

## Algorithms for Comp. Biol. | End Semestral Examination

Time: 1 hour 30 minutes | Total points: 50

1. Answer ALL questions in brief (2 points each)

- a. What is an allele?
- b. Approximately what fraction of human DNA is protein coding?
- c. What do 5' and 3' mean?
- d. What is the role of DNA polymerase in NGS?
- e. What is 'transition'? What is 'transversion'?
- f. What is a 'contig'?
- g. What type of graph can be used to describe miRNA-mRNA interactions?
- h. State appropriate applications of local and global alignments.
- i. How does top down approach differ from bottom up approach in dynamic programming?
- j. What is the complexity of matrix multiplication operation? Explain in brief.

2. Answer any THREE questions. (10 points each)

- a. Write the steps for motif finding with Gibbs' sampling.
- b. Find the best local alignment between TCAGTTGCC & AGGTTG considering +1 for match, -2 for mismatch and -2 for gap. Show tracing of the alignment.
- c. Perform Burrows Wheeler Transform (BWT) of ACAACG. Show the steps of reversing the same.
- d. Given reads GTAAGTC & GTAAGAG construct the de Bruijn graph considering k-mer length as 5. Clearly chart the steps and figures.