Avinashilingam Institute for Home Science and Higher Education for Women
Coimbatore – 641 043
Continuous Internal Assessment I – February 2025
Semester - II

Class : I PG **Max. marks : 60**
Major : Biotechnology **Time : 2 hours**

23MBTC09 – Bioinformatics

Course Outcomes:

After completing this course, the student will:

1. Explain the contents and layout of the important biological databases and to search and retrieve.
2. Apply bioinformatics tools for sequence alignment and to find the evolutionary relationships
3. Explain the theory behind the gene-finding tools, different types of genomics and proteomics
4. Understand the steps involved in the analysis of structures of biomolecules and predicting their secondary and tertiary structures with various bioinformatics tools.
5. Develop a protein model/design a drug and predict its structure and function with various tools.

Part – A (6 x 1 = 6)

Answer the following

1) ___________is a database of current sequence map of human genome (CO1; K1)

(a) OMIM (b) HGMD (c) Golden Path (d) GeneCards

2) BLAST program is used in (CO2; K2)

(a) DNA sequencing (b) Amino acid sequencing (c) DNA barcoding (d) Bioinformatics

3) Alignment method suitable for aligning closely related sequence is (CO2; K1)

(a) Multiple sequence alignment (b) Pairwise alignment

(c) Global alignment (d) Local alignment

4) All are sequence alignment tools except (CO2; K4)

(a) Rasmol (b) BLAST (c) FASTA (d) Clustal W

5) Which of the following is NOT a gene finding program? (CO4; K1)

(a) GeneMark (b) GeneLynx (c) GenScan (d) GRAIL

6) Which of the following is NOT a secondary structure prediction method for proteins? (CO4; K2)

(a) SOPMA (b) GOR (c) PSSpred (d) Mfold

Part – B (3 x 6 = 18)

Answer ALL questions.

Answer should not exceed 200 words or one page.

7) a) Comment on the branches and applications of bioinformatics. (CO1; K3)

Or

7) b) Give an account on Entrez. (CO2; K4)

8) a) Write a note on global alignment algorithms. (CO2; K2)

Or

8) b) Discuss about PAM and BLOSUM. (CO4; K6)

9) a) Write a note on ORF databases. (CO2; K1)

Or

9) b) Write a note on primer designing. (CO3; K4)

Part – C (3 x 12 = 36)

Answer ALL questions.

Answer should not exceed 600 words or three pages.

10) a) Write an elaborate note on genome and literature databases. (CO1; K2)

Or

10) b) Explain in detail about classification of biological databases. (CO2; K3)

11) a) Elaborate the need and importance of sequence alignment and add a note on pairwise alignment. (CO2; K2)

Or

11) b) Give an account on multiple sequence alignment. (CO2; K4)

12) a) Discuss the approaches used by popular gene finding programs. (CO4; K6)

Or

12) b) What are the methods developed for the prediction of RNA secondary structure? (CO5; K3)

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Staff in-charge: Dr.A.Shobana **No. of copies: 10**