Linux Basics

$ ls *List everything in directory*

$ pwd *What directory am I in?*

$ mkdir modelling *Make a directory called modelling*

$ cd modelling *Go into the modelling directory*

$ cp test.pdb protein.pdb *Copy test.pdb to protein.pdb*

$ cp test1.pdb modelling/protein.pdb

$ cp * modelling/. *Move everything into modelling*

$ mv crap.pdb important.pdb *Changing filenames*

$ rm crap1.pdb *Removing files*

$ more important.pdb *View the file*

$ head important.pdb *View the first 10 lines*

$ tail -100 important.pdb *View the last 100 lines*

Find the Trajectory Files

You will find copies of the pdb, topology and trajectory files in:

$ cd $WORKDIR
$ ls $DATADIR
Uncompress the files:
$tar –zxvf $DATADIR/workshopSAH.tar.gz

Look at what you've got.

$ ls

Your Starting Structure: PDB Search

Go to the protein data bank (type pdb into google).

Before you start, scroll down and have a look at “Molecule of the month”. If you click on “Structural view of biology” you can access the archive. This is highly recommended reading!

In the pdb search facility, find human ubiquitin
1UBQ.pdb (X-ray crystal structure)
1D3Z.pdb (NMR) by typing in the codes.

Download the files. They will go into the “downloads” directory (~/Downloads). Move them into your working directory.
$cp ~/Downloads/*.pdb $WORKDIR/

VMD ~ “Hot” Keys

VMD has particular “hot keys” that make the program easy to use.

“r” Rotate structure
“t” Translate structure
“s” Scale structure (eg zoom in or out)
“1” Label an atom
“2” Measure a bond between 2 atoms
“3” Measure the angle between 3 atoms
“4” Measure the dihedral between 4 atoms

VMD for Visualisation ~ X-ray Structure

1. Load your X-ray structure into VMD.

$VMD

2. Play with the different representations (eg VdW, cartoon). Display the backbone only.

3. When you colour the structure by “name” (default), notice which elements have which colours (eg hydrogens are white).

What else is there in the file, apart from the protein?

4. In cartoon representation, colour the protein by "secondary structure".

5. Make the LYS residues VdW while the rest of the protein is licorice.

6. Make LYS 63 and 48 green but LYS 27 red.

7. Put the molecule in cartoon representation and then display all of the charged residues in VdW.

8. What do you notice? Be sure to rotate the molecule and look at it in different orientations.

9. Now display the hydrophobic residues as well. What else to you notice? (hint: what is on the outside/inside of the protein?!)

10. Colour the protein by B-factor (the largest B-factors show the most flexible regions).

11. Plot a Ramachandran plot (under Extensions/ Analysis).
You will need to click on “Molecule” to select your structure – the angles for your protein will appear as yellow squares.

Visualising NMR Structures with VMD

1. Delete the X-ray structure and read the NMR structure into VMD.

2. What two very obvious differences are there with the X-ray structure?

3. Use the cartoon representation to display all of the structures simultaneously.

4. Compare the regions of highest flexibility with those you detected using crystallographic B-factors (switch from RWB to BWR under "graphics/colours"!!)

NMR Structure ~ Distances and Angles

1. For one of your structures, measure the distance between one of the OD1/OD2 oxygen atoms of ASP 52 and the NZ on LYS 27. Use:

Graphics/labels/bonds

2. Display the hydrogen bonds between the side chains only. Are there any hydrogen bonds between ASP 52 and LYS 27? If “yes”, does this hydrogen bond persist for all NMR structures?

3. Delete all bond and atom labels. Now pick two different interesting atoms in your structure (e.g. a hydrogen bonding pair). How does this distance change throughout the ensemble? Plot a graph of your results.

MD trajectory of a Protein/DNA Complex

You have been provided with two pdb files, two topology files and their two corresponding trajectory files.

1. In a terminal window type look at the size of your files by typing:

   $ls –l

Which of the files do you think are the trajectory files?

2. Look at one example of each of the three file types using the “more” linux command. Do the files contain what you expected?

Read the pdb file for the protein into VMD and load the corresponding trajectory file.

The topology file is of type “amber7 parm”
The file is of type “amber trajectory”

What happens if you load the file as type “amber coordinates with periodic box”? What has gone wrong and why?

Now load in the topology file and the trajectory file for the protein DNA complex.
Can you think of an advantage to using a topology file instead of a pdb file to watch your trajectories?

This trajectory was sampled every 50ps for visualisation purposes. How long was the simulation run for?

Use the smoothing tool under:

Graphics/representations/trajectory/

to explore how the visualisation of the dynamics changes as you change the level of trajectory smoothing from none to 100.

Make a Nice Picture

Using “graphics/representations”:

1) Display the protein as “new cartoon”, and colour by secondary structure.

2) Represent the DNA as vdw, and colour by atom type.
3) Switch off the axes:
   Display/axes/off

4) Change the colour of the background to white:
   Graphics/colors/display/background

5) Change into a “Goodsell” representation

Graphics/materials/goodsell

6) Switch on the ambient occular settings:

Display/Display Settings/External renderer options

7) Look at these settings on the screen

Display/Rendermode/GLSL

8) Render the image using “Internal Tachyon” and look at the results.

The “tga” file format can be converted into conventional windows compatible formats (e.g. jpg or bmp) using the Gimp.

8) Switch back to an opaque material for the DNA and the protein.

9) Change the DNA representation to “lines”, but increase the thickness of the lines to make them more visible.

10) Switch to a backbone representation for the DNA.

11) Change the protein representation to “tube” representation.

12) Using:

Graphics/representations/trajectory

for the protein display frames 1 to 2000 in steps of 10, and colour these by MD timestep.

13) Change the colour representation from RWB to RGB.

14) Make another picture using a non-white background colour and material of your choice! The more lurid the better!

Comparing Structures in VMD

1) Delete the protein/DNA complex, and load in the protein only trajectory using the appropriate topology file.

2) Now load in the protein pdb file separately using:
   File/new molecule

3) Display and undisplay the pdb file and the trajectory file.

4) Translate the protein pdb file but not the trajectory.

5) By changing which molecule is selected, colour the pdb file pink and the trajectory file blue.

6) Make the pdb file the “top” structure by selecting it in “main” and then:

Molecule/make top

7) In:

Extensions/analysis/RMSD trajectory tool

click on “add all”, select “top” to be the reference molecule and the plot the RMSD.

8) Does the structure undergo a conformational change during the simulation, or not?

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