Reg. No. \_\_\_\_\_\_\_\_\_\_\_\_\_



**End Semester Examination – Nov / Dec – 2019**

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| **Code :** | **17BI2001** | **Duration :** | **3hrs** |
| **Sub. Name :** | **ANALYTICAL BIOINFORMATICS** | **Max. Marks :** | **100** |

**ANSWER ALL QUESTIONS (5 x 20 = 100 Marks)**

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| **Q. No.** | **Sub Div.** | **Questions** | **Course**  **Outcome** | **Marks** |
| 1. | a. | Breifly describe the importance and scope of bioinformatics. | CO1 | 6 |
| b. | Explain in detail the types of databases that are used in bioinformatics. | CO5 | 6 |
| c. | Write a short note on elementary commands and protocols of internet. | CO1 | 8 |
| **(OR)** | | | | |
| 2. | a. | Let S1= AATTCGCGTA & S2 = TATCGCTACA(a) Build the complete dynamic programming table for these strings . | CO2 | 4 |
| b. | What is the edit distance between S1 and S2? | CO2 | 2 |
| c. | List all optimal global alignment between S1 and S2. The score of Match +2 . Mismatch -1, Gap penalty -1. | CO3 | 14 |
|  |  |  |  |  |
| 3. |  | Compute the dynamic programming table, alignments and associated sequence identities for the two strings WATER and WINE, where Symbol mis-match -5; gap insertion -1; match 5. | CO3 | 20 |
| **(OR)** | | | | |
| 4. | a. | Describe the uses of various protein secondary structural databases. | CO5 | 6 |
| b. | Write the file format of EMBL Nucleotide Sequence Database. | CO5 | 7 |
| c. | Define DBMS and DBMS System. What is the difference between a Database and a Database System? | CO5 | 7 |
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| 5. | a. | What is Pattern matching? Give some of its applications. | CO2 | 7 |
| b. | Explain briefly the types of sequence alignment. | CO2 | 5 |
| c. | Illustrate the algorithm of Dynamic programming and its types. | CO2 | 8 |
| **(OR)** | | | | |
| 6. | a. | Explain the importance of Heuristic algorithms in biological sequence analysis and detail the history of alignment tools. | CO3 | 12 |
| b. | Compare and contrast the algorithm scheme of BLAST with FASTA. | CO2 | 8 |
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| 7. | a. | Briefly explain the biomechanics of protein protein interaction with database Resources. | CO4 | 8 |
| b. | Explain promoter prediction in E.coli, and in eukaryotes. | CO6 | 12 |
| **(OR)** | | | | |
| 8. | a. | What is HMM? How is it used in gene prediction? | CO4 | 10 |
| b. | Explain the basic machine learning process with neat diagram. Describe following the machine learning process in brief:  i) Neural Networks ii) Decision trees. | CO4 | 10 |
|  | | **Compulsory**: |  |  |
| 9. | a. | Give one major advantage of DNA computing. | CO1 | 4 |
| b. | Explain the classification of biological databases. Give some information about applications of databases in molecular biology. | CO5 | 16 |