In course examination

Fundamentals of Genomics and Proteomics, CSE: 4223

Handed on : 22-02-2021 Due on: 28-02-2021

Answering Guideline

Put all your code (preferably in Java) in a single file named (**roll_firstname.pdf**) and upload it in the classroom.

Answer the following questions Marks: 3×10=30

1. Consider the sequence v=TACGGGTAT and w=GGACGTACG. Assume that the match premium is +5 and that the mismatch and indel penalties are -5. Implement the dynamic programming algorithm for global alignment and show the tables for global alignment. Also show the score of this global alignment. **10**

2. Implement de Bruijn graph algorithm for finding shortest superstring of the following 3-mers {AGT, AAA, ACT, AAC, CTT, GTA, TTT, TAA}. **10**

3. Given a long test string *T*, one shorter pattern string *s*, and an integer *k*. Implement an algorithm to find the first occurrence in T of a string (if any) s' such that hamming distance $d_H(s, s') \leq k$. **10**