ABOUT THE LAB:

We will begin our study of graphs. First, we will become familiar with the adjacency matrix and its visualizations. Next, we will generate matrices stochastically and study them using in- and out-degrees and degree distributions.

Exercises:

1. Graphs and their adjacency matrix.
Download the Matlab file "clickgraph.m" from Lab 1. (It's under "Making a graph (M. Stobb)." Use this program to create the adjacency matrix for a graph with 7 nodes and 21 edges. Save the figure that shows the graph and also copy the adjacency matrix. Explain how the adjacency matrix represents or encodes the graph. Now draw the graph that is represented by the adjacency matrix

$$A = \begin{bmatrix} 0 & 1 & 0 \\ 1 & 0 & 1 \\ 1 & 0 & -0 \end{bmatrix}$$

2. Creating random graphs and saving the adjacency matrix.
We will talk about creating a random graph and saving the adjacency matrix. Download the m-file called "saving_data.m" from moodle. Use this to create the adjacency matrix for graph with 500 nodes. Save the graph as a .dat file and also as .mat. (You do not need to turn in anything from this exercise.)

3. Visualization of the graph.
Use the 'spy' command to look at the graph you created in Exercise 2. Now create a bio graph using the command 'BGobj = biograph(CMatrix)' and look at the graph using 'BGobjHandle = view(BGobj)'. Save both figures and turn them in. Explain how the figures represent the graph.

4. Degrees and degree distribution.
Find the indegree and outdegree of the nodes in your random graph. Turn in matlab script you write to do this. After you are done, you can go to Olaf Sporn's website (`http://www.indiana.edu/\~cortex/CCNL_main_menu.html`) and download his script 'degrees_und.m' from his 'Brain Connectivity Toolbox' (Connectivity Research to Brain Connectivity Toolbox to Network measures) to check your calculations.

5. Bioinformatics toolbox.
Look at the Graph Theory functions in the Bioinformatics toolbox of Matlab: `http://www.mathworks.com/help/toolbox/bioinfo/ref/a1052308804.html#bqur9d7-1` Choose one of the commands, describe what it does. Explain how you can use this function to explore a graph that represents a biological graph - i.e. what kind of information would this analysis provide and why would it be useful?