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



**UNIVERSITY**

(Karunya Institute of Technology & Sciences)

(Declared as Deemed-to-be University under Sec.3 of the UGC Act, 1956)

**End Semester Examination – Nov/Dec – 2017**

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| **Code :** | **14BI2001** | **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. | Illustrate the classification of biological databases. | CO1 | 5 |
|  | b. | Give a detailed account on any two primary nucleotide sequence databases. | CO1 | 15 |
| (OR) | | | | |
| 2. | a. | Explain local and global sequence alignments using suitable examples. | CO1 | 10 |
|  | b. | Illustrate blast tool working methodology and discuss in detail blast scoring system for sequence analysis. | CO1 | 10 |
|  |  |  |  |  |
| 3. |  | Align the following Sequences using Needleman -Wunch-Algorithm  Sequence 1 : A C A C T C C G T  Sequence2 : A C G G T C G T  Scores : Match = 2 ; Mismatch = -3 ; Gap = -2 | CO1 | 20 |
| (OR) | | | | |
| 4. |  | Establish the procedures of dynamic programming algorithms in performing sequence alignments. | CO1 | 20 |
|  |  |  |  |  |
| 5. | a. | List out various structural databases. Discuss about protein data bank in detail. | CO2 | 10 |
|  | b. | Write a short note on Protein motif and domain prediction. | CO2 | 10 |
| (OR) | | | | |
| 6. |  | Explain the algorithms used for protein secondary structure prediction. | CO2 | 20 |
|  |  |  |  |  |
| 7. | a. | Define newick format. Discuss different types of newick representation for building phylogenetic trees. | CO3 | 10 |
|  | b. | Give examples i. Cladogram ii. Phylogram iii. Dendogram | CO3 | 10 |
| (OR) | | | | |
| 8. |  | Define an example on your own and construct a phylogenetic tree using distance matrix method. Write the procedure of distance based approach. | CO3 | 20 |
|  | | **Compulsory**: |  |  |
|  | |  |  |  |
| 9. |  | Explain computational gene finding programs and gene prediction in prokaryotes and eukaryotes. | CO3 | 20 |

ALL THE BEST