

Shree Manibhai Virani and Smt. Navalben Virani Science College (Autonomous), Rajkot
Affiliated to Saurashtra University, Rajkot

SEMESTER END EXAMINATION APRIL - 2018

M.Sc. Microbiology / M.Sc. Biotechnology

16PMBCC14 / 16PBTCC14 - BIOINFORMATICS

Duration of Exam – 3 hrs

Semester – IV

Max. Marks – 70

Part A (5x2= 10 marks)

Answer **ALL** questions

1. Define biological databases? Differentiate between primary and secondary databases?
2. What do you mean by sequence alignment? Give the example.
3. Differentiate between pair wise and multiple sequence alignment.
4. Define Molecular Phylogeny?
5. What do you mean by molecular docking?

Part B (5x5= 25 marks)

Answer **ALL** questions

- 6a. Explain Regular expression with suitable example.

OR

- 6b. Write a note on important secondary databases?

- 7a. Explain the types and algorithm of any sequence similarity search tool.

OR

- 7b. Write a note on Drug Bank databases?

- 8a. Discuss different types of scoring matrices used in the sequence alignment.

OR

- 8b. Explain the principle for PCR Primer Designing.

- 9a. Describe bootstrap method for phylogenetic tree evaluation?

OR

- 9b. Explain the concept of sequence homology and their types along with suitable examples.

- 10a. Describe structural bioinformatics in detail?

OR

- 10b. Explain protein secondary structure prediction methods in detail.

Part C (5x7= 35 marks)

Answer **ALL** questions

11a. Explain Genbank flat file in detail

OR

11b. Write down the names of members of INSDC? And discuss the EMBL file format in detail?

12a. Perform the global alignment between two sequences S1=CGTAGC and S2 =CTAGC. Apply the scores for match, mismatch and gap as 1, 0 and -1 respectively.

OR

12b. Outline the difference between global and local alignment. Explain the global alignment algorithm to generate the optimal global alignment.

13a. Discuss the Protein Databank in detail.

OR

13b. Explain multiple sequence alignment in detail.

14a. Describe distance based phylogenetic analysis by using UPGMA method?

OR

14b. Discuss in detail about Character based methods in phylogenetic Analysis?

15a. Explain homology modeling in detail? Discuss any one method in detail? Also mention the software available in public domain.

OR

15b. Discuss the drug discovery process in detail with emphasis.
