VMD Analysis Tutorial - Trypsin with Benzamidine

Let us explore some of the analysis tools available in VMD. This tutorial assumes that you have some proficiency with using VMD to visualize proteins and load/display trajectories.

Download or otherwise obtain the trajectory file “tryp_benz.pdb”. This trajectory file contains 100 frames of a simulation of the trypsin protein with a small-molecule inhibitor benzamidine.

Now open VMD and load the tryp_benz.pdb trajectory file.

Using the Graphical Representations window, show the protein in “New Cartoon” style.

RMSD Analysis:

Most analyses require the protein to be structurally aligned (to remove protein translation and rotation).

In the menu of the VMD Main window, select Extensions -> Analysis -> RMSD Trajectory Tool.

The RMSD Trajectory Tool window will appear. Make sure the “protein” is the selection in the main window in the top left, and make sure that “noh” is selected. This will align the protein by all non-hydrogen (heavy) atoms. Now click the ALIGN button.

If you move the frame slider in the VMD Main window, you should see that all protein translation and rotation is removed. Now only internal degrees of freedom remain.

Researchers will commonly plot the RMSD of a trajectory to assess whether the simulation was stable. To do this, select the Plot checkbox, and then click the RMSD button. A plot will appear, showing how the RMSD of the trajectory changes with time. A stable, equilibrated trajectory will typically have an RMSD that has “leveled off” by the end of the simulation.

Ramachandran Plot:

Ramachandran plots are frequently used in bioinformatics to examine protein conformational states.

In the menu of the VMD Main window, select Extensions -> Analysis -> Ramachandran Plot.

For “Molecule”, select “0 tryp_benz.pdb”. A series of points should appear on the Ramachandran plot, indicating the values of the various phi-psi angles of the protein backbone.

You can create a rudimentary histogram by clicking “Create 3-d Histogram”. You may delete the histogram by clicking “Delete 3-d Histogram”.

Solvent Occupancy:

Researchers frequently wish to know whether structured waters exist within or around the protein. These structured waters may mediate key interactions within the protein or between the protein and other molecules.

In the menu of the VMD Main window, select Extensions -> Analysis -> Volmap Tool.

In “selection”, type “water”.
In “volmap type” select “occupancy”.
Select the box for “compute for all frames, and combine using”, then make sure “avg” is selected.
Click “Create Map”.

A volmap will appear. In the Graphical Representations window, with the Isosurface Rep selected, you can slide the Isovalue slider to a larger value (like 0.80), and the volmap will reveal possible structured water locations.

The more frames in the trajectory, the “cleaner” the volmap will appear, and the clearer the water occupancy will be.

Visualize APBS Results:

Load the file “trypsin.pqr” into VMD. In the VMD Main window, click the “D” symbol next to “tryp_benz.pdb” to hide it. Feel free to change the visualization state

In the Molecule File Browser window, make sure the “Load files for” has the trypsin.pqr file selected. Then click “Browse...” and find “trypsin.dx”. Load the DX file into the existing structure.

First, let us view the isosurfaces of the electric potential field itself.
In the Graphical Representations window, “Create Rep”.
In “Drawing Method”, select “Isosurface”.
In “Coloring Method”, select “Volume”.
Select the “Trajectory” tab. For “Color Scale Data Range”, enter -2.0 and 2.0 in each of the two windows, respectively. Click the “Set” button.
Return to the “Draw Style” tab and move the Isovalue slider to visualize the electric potential around the protein.

Another interesting representation is to view the electric field lines. In “Drawing Method”, select “FieldLines”.

Let us visualize the field on the protein surface.
Double-click the “Isosurface” rep to hide it.
Click on the rep that displays the protein, and change “Coloring Method” to “Volume”, and change “Drawing Method” to “Surf”.
Select the “Trajectory” tab. For “Color Scale Data Range”, enter -2.0 and 2.0 in each of the two windows, respectively. Click the “Set” button.
Notice the negative electric potential within the trypsin binding pocket.