Single Small PDB and Fit

<https://youtu.be/8-7Y_QDM_XA>

This tutorial will show you how to calculate the scattering curve from PDB files, and how to use the fitting options in D+

First, in the Domain View, we select PDB File model, press Add, select a PDB file (in this case the PDB of Lysozyme), and press Open.

Notice we are at low level of details. At a higher level of details, you can see the atoms as spheres. Especially with large PDB files, it is important to keep low level of details.

In our example, the center of mass of the Lysozyme protein is not located at the origin. By checking on the "Center PDB" option, when loading the PDB, we shift the center of mass of the structure to the origin. For single PDB files, this is the correct way of calculating the scattering curve. Off center structures require a larger grid size, and as a consequence longer calculation time (to attain the same level of accuracy).

We are now deleting the first off-centered PDB, and add a cylinder to approximate the size of the PDB structure, for a later use in the Suggest Parameters accessory tool.

We are now opening Suggest Parameters, and entering the enveloping cylinder dimensions, to get the appropriate calculation parameters for our PDB model

We are now entering the suggested parameters into D+: Monte-Carlo integration, Iterations of one E to the sixth, and so forth, and… are clicking: Generate.

In the log-log intensity curve, you can see the scattering curve of Lysozyme. We decrease a little bit the convergence field, to produce a smoother curve, but the initial convergence of zero point zero zero one is sufficient for most calculations.

When we select the PDB in the objects tree, more options appear at the bottom, in the "Parameters Editor" pane. We changed the "Outer Solvent Electron Density" from zero, which means that no solvation layer is taken into account, to three hundred and sixty four, so that D+ will calculate the contribution from the solvation layer. We then select the "Fill Holes" option, to add solvation in cavities in the structure that are sufficiently large to contain solvation layers.

In the console window, which runs in the background whenever the GUI of D+ is open, we see the calculation time. Without including the solvation layer, the PDB calculation took less than a second. When the solvation was included, it took nearly twenty seconds. If we want to fit the solvation layer parameters, this may take many evaluations of similar length, and will take a long time.

We shall now show a faster method for using the fitting option of D+ with a PDB file.

We load an experimental signal of Lysozyme, downloaded from the SASBDB database. We then click the "Mutable" option for both the "Domain Scale" and "Domain Constant", and generate the initial curve.

We ensure the appropriate fitting preferences are selected, in the bottom right "Fitting preferences" pane (based on the Suggest Parameters tool).

When we see the resulting initial state curve, we click "Fit" to fit the mutable parameters (scale and background, so far).

The resulting fitted curve appears in blue, as always.

As you can see it converged after two iterations, and it looks better.

We now close D+, and re-open it to show a more elaborate fitting procedure.

The experimental data that was loaded before is reloaded automatically, we add again the PDB, but this time we add two instances of the same PDB model. The first will be used for the solvent subtracted scattering curve without a solvation layer, and the second will be used only for the solvation layer contribution.

A Manual Symmetry model is added and then the second PDB model is placed within the manual symmetry model, which has, in this case, only one layer. In the second PDB model we will only calculate the solvation layer contribution. As you can see, we clicked on the "Solvent Only" option in the Parameter Editor pane, and we set the "Outer Solvent Electron Density" to one, and the "Solvent Electron Density" to zero.

The scale of the Manual Symmetry, which envelopes the solvation layer of the PDB structure, will essentially give us the electron density contrast between the solvation layer and the solvent.

We used four as our initial guess, and used constraints for the fitting.

The "Domain Scale" and the "Domain Constant" on the right pane are still mutable and will be fitted simultaneously.

After the initial generation of the signal we click "Fit". We open the console and see the iterations flying by.

The fitting is done, reached convergence, after two iterations. This of course takes much more time when you fit the solvation layer thickness as well. The solvation layer scale that best fit the data was three point nine eight.