**Each question carries 10 points**

**Total: 50**

**Total time: 2 hours**

1. Write a pseudocode for UPGMA (a phylogenetic tree construction algorithm). Derive the time complexity for the same.

2. Construct BWT matrix for “missippissi” and show how “is” can be searched efficiently using it. Answer pictorially.

3. Write a pseudocode for shortest common superstring (SCS) algorithm for genome assembly. Explain its loophole using an example.

4. Compute the time complexity of the Pattern Branching algorithm.

5. Write short notes (each carries 2.5 points).

A) Motif logo

B) Sequencing by synthesis

C) Epigenome

D) Maximum parsimony in context of phylogenetic tree construction