

**GUJARAT TECHNOLOGICAL UNIVERSITY****BE - SEMESTER-VI (NEW) - EXAMINATION – SUMMER 2017****Subject Code: 2160410****Date: 08/05/2017****Subject Name: Bioinformatics - Department Elective I****Time: 10:30 AM to 01:00 PM****Total Marks: 70****Instructions:**

1. Attempt all questions.
2. Make suitable assumptions wherever necessary.
3. Figures to the right indicate full marks.

**MARKS**

<b>Q.1</b>	<b>Short Questions</b>	<b>14</b>
	1 What is the role of CpG island in bioinformatics?	
	2 Define: Evolutionary systematics	
	3 What is rooted tree and unrooted tree?	
	4 Enlist any two library databases.	
	5 Give the optimality criteria for maximum parsimony method.	
	6 Name any two sequence alignment tools.	
	7 GeneBank is maintained by _____.(Fill in the gap)	
	8 _____ is the protein structure database. (Fill in the gap)	
	9 Nucleotide sequence submission system and Mass Submission system are submission tools of _____. (Fill in the gap with options: GenBank, DDBJ, EMBL, UniProt)	
	10 What is the significance of P value and E Score?	
	11 Smith-Waterman Algorithm algorithm is used for global alignment. Is this true?	
	12 Motifs are independently stable. Is this statement true?	
	13 What does divergence of protein means?	
	14 Define domain swapping.	
<b>Q.2</b>	(a) What is bootstrapping?	<b>03</b>
	(b) How does molecular biology relate the bioinformatics?	<b>04</b>
	(c) Enlist and explain the databases for Protein.	<b>07</b>
	<b>OR</b>	
	(c) Write a note on: ENTREZ	<b>07</b>
<b>Q.3</b>	(a) What is global and local alignment? Give example and explain.	<b>03</b>
	(b) Give the functions of NCBI and write about its major contribution to the Bioinformatics fraternity.	<b>04</b>
	(c) Summarize the usefulness of bioinformatics tools/software for agricultural and medical fields.	<b>07</b>
	<b>OR</b>	
<b>Q.3</b>	(a) Give the base for gene prediction? How does Exon and Introns contribute in that?	<b>03</b>
	(b) Differentiate between <i>Smith-Waterman</i> and <i>Needleman-Wunsh</i> algorithm.	<b>04</b>
	(c) Discuss gene prediction tools.	<b>07</b>

- Q.4** (a) Narrate the basic features of SRS. **03**  
(b) Enlist and explain the domains of Proteomics. **04**  
(c) Narrate the steps for GOR-IV and Chau-Fasman methods. **07**

**OR**

- Q.4** (a) Give the importance of scoring matrix. **03**  
(b) What is the molecular phylogeny? **04**  
(c) What are the methods to predict the genes? Explain any one of them. **07**

- Q.5** (a) Narrate the principle of 2D-PAGE. **03**  
(b) Write the steps for drug discovery. **04**  
(c) What is the role of SNP in bioinformatics? **07**

**OR**

- Q.5** (a) Write a note on: DNA microarrays **03**  
(b) Exemplify the homologs and orthologs. **04**  
(c) Discuss the steps of homology modeling. **07**

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