



Avinashilingam Institute for Home Science and Higher Education for Women

Deemed to be University Estd. u/s 3 of UGC Act 1956, Category 'A' by MHRD (now MoE)

Re-accredited with 'A++' Grade by NAAC. CGPA 3.65/4, Category I by UGC

Coimbatore - 641 043, Tamil Nadu, India

**Continuous Internal Assessment Test I – February 2025
Semester-II**

**Class: I PG
Major: Biotechnology**

**Time: 2 hours
Max. marks: 60**

23MBTC09–Bioinformatics

Course Outcomes:

After completing this course, the student will:

CO1: Explain the contents and layout of the important biological databases and to search and retrieve.

CO2: Apply bioinformatics tools for sequence alignment and to find the evolutionary relationships

CO3: Explain the theory behind the gene-finding tools, different types of genomics and proteomics

CO4: Understand the steps involved in the analysis of structures of biomolecules and predicting their secondary and tertiary structures with various bioinformatics tools.

CO5: Develop a protein model/design a drug and predict its structure and function with various tools.

Part– A

(6 x 1= 6)

Choose the correct answer

- 1) _____ is a database of current sequence map of human genome (CO1; K1)
(a) OMIM (b) HGMD (c) GoldenPath (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 sequences 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) ClustalW
- 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.

Answers should not exceed 400 words or two pages

- 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

(3x 12 = 36)

Answer ALL questions.

Answers 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)

Staff in-charge: Dr.A.Shobana

No. of copies: 10