BIOE 210, Spring 2022

Homework 13

Due Monday, 4/25/2022 by 5:00pm. Upload your answers to Gradescope. If submitting a single PDF, you must mark the location of all answers.

You can use Matlab or a calculator to answer the following questions.

1. Consider the matrix

$$\mathbf{A} = \begin{pmatrix} 5 & 3 & 1 \\ 3 & 2 & 1 \\ 1 & 1 & 1 \end{pmatrix}$$

Use the following steps to calculate the leading eigenvector using the Power Iteration Method.

- (a) Choose a random, nonzero starting vector **b** and normalize it.
- (b) Multiply **b** by the matrix **A** and normalize the resulting vector.
- (c) Compute the associated eigenvalue λ_{max} using the Raleigh quotient

$$\lambda_{\max} = \frac{\mathbf{b} \cdot \mathbf{A}\mathbf{b}}{\mathbf{b} \cdot \mathbf{b}}$$

- (d) Go to step (b) and repeat for a total of 10 iterations.
- (e) Use Matlab to compute the eigenvectors and eigenvalues of the matrix **A**. Did you find the leading eigenvector?
- (f) Plot the value of λ_{max} for each iteration. How long does it take to converge?
- (g) Use the eigenvalue you computed with Matlab to explain the rate of convergence of your Power Iteration.

2. The following figure depicts protein-protein interactions in a human signal transduction network. Your goal is to find the most central and least central proteins in this network.



- (a) Construct an adjacency matrix to represent the connections in the network.
 - An adjacency matrix is a square matrix **A** such that each element *a*_{*ij*} equals 1 if node *i* is directly connected to node *j*.
 - Since the above graph is undirected, your adjacency matrix should be symmetric. If $a_{ij} = 1$, the $a_{ji} = 1$.
 - The diagonal elements (*a_{ii}*) must be left zero, since no node is "connected" to itself.
- (b) Calculate the leading eigenvector for the adjacency matrix. The leading eigenvector is associated with the eigenvalue with the largest magnitude.
- (c) Using the magnitude of the entries in the leading eigenvector, report the most central and least central proteins in the network. How does the centrality of these proteins compare with the number of connections involving these proteins? Is the most central protein always the protein with the largest number of direct connections?