Analysis of an RNA molecular dynamic simulation

In this computer lab you will learn to visualize and analyze he MD trajectory of an RNA molecule using the visualization program VMD. You will analyze two different trajectories for the same system, one at atomistic resolution, generated with the Amber force field, the other at a coarse-grained resolution using the HiRE-RNA model.

1 Practical set up

If not done already, install the program VMD on your machine.

From the USB-key download the directory named **TP-simulation**.

- In the directory you'll find two sub-directories : atomistic and coarse-grained.

- In the atomistic directory the file containing static representations of the molecule is **start.gro**.

- In the coarse-grained directory the file containing static representations of the molecule is **RNA_cg.pdb**.

- Files with extension ".xtc" contain the simulation trajectory.

To open a trajectory of the molecule, from shell type the command:

vmd start.gro md_atom.xtc

or

vmd RNA_cg.pdb md_cg.xtc

for atomistic and coarse-grained respectively.

Alternatively, you can open the molecule with VMD and then from the main menu select the option *Load data into molecule* to load the trajectory choosing the appropriate .xtc file.

2 Visualize different components

From the main menu select *Graphics → Representations*. A new panel will open named *Graphical Representations*. From this panel you can create (and delete) new representations that will be added to your visualization. You can hide/show a given representation by double-clicking on its name in the list.

In the *Graphical Representations* panel under *Selected Atoms* you can make a selection of different parts of the molecule. For example to select atom 127 type "index 127", to select residue 4 type "resid 4", to select all guanines type "resname G", etc. You can also make a selection using the buttons in the pannel. You can choose a different representation of the selection in style and colors using the panels *Coloring Methods* and *Drawing Methods*.

3 Trajectory analysis

The atomistic trajectory file has already been processed to contain only the protein and the ligand and not the solvent and the ions.

3.1 Alignment

The first thing to do is to align the all frames of the trajectory with respect to the first one in order to visualize just the internal motion of the different parts of the molecule. To so do from the main menu select *Extension → Analysis → RMSD Trajectory tool*. A new panel will open. On the left side of the panel under *Selection Modifier* erase *protein* and type *all*. You can now align the proteins by clicking the *Align* button.

You can also obtain a measure of the structural difference of the two conformation by computing the Root Mean Square Deviation (RMSD) which gives the average displacement of any two corresponding atoms of the two structures. Click on the *RMDS* button to obtain this measure. A graph will open.

3.2 Visualization of the molecule's movements

In order to better detect global movements we are going to smooth the trajectory averaging over several frames. From the *Graphical Representations* panel click on the *Trajectory* button. Make a choice of 10 for the *Trajectory Smoothing Window Size*, at the bottom of the panel.

To obtain a better view of the molecule's motion we are now going to superpose many frames at once. From the *Graphical Representations → Trajectory* in the *Draw Multiple Frames* box erase "now" and type **b:s:e**, where **b** is the first frame you want to analyze, **e** is the last frame, and **s** is the step size. This command will superpose frames from **b** to **e** selecting one every **s**.

3.3   Distance measurements

VMD allows you to measure distances between elements of the structure and follow their evolution over time. To select the distance between two elements you from the main menu select *Mouse → Label → Bonds*. Then in the visualization window click on two atoms of the system. The name of the selected atoms will appear, together with a dashed line between the two elements and a text indicating the value of the distance measured in Å.
To observe the evolution of this quantity over time from the main menu select *Graphics → Labels*. A new panel will appear named *Labels*. From the box on the upper left side select *Bonds* (when the panel opens it says "Atoms"), click on the distance or distances you want to follow over time, click the *Graph* panel below and finally click the *Graph* button to obtain the graph of the distance over all frames.