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 June – 2021
VI Semester

Class : III UG **Time : 3 Hours**
Major : Biochemistry & Biotechnology **Max. Marks: 100**

18BBTC16 Computational Biology

Course Outcomes:

1. Understand Bioinformatics and its applications in Pharmaceutical industry.
2. Familiar with biological databases , data storage and querying.
3. Understand algorithms and applying tools in sequence analysis.
4. Apply Bioinformatics tools and interpret results.

Part A 10 x 1 = 10
Choose the Correct Answer

1.Label the establishment year of European Bioinformatics Institute CO1 K1
a.1994 b. 1984
c. 1987 d.1997

2. Identify the funding agency of Human Genome Mapping Project – Resource Centre CO1 K1
a.USA Medical Research Council b. UK Medical Research Council
c. Japan Medical Research Council d. German Medical Research Council

3. Select the Protein sequence database CO2 K1
a. EMBL b. Gen Bank
c. PIR d. DDBJ

4. Name the level of CATH hierarchy gives a description that encompases both the overall shape and the connectivity of secondary structure CO2 K1
a. Architecture b. Class
c. Topology d. Homology

5. Identify the local Alignment technique. CO3 K1
a. Needleman and Wunsch Algorithm b. Smith and Wunsch Algorithm
c. Needleman – Waterman Algorithm d. Smith – Waterman Algorithm

6. Select the type of BLAST searches protein sequence databases for polypeptide sequences. CO2 K1
a. BLASTP b. BLASTN
c. BLASTX d. TBLASTX

7. Name the phylogenetic tree concept specifies relationships among things, but not evolutionary paths CO3 K1
a. Rooted tree b. Un rooted tree
c.Internal nodes d. Leaves

8. Locate the method used to develop a phylogenetic tree in CLUSTAL. CO3 K1
a. Maximum parsimony method b. Maximum Likelihood
c. Fitch – Margoliash Method d. Neighbor – Joining Method

9. Name the molecular visualization form, which shows the flat arrows to represent β Strands. CO4 K1
a. Wire – frame diagram b. Balls and Sticks
c. Space – filling spheres d. Ribbon diagrams

10. Which of the following is molecular visualization? CO4 K1
a. Rasmol b. BLAST
c. FASTA d. CLUSTALW

Part B 5 x 6 = 30

Answer ALL questions

Each answer should not exceed 400 words or two pages

11.a. Write short notes on data mining. CO1 K3
(or)
11.b. Explain the problems, which are faced in Bioinformatics area. CO1 K2

12.a. Discuss in detail on the protein database PIR. CO2 K2
(or)
12.b. Examine the role of TIGR in Human Gene Index. CO2 K3

13.a. Show the steps in the global alignment of sequence analysis. CO3 K2
(or)
13.b. Illustrate the FASTA programs in similarity searches. CO3 K2

14.a. List out the applications of multiple sequence alignment. CO3 K3
(or)
14.b. Explain the rooted and un rooted tree concepts in phylogenetic analysis. CO3 K3

15.a. Sketch the various molecular visualization forms. CO4 K3
(or)
15.b. Examine the importance's of PDB file format in molecular visualization. CO4 K3
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Part C 5 x 12 = 60

Answer ALL questions

Each answer should not exceed 800 words or fourpages

16.a. Explain in detail on various opportunities in Bioinformatics. CO1 K4
(or)
16.b. Evaluate the important role of Bioinformatics in Pharmaceutical industries. CO1 K4

17.a. List out and explain the structural databases. CO2 K3
(or)
17.b. Write in detail on different types of Nucleotide sequence databases. CO2 K3

18.a. Outline the approaches of Dot plot in comparison of two sequences. CO3 K4
(or)
18.b. Illustrate the important concepts of BLAST program . CO3 K4

19.a. Summarize the steps in phylogenetic tree construction. CO3 K5
(or)
19.b. Explain the multiple sequence alignment by CLUSTAL progressive method. CO3 K4

20.a. Illustrate the protein structure databases in detail. CO4 K4
(or)
20.b. Write in detail on RasMol. CO4 K3

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