**Instructions for Sedview**

To use Sedview:

1. Extract the Zip into any directory (or to the desktop)
2. Double-click on Sedview.exe to run the program.
   1. It will ask you to select a JPEG file to use as a logo in the Report that the program generates. The report and the use of a logo was added for companies. I’ve included a ReportLogo.JPG in the Zip file that can be used. Alternatively, you can click Cancel and the program will continue without using a logo. At this time, you will have to click Cancel every time you start the program (or find a JPEG you’d like to appear at the top of the report)… family photo maybe 😊
3. Follow the directions to select a ‘Root folder.’ This is the folder where the data directories will be found.
4. The program will list all of the directories that have XLI data in them in the top list box.
5. Select a directory by clicking on it
6. The program will list all of the data files in that directory, and radio buttons will appear that specify the types of data available, with the first button selected. A list of the files in the directory will show up in the list box at the lower left. Clicking on one of the files will graph the contents to the right. This is there just to let you preview raw data. If there are more than one sets (e.g. cells) of files in the directory, there will be a radio button for each file. You can click on these and view files as you wish.
7. Once you have selected which data to examine, click on the ‘Launch a viewer’ button and an analysis tab for that data set will appear.
   1. You can always go back to the ‘Select data’ tab… it is the blue tab at the top of the program.
8. Click on and drag the red ‘Meniscus’ bar and place it at the meniscus.
9. You are ready to look at your data as a g(s) graph.
   1. Click on the ‘Corrected t dc/dt’ tab and, voila, you should see the curve.
      1. Ignore the “Average t dc/dt’ and ‘Extrapolation’ tabs… they are not important, trickier to get to work and not of any real use (in my opinion).
      2. However, the “Time course” tab, allows you to view a ‘movie’ of your run, or view a movie of the analysis as a function of the run. This can be useful to see if there are bad scans, or a slow leak in your cell, etc.. The time course also is fun to view.
   2. If you want, you can change the Mw used for the analysis by clicking on the ‘Enter Mw for data span.’ I usually try this to see if the data can be made cleaner. Usually, I click it, enter a molecular weight, then unclick it if there is not a substantial change in the graph.
10. Select more data sets (they can be in different Root folders), and repeat steps 7 – 9.
    1. Notice that the graphs all have a ‘Copy to report button.’ Click on this and the graph image will be added to the report page (Report is the yellow tab at the top of the program).
11. To compare data, click on the ‘Compare’ tab (green tab at the top of the program)
    1. Select which data sets you wish to compare, then click the ‘Refresh data’ button to see the overlay of the selected scans.
    2. For data acquired at different concentrations, you will want to click the ‘Normalize data’ button. This will adjust the data so that the peak areas are all the same.
    3. Again, you can copy the graph to the report when you are done
    4. If your data do not superimpose, there is either:
       1. A problem in the raw data from one or more data sets (e.g. a leak), noisy scans, etc.
       2. If the t dc/dt curves shift towards higher s with increasing concentration, you have mass-action association in your system. This is thermodynamic proof of the interaction. Other programs (e.g. Sedphat) would need to be used to dissect/refine the analysis.
12. The ‘Report’ tab keeps track of which data sets you used, and contains any graphs you may have saved.
    1. You can edit this file and save it (it is an .RTF file, which can be read by Word, WordPerfect, WordPad). If you do not save it, it will be discarded when you exit the program.