Steps to Running Software:

1. Open a Terminal. This is done by opening the Finder, going to the Applications folder, opening the Utilities folder, and double clicking on “Terminal”.
2. Locate the file titled “drag\_me\_to\_terminal.py” that was downloaded from GitHub. Drag and drop this file into the Terminal.
3. Go to the Terminal and press the “Enter” key. This will begin running the software. (From here on, the software will guide you through using it)
4. Provide the prompt with the two times that data was collected at.
5. Select each of the data files to analyze.
6. Select the proteins to construct the network from.
7. Draw the network.
8. The simulation will begin. To see the status of it, the bottom line displayed in the Terminal should show “Run [X] out of 2000”. The simulation will complete when it reaches 2000.
9. Once complete, you may view the values of the flux between network connections by hovering over the arrows you drew previously.
10. The final results are created in a folder named after the time you began the simulation. The flux values can be found in the file titled “final\_fluxes.csv”. If desired, these can be visualized fairly easily using the free, open-source software CytoScape.