Avinashilingam Institute for Home Science and Higher Education for Women
Coimbatore - 641043.

Master's Degree Examination – NOVEMBER 2017
First Semester

Class : I PG **Time: 3 hours**
Major : Bioinformatics **Max. Marks: 60**

17MBIC04-Basic Bioinformatics

Part-A (10 x 1/2 = 5)

Choose the correct Answer

1. Literature databases include
   (a)PubMED and PDS (b) MEDLINE and PDB (c)MEDLINE and PubMED (d)PubMED and PDB
2. The information retrieval tool of NCBI GenBank is
   (a)Entrez (b)STAG (c)Seqin (d)Text Search
3. Which of the following is a sequence alignment tool provided by NCBI
   (a)Chime (b)BLAST (c)FASTA (d)ClustalW
4. BLOSUM matrices are used for
   (a)Multiple sequence alignment (b)Pairwise sequence alignment (c) Phylogenetic analysis (d) All of the above
5. Which of the following gene finding signals is not used in prokaryotic gene finding methods?
   (a) ORF (b) Pribnow box (c) Poly-A tails (d) Stop codon
6. Which of the following is not a stop codon?
   (a)TAG (b)TAA (c)TGA (d)ATG
7. The most common secondary structure seen in proteins
   (a)alpha helix (b)beta-pleated sheet (c)beta-pleated sheet parallel (d)beta-pleated sheet non parallel
8. The anticodon region is an important structural component of
   (a) mRNA (b) tRNA (c) rRNA (d)DNA
9. Which of the following is a molecular visualization tool?
   (a) RasMol (b)SWISS-PROT (c) PDB (d) BLOSUM
10. Homology modelling of a target protein requires
    (a)Only target sequence (b)Good alignment between target and template sequence (c) Poor alignment between target and template sequence (d) Template without a known structure

Part-B (5 x 4 =20)

Answer ALL questions.

Each answer should not exceed 200 words or one page

11. (a)Write an account of MSDN.

Or

(b)Explain in brief any two specialized databases in bioinformatics.

12. (a)Explain the utility of motifs and pattern search in protein bioinformatics.

Or

(b) Describe in brief the principles and tools for phylogenetic analysis.

13. (a)Discuss in brief restriction mapping.

Or

(b)Discuss the features of standard codon table.

14. (a)Discuss briefly the methods and tools for prediction of 3D structure of proteins and nucleic acids.

Or

(b)Explain the usage of PredictProtein, ssPRED and SOPMA in predicting protein structure.

15. (a) Explain in detail the simulation of enzyme-substrate complex.

Or

(b)Discuss in brief the stereodynamic concepts of molecular interactions

Part-C (5 x 7 =35)

Answer ALL questions.

Each answer should not exceed 600 words or three pages

16. (a)Explain in brief the classification of biological databases. Or
(b)Describe the application of bioinformatics databases for storage and analysis of biological data

17. (a)Expand and explain the usage of BLAST. Or
(b)Discuss the scoring and substitution matrices used for protein sequence alignment.

18. (a)Explain the principles of primer design in bioinformatics. Or
(b)Discuss the various gene finding methods and tools in bioinformatics.

19. (a)Explain the structural classification of proteins. Or
(b)Discuss in brief the methods for structure prediction of rRNA.