Enrollment No.

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 hrsSemester - IVMax. Marks - 70

<u>Part A</u> (5x2= 10 marks) Answer <u>ALL</u> 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?

<u>Part B</u> (5x5= 25 marks)

Answer <u>ALL</u> 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.

<u>Part C</u> (5x7= 35 marks) Answer <u>ALL</u> 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.