BNFO 262 2024
Homework 2: single cell RNA-seq and Networks (Robert Morey and Hannah Carter)

Instructions
Answer the following questions in your own words and upload a PDF of your answers to Gradescope. Make sure to write your name and PID at the start of your answers. This assignment is due **2/15/24 at 9:00AM**.

Part 1: Single cell RNA-seq

1. Describe the experimental differences between droplet based methods and physical separation methods. Start by explaining each. Then discuss when it might be better to use one or the other. Limit 5 sentences. (3 points)

2. When analyzing scRNA-seq data, how do you know which cell a read comes from? Limit 5 sentences. (1 point)

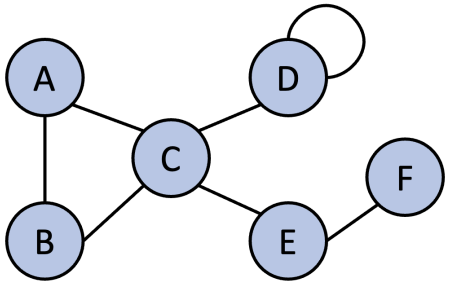
3. Describe what a doublet is and how it is generated. Why do you not want doublets in your dataset when you perform analysis? Limit 5 sentences.(2 points)

4. When preprocessing scRNA-seq data, there are multiple metrics to perform QC on. Please list three QC metrics and explain what each controls for? Limit 5 sentences. (3 points)

5. Come up with an experiment in which you'd prefer to use scRNA-seq rather than RNA-seq. Justify why you believe this assay would be preferable for this experiment. Limit 5 sentences. (2 points)

Part 2: Networks

6. Answer the following questions according to the graph (3 points)



   a. What is the adjacency matrix of this graph? (1 point)

   b. List the degree of each node in this graph (1 point)

   c. Which node has the highest degree of centrality? Why? (1 point)

7. Give an example of a biological network. Describe the node and edge. Explain what is the biological meaning of a node with high centrality in this network. Limit 5 sentences. (3 points)