

**Avinashilingam Institute for Home Science and Higher Education for Women  
(Deemed to be University), Coimbatore – 641 043**

**Semester Examination- November 2018  
Semester – I**

**Class: I PG  
Major: Bioinformatics**

**Max. Marks: 60  
Time: 3 hours**

**17MBIC04 BASIC BIOINFORMATICS**

**Part - A  
Choose the correct answer**

**(10 X 1/2 = 5)**

1. Which of the following is a Pair wise sequence alignment tool?  
a) Clustal W                      b) PDB                      c) Chime                      d) BLAST
2. The sequence retrieval tool of NCBI Genbank is  
a) Entrez                      b) Seqin                      c) text search                      d) STAG
3. Which algorithm is used by local alignment?  
a) Needleman and Wunsch                      b) PAM  
c) Smith-Waterman                      d) All the above
4. Define PAM.  
a) Parallel Align Mutation                      b) Point Altered Mutation  
c) Point Accepted Mutation                      d) Point Arranged Mutation
5. PRINTS are software used for  
a) Detection of genes from genome sequence                      b) Detection of tRNA genes  
c) Prediction of function of a new gene                      d) Identification of functional domains/motifs of proteins
6. Which of the following is a protein domain database  
a) PDB                      b) NCBI                      c) UniProtKB                      d) Pfam
7. Which of the following is NOT a secondary structure of RNA?  
a) Hairpin loop                      b) Bulge loop                      c) Inverse loop                      d) Multifurcation loop
8. Which of the following a tool for secondary structure prediction.  
a) Modeller                      b) SWISS Model                      c) SOPMA                      d) Clus Pro
9. The most commonly used database of atom coordinate information of protein structure is  
a) PIR                      b) Swiss-Prot                      c) PDB                      d) Prot3D
10. Deep view is more popularly referred to as  
a) Spdbv                      b) Weblab Viewer                      c) mm3D Viewer                      d) RasMol

**Part B**

**(5 X 4 = 20)**

**Answer all questions**

**Answer should not exceed 200 words or one page**

11. (a). Write short notes on Microbial and cellular databanks.

or

11. (b). Write notes on the databases available for proteins

12. (a). Write short notes on PAM and BLOSUM.

or

12. (b). What is multiple sequence alignment? Explain the different approaches.

13. (a). Write short notes on the gene finding methods.

or

13. (b). Write notes on restriction mapping.

14. (a). Write short notes on Secondary structure and folding classes.

or

14. (b). Give the features of any one protein structure prediction tool.

15. (a). Discuss on simulation of substrate-ligand binding

or

15. (b). Write short notes on force field.

**Part C**

**(5 X 7 = 35)**

**Answer all questions**

**Answer should not exceed 600 words or three pages**

16. (a). Write in detail about database searching.

or

16. (b). What are biological databases? Explain its types in detail.

17. (a). What is alignment? Explain in detail about local and global alignment.

or

17. (b). Elaborate the phylogenetic tree construction methods.

18. (a). What are protein motifs? Explain the motif prediction methods.

or

(b). Explain in detail about codon distribution and codon bias.

19. (a). What is structure prediction? Explain the methods for predicting the three dimensional structure of proteins

or

(b). Explain in detail the RNA secondary structure prediction methods.

20. (a). Explain the features of Rasmol for the visualization of Biomolecules

or

(b). Explain in detail on virtual reality and its applications

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