

Assignment 2

BT5240 Computational Systems Biology | Jan - May 2025

Network Biology

February 11, 2025

Due Date: 25th February 2025, 5:00 PM

Maximum Marks: 25

Academic Integrity: You can discuss the problems verbally with your friends, but copying or looking at codes (either from your friend or the Web) is not permitted. Transgressions are easy to find and will be reported to the “Sub-committee for the Discipline and Welfare of Students” and dealt with very strictly. Mention any collaboration (discussions only!) in your solutions.

Submission: Since this is a computational assignment, we would also like to look at your codes. Submit your assignment as one zip file by uploading it at <https://tinyurl.com/bt5240-a2>. Your zip file should be named something like BTyyBxxx.zip based on your roll number. This zip file must contain a single neatly typeset PDF of your solutions (named BTyyBxxx.pdf), including well-annotated plots and figures of legible font size, as well as the codes used for each of the problems in a separate folder code with proper annotations.

Problem 1: Watts-Strogatz network vs. random network (10 marks)

Consider a Watts-Strogatz network with 100 nodes where each node is initially connected to 10 nearest neighbors. Investigate the following:

- A. Generate networks with rewiring probabilities $p = 0.3, 0.7,$ and 1.0 . For each network:
 - a. Calculate and plot the degree distribution
 - b. Compute the average clustering coefficient
 - c. Determine the characteristic path length
- B. Compare these networks with Erdős-Rényi random networks with the same nodes and edges. What conclusions can you draw about the network properties as p approaches 1.0 ?

Hint: Consider generating multiple random networks for comparison. Your analysis should include quantitative results and qualitative interpretation of the network properties.

Problem 2: Network centrality analysis (15 marks)

- a. Use the edge list of the E.coli transcription network given [here](#) and visualize the network with Matlab. The transcription network consists of operon and transcription factors and the type of regulation (Activator/ Repressor/ Both) of transcription factor on the operon (3 marks).
- b. Calculate the following properties for each node in the network and report the top five transcription factors according to each of these centrality measures. (6 marks)
 - i. Degree centrality
 - ii. Closeness Centrality
 - iii. Shortest Path Betweenness Centrality
- c. Compute the top five transcription factors that facilitate a higher fraction of activation in a network, remove the nodes, and recompute the properties in an activator network (3 marks)
 - i. Degree Distribution
 - ii. Degree Centrality
 - iii. Closeness Centrality
- d. Compute the top five transcription factors that facilitate a higher fraction of repression in a network, remove the nodes, and recompute the properties involving only repression and dual-type regulation (3 marks).
 - i. Degree Centrality
 - ii. Degree Distribution
 - iii. Closeness Centrality