M. Sc. Bio-Technology Examination 1st Year 2nd Semester, 2023
BIOINFORMATICS
PAPER- SC/BT/PG/235T/2023
Answer all the questions.
Total Marks – 40

1. Answer **any ten** questions: 10×1=10

a) Name the methods used for predicting the Tertiary structure of a globular protein.
b) What makes BLAST more useful than FASTA for database search?
c) What is the basic structure of a GenBank and an EMBL entry?
d) Define propensity scores in the secondary structure of a protein.
e) For what purpose BLOSUM matrices are used?
f) What is the PSIPRED tool?
g) Write a note on RMSD.
h) If you want to BLAST the non-redundant database using a new protein sequence as a query, which is the BEST search program to use?
i) blastp ii) blastn iii) tblastx iv) blastx
i) Submission to GenBank include
i) Sequin and Banklt ii) Sequin
iii) Banklt iv) Banktl and sequeen
j) Write a note on the importance of SWISS-MODEL for protein structure prediction.
k) What is the T-Coffee algorithm?
l) Define the "Sum of pairs" method for scoring the multiple sequence alignments

2. Answer ***any five*** of the following: 5×2=10

a) Write the two most commonly used scoring matrices.
b) Write down the differences between CLUSTALW and MUSCLE in multiple sequence alignments.
c) What are the phylogenetic tree construction methods that use direct sequence information?
d) What are Cladogram and Phylogram in phylogenetic analysis? Explain with schematic diagrams.
e) Write a short note on the two most important methods used in protein structure classification.
f) Define the Progressive alignment method and its cons and pros in multiple sequence alignments.

3. Answer ***any three*** of the following: 4×3=12

a) Write a short note with a schematic diagram of Chou–Fasman and GOR methods. 2+2
b) What are Homologs, Paralogs, and Orthologs? Explains them with examples. 2+2
c) Describe the wire-frame diagram, Balls and sticks, space-filling representation, and Ribbon diagrams of the protein structure. 4
d) Define the Total Score, Max Score, Query coverage and E-value, and Identity in the context of sequence alignment 4
e) Define the Markov chain and Viterbi algorithm in multiple sequence alignments. 2 +2

4. Answer ***any one*** of the following: 8×1=8

a) What would be an optimal alignment of the following two sequences using a Dynamic programming algorithm (with diagram)
Sequence A: CAATTGA
Sequence B: GAATCTGC 8
b) Define with the schematic diagram on the *ab-initio* and template-based modeling on the tertiary structure of proteins 4+ 4

c) Write a note on Position-Specific Scoring Matrices (PSSMs), Profiles, and Hidden Markov Models (HMMs) 8