Cluster Innovation Centre, University of Delhi, Delhi-110007

Examination	: End Semester Examination – May 2022
Name of the Course	: B. Tech. (Information Technology and Mathematical Innovations)
Name of the Paper	: *in silico* Biology
Paper Code	: 32864404
Semester	: IV
Duration	: 2 Hours + 30 minutes
Maximum Marks	: 35

Instructions:

The first question is compulsory. Attempt any three from the rest (all of which carry equal marks).

1. Explain the following abbreviations: PUBMED, MSA, SRS, PDB, DDBJ (1X5=5)

2. What are Global and Local alignments? Name the two most common algorithms used for Global and Local alignments. If you are given two sequences which are evolutionary far distant from each other which alignment would you prefer and why?   (2+2+6=10)

3. Differentiate pBLAST and nBLAST. Why is BLAST so important in sequence analysis? Name two scoring matrices used in BLAST. What are the limitations of BLAST?   (2+2+2+4=10)

4. Draw a matrix for aligning COVIDNINETEEN and CALLNINEONEONE. Justify your scoring pattern and method of alignment.   (8+2=10)

5. What is a phylogenetic tree? How is it different from a family tree? Differentiate the Distance, Maximum Likelihood and Maximum Parsimony methods.   (2+2+6=10)

6. Explain with examples/diagrams/flowcharts any five of the following:
Rigid Docking, DNA Profiling, Dynamic Programing, Bootstrapp, Proofreading, FASTA.   (2X5=10)