

Global Analysis of AUC data

Homework Assignment:

(your chance to make up some points – the homework is worth 100 points)

Perform a complete global analysis of the demo1_intensity dataset using the appropriate workflow for all five triples with BSA signal (ranges: $s=1-10$, $f/f_0=1-4$, the defaults will work fine):

- 1. 2DSA+TI noise, 2. 2DSA + TI and RI noise, fitting both meniscus + bottom, 2DSA-IT**
- 2. report the bottom of the cell position as fitted in your 2D plot as shown in class for each of the 5 triples.**
- 3. perform a global fit as shown in class, but use a 2DSA-MC fit with 100 iterations, but without any additional noise fitting.**
- 4. report the total concentration (from Analysis Report) of the 2DSA-IT, 2DSA-MC-SG, 2DSA-MC-SC, and 2DSA-MC-VR models for each triple by comparing it in a bar plot for each triple (4 bars for each triple).**
- 5. report the RMSD of the 2DSA-IT, 2DSA-MC-SG, 2DSA-MC-SC, and 2DSA-MC-VR models for each triple by comparing them in a bar plot for each triple (4 bars for each triple). Make 4 discrete distributions overlay plots (one for each model type) for the s-value distributions for all 5 triples. **50 pts.****
- 6. explain what the results mean, based on the lecture notes in the 19th lecture. Knowing that the same sample was loaded, and all samples were at the same loading concentration in each triple, discuss which triple is an outlier (and why?); what gives rise to different concentrations? Why do we have different RMSD values for the different models? Can we determine from these results if the sample is reversibly self-associating - y/n? Why? Can we determine from these results if the sample is non-interacting - y/n? Why? Can we determine from these results if the centerpieces are identical - y/n? Why? Discuss your answers.**

Please type out your answers and provide a PDF document with the graphs included. **50 pts.**