

# GUJARAT TECHNOLOGICAL UNIVERSITY

BE - SEMESTER-VI(NEW) – EXAMINATION – SUMMER 2019

**Subject Code:2160410**

**Date:21/05/2019**

**Subject Name: Bioinformatics**

**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.

- Q.1**
- |     |  |           |
|-----|--|-----------|
| (a) | Give the historical overview of Bioinformatics.          | <b>03</b> |
| (b) | What is consensus sequence?                              | <b>04</b> |
| (c) | Briefly explain the role of NCBI. Further, discuss MMDB. | <b>07</b> |

- Q.2**
- |     |  |           |
|-----|--|-----------|
| (a) | Enlist the tools of Entrez.  | <b>03</b> |
| (b) | Write with an example: global alignment.                                     | <b>04</b> |
| (c) | Discuss the importance of molecular biology in understanding bioinformatics. | <b>07</b> |

**OR**

- Q.3**
- |     |   |           |
|-----|---|-----------|
| (c) | For what attributes, do the phylogenetic analysis help?   | <b>07</b> |
| (a) | What is cladistics and systemics?   | <b>03</b> |
| (b) | How is the score calculated for BLAST and transition-transversion matrices?                             | <b>04</b> |
| (c) | Explain the terms: target identification and validation, lead molecule identification and optimization. | <b>07</b> |

**OR**

- Q.3**
- |     |   |           |
|-----|---|-----------|
| (a) | Describe Hidden Markov Model.                       | <b>03</b> |
| (b) | Narrate the major features of PDB.                  | <b>04</b> |
| (c) | Give the importance of multiple sequence alignment. | <b>07</b> |
- Q.4**
- |     |   |           |
|-----|---|-----------|
| (a) | Write the steps of <i>Chau-Fasman</i> method for secondary structure prediction.  | <b>03</b> |
| (b) | What is DNA microarray?   | <b>04</b> |
| (c) | Make a clear list of applications of Bioinformatics and briefly important of all. | <b>07</b> |

**OR**

- Q.4**
- |     |  |           |
|-----|--|-----------|
| (a) | Make a list of all the tools for gene prediction.                              | <b>03</b> |
| (b) | Discuss maximum parsimony method representing phylogeny.                       | <b>04</b> |
| (c) | What are the major tools or techniques in proteomics? Explain any two of them. | <b>07</b> |
- Q.5**
- |     |  |           |
|-----|--|-----------|
| (a) | “Protein structure is related with its function”. Discuss briefly. | <b>03</b> |
| (b) | Write the steps for GOR IV method.                                 | <b>04</b> |
| (c) | What is Single nucleotide polymorphism? Explain.                   | <b>07</b> |

**OR**

- Q.5**
- |     |  |           |
|-----|--|-----------|
| (a) | Define: Progressive alignment.   | <b>03</b> |
| (b) | What is clinical trial? What are its phases?                             | <b>04</b> |
| (c) | Explain the types of proteomics studies, based on their characteristics. | <b>07</b> |

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