in the force field. You will optimize the structure in the gauche and anti conformations, calculate the normal modes of vibration for each optimized structure, and display them with the visualization software VMD.

Lab report:

- Abstract: a dozen lines or so. After reading it, it should be clear what the goal of your research is, how you proceeded towards the goal, and your main results.
- Introduction: from half a page to a page. Provides a framework for your research. Mention and describe the important theory behind your research, with some equations. For this lab you could focus for example on describing some of the theory behind normal modes analysis.
- Material and methods: By reading the methods, someone else should be able to reproduce your experiment. Keep it simple, avoid lengthy descriptions, but include all necessary details. If you need to provide large data sets (topology files, coordinates, etc.), you may want to create an additional file for "Supporting Information". This file could be a word-processor file where you organize the data in tables. Notice if you copy and paste from linux terminal, it helps keeping things neat and aligned to use "Courier New" font, and maybe reduce its size (no smaller than 8 though) to fit the text in a line. In alternative, you can create a directory containing ASCII files in linux, compress it, and attach it as a zipped file. If you choose this path, you need to provide either a README file in the directory describing the content of each file, or describe them in a word-processor file.
  For this lab module, some things you may want to include are:

    - What software did you use?
    - What force field did you use?
    - How did you modify the FF to include your 1-propanol? (Table from topology file).
    - Where did you obtain your initial structures? If they are not publicly available, you should include them in the material and methods.
    - What cutoffs have you used? Did you use boundary conditions?
    - What optimization algorithm? What threshold for convergence? Any constraints?
- Results and discussion: *Present* your results, organizing the relevant data in tables and figures with captions. *Describe* your results first (table 1 shows that the frequency XX is greater than YY…), and then *discuss* them (a possible explanation is that in the ZZ conformation the O-H group is hydrogen-bonded with the C=O group of the QQ residue, which may contribute to lowering its stretching frequency). For this lab, some possible topics you want to discuss and material you want to provide include:
    - What are the coordinates of your optimized structures, their energies, their frequencies?
    - Show the optimized gauche and anti structures in a figure. Highlight the main structural differences.
    - How did the energy change along the optimization? What about the structure?
    - Energy and structural differences between the anti and gauche conformers.
    - Normal modes, how do they relate to what expected from IR spectrum and characteristic IR absorption frequencies? What do the lowest frequency modes correspond to? Does it make sense? What are the force field potential energy functions that appear contributing the most to these modes?
    - What is the force constant for the C2-C3 bond? What frequency do you expect that force constant correspond to in cm^{-1} if you treat it as a harmonic oscillator (remember to use the reduced mass for the carbons)? How well does it match what you found from the frequency analysis? Comment.
    - Are there any differences in the normal modes between anti and gauche?
    - Do you expect there could be other conformers? What atoms and dihedrals could be involved? What energy difference and energy barriers would you expect for these conformers? Do you think they would be populated at room temperature?
- Conclusions: reiterate the abstract, but shifting the focus on the results. If you are planning to use what you found in the near future, comment on that. In this case you may want to look at the next lab module.

Useful resources:

- GROMACS and GROMACS 5.0 Manual
- VMD and manual
- CHARMM36
- IR Characteristic Frequencies