DONWLOADING:

1. Install gfortran using the following link: <https://gcc.gnu.org/wiki/GFortranBinaries>

You’ll see several options for installers. Select the one that corresponds to your operating system and follow all instructions for installation. You will have to ‘open’ the downloaded package to install it.

1. Install Xcode Command Line Tools. This does not *have* to be done ahead of time, running the code once should prompt you to install it. The following link provides helpful instructions: <http://railsapps.github.io/xcode-command-line-tools.html>

You can skip to the instructions titled “Install Xcode Command Line Tools” to install it.

1. Download the files to run the software from the following link: XXXX

THINGS YOU’LL NEED TO HAVE/KNOW:

1) Two .fcs files that will provide details of the expressions levels of different measured molecules and the names of these molecules.

2) The time after t=0 at which the data for the two .fcs files were collected (for example, 8 minutes and 16 minutes).

3) The network of molecules from your data you’d like to analyze.

4) Time. The simulation will take several hours, sometimes several days on slower computers. You can still use your computer for other tasks during this time, but be aware of the time requirements.