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

Continuous Internal Assessment – I February, 2025

II Semester

Class: I PG **Time: 2 Hours**
Branch: Zoology **Max. Marks: 60**

23MZOC10 Bioinformatics

Course Outcomes:

CO1	Locate and use the main databases at the NCBI and EBI resources and know the difference between databases, tools, repositories and be able to use specific information
CO2	Extract data from specific databases using accessions numbers and gene names
CO3	Able to perform simple genome sequence analyses using existing tools
CO4	Interpret correctly the outputs from tools used to analyse biological data and make meaningful predictions from these outputs.
CO5	Able to describe and comprehend the fundamental concepts of molecular modelling and computational driven drug discovery

Part A 6 x 1 = 6

Choose the Correct Answer

1. The primary nucleotide sequence database is CO1 K1
   a) PDB b) DDBJ c) BLAST d) UniRef
2. What data does PDB provide? CO1 K1
   a) Genomic data b) 3D structures c) Protein families d) RNA sequences
3. FASTA used to search similar sequences in CO1 K2
   a) DNA or Protein b) Nucleotides c) RNA d)mRNA
4. Bioinformatics tool used for phylogenetic analysis is CO2 K2
   a) GLSEARCH b) PANTHER c) t blast n d) FASTX, FASTY
5. Which method is used for the graphical method for assessing similarity? CO2 K1
   a) BLOSUM b) BLOSUM80 c) TreeFam d) DOTPLOT
6. Which of the following organizations was involved in the HGP? CO3 K2
   a) RCSB b) NIH c) EBI d) NLM

Part B 3 x 6 = 18

Answer ALL questions
Each answer should not exceed 400 words or two pages

7. a)Compare and contrast nucleotide sequence databases (GenBank and EMBL) CO1 K5

OR

7. b)Explain the applications of FASTA and BLAST CO1K4

8. a)Explain the role of GEO and OMIM in genome expression studies CO1 K4

OR

8 b) Discuss about CLUSTALW in Multiple sequence alignment CO2 K2

9. a) Write an account on the scope of Pharmacoinformatics CO1 K3

OR

9. b)Write short notes on goals and applications of HGP CO3 K3

Part C 3 x 12 = 36

Answer ALL questions
Each answer should not exceed 800 words or four pages

10. a)Discuss the importance of PDB, and InterPro CO1 K2

OR

10. b)Give notes on PAM and BLOSUM scoring matrices CO2 K2

11. a)Explain Pair wise sequence Alignment methods CO2 K4

OR

11. b)Describe any two the protein sequence Databases CO1 K2

12. a) Compare and contrast eukaryotic, bacteria, archaea and viral genomes CO3 K5

OR

12. b)Explain the main steps involved in constructing a Phylogenetic tree CO2 K4

No. of Copies: 20 **Name of the staff: Dr. K.S.Santhy**