

S.No. 6123

P 16 BTE 2

(For candidates admitted from 2016–2021 Batch)

M.Sc. DEGREE EXAMINATION, NOVEMBER 2023.

Biotechnology — Elective

BIO INFORMATICS

Time : Three hours

Maximum : 75 marks

SECTION A — (10 × 2 = 20)

Answer ALL questions.

1. Define NCBI.
2. Define DNA.
3. Tomology.
4. Paralogues.
5. FASTA.
6. MSF.
7. Motif.
8. Sequence alignment.
9. HMM.
10. Neighbouring joining.

SECTION B — ($5 \times 5 = 25$)

Answer ALL questions, choosing either (a) or (b).

11. (a) Write a note on role of Internet and WW in bio-informatics.

Or

- (b) Give an account on basic concept of protein and amino acids.

12. (a) Write a basic concept of sequence similarity, identity, homology of paralogues.

Or

- (b) Write a basic concept of sequence similarity, identity, homology of orthologues.

13. (a) Write a short note on analysis tool for assign homology using database search engine for BLASTA.

Or

- (b) Write short note on bio molecular sequences of GCG.

14. (a) Explain in details on basic concept and sequence pattern and profile of consensus and regular expression.

Or

- (b) Explain the concept of behind multiple sequence alignment of clustalW and TCOffee.

15. (a) Write the advantage and disadvantage of various sequence analysis method.

Or

- (b) Write the uses of assigning the homology of hidden Markov model.

SECTION C — ($3 \times 10 = 30$)

Answer any THREE questions.

16. Give a brief account on organization of databases of data contents, purpose and utility.

17. Give a brief account on basic concepts of sequence similarity of PAM and matrices.

18. Write a detailed note on various file formats and storing sequences of bio-molecular sequence with four examples.

19. Give a brief note on pairwise alignment methods of Smith-Water-man and Needle man Wunsch.

20. Give a brief account on Phylogenetic tree, Neighbouring joining and UPGMA.