Avinashilingam Institute for Home Science and Higher Education for Women

(Deemed to be University under Category 'A' by MHRD, Estd. u/s 3 of UGC Act 1956)
Re-accredited with 'A+' Grade by NAAC. Recognised by UGC Under Section 12B
Coimbatore - 641 043, Tamil Nadu, India

Bachelor's Degree Examination – August 2020
VI Semester

Class : III UG **Time : 2 Hours**
Major : Biochemistry and Biotechnology **Max. Marks: 50**

15BBTC16 Computational Biology

Part A 10 x 1 = 10
Choose the Correct Answer

1. A single piece of information in database is known as
   a. file b. field
   c. record d. data set

2. A database of current sequence map of the human genome is called as
   a. OMIM b. HGMD
   c. Golden path d. Gene cards

3. Which of the following is a protein sequence database?
   a. DDBJ b. EMBL
   c. GenBank d. PIR

4. Which of the following is a sequence alignment tool?
   a. BLAST b. PRINT
   c. PROSITE d. PIR

5. Which of the following is not a protein sequence database?
   a. PIR b. PSD
   c. Swiss prot d. EMBL

6. Margaret Dayhoff developed the first protein sequence database called
   a. Swiss prot b. PDB
   c. Atlas of protein sequence anstructure d. Protein sequence database

7. Alignment method suitable for aligning closely related sequence is
   a. multiple sequence b. pair wise
   c. global d. local

8. All are sequence alignment tools except
   a. Rasmol b. BLAST
   c. FASTA d. Clustal W

9. ------ is the smallest amino acid, has a hydrogen atom as the R group.
   a. Valine b. Proline
   c. Glycine d. Threonine

10. A linear polymer of more than 50 amino acid acids are referred as
    a. dipeptide b. oligopeptide
    c. peptide d. polypeptide

Part B

3 x 6 = 18

Answer Any Three questions

Each answer should not exceed 400 words or two pages

11. Write about the history of Bioinformatics.
12. Enlist the problems faced in bioinformatics and its applied research.
13. Explain nucleotide sequence databases.
14. Explain the data retrieval tools.
15. Illustrate dot plot sequence alignment method.
16. Write a note on local alignment.
17. Write a note on phylogenetic tree construction.
18. Demonstrate global pair wise alignment.
19. Discuss the parameters employed in structural analysis of proteins.
20. Write a note on Rasmol.

Part C

2 x 11 = 22

Answer Any Two questions

Each answer should not exceed 800 words or four pages

21. Discuss in detail about the opportunities in bioinformatics.
22. Write an account on knowledge discovery and data mining.
23. Write an essay on structural databases.
24. Give a brief account types of biological databases.
25. Explain the application of FASTA tool.
26. Discuss in detail about BLAST.
27. Write an essay on progressive alignment method.
28. Explain PHYLIP and its role in phylogenetic tree construction.
29. Explain 3D analysis of biomolecules.
30. Write an account characterization and comparison of on CPK.

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