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



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

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|  |  |  |  |
| **Code :** | **15BI3002** | **Duration :** | **3hrs** |
| **Sub. Name :** | **COMPUTATIONAL GENOME AND PROTEOME ANALYSIS** | **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. | Explain Sanger’s method of sequencing DNA. | CO1 | 10 |
| b. | Describe sequence assembly by shotgun method with *Haemophilus influenza* genome assembly as an inference. | CO1 | 10 |
| (OR) | | | | |
| 2. | a. | Describe the implications of the Human Genome Project and the evolution of Computational Genomics. | CO1 | 10 |
| b. | Explain sequence assembly by clone contig approach along with its limitations. | CO1 | 10 |
|  |  |  |  |  |
| 3. | a. | Describe Illumina’s RNA sequencing workflow. | CO1 | 10 |
|  | b. | Illustrate how the Burrow Wheel Transform Algorithm is applied to mapping reads. | CO1 | 10 |
| (OR) | | | | |
| 4. |  | Describe methods to find genes within genomic DNA computationally. | CO2 | 20 |
|  |  |  |  |  |
| 5. |  | Describe how LAGAN serves as an efficient tool for multiple alignment of genomic DNA. | CO2 | 20 |
| (OR) | | | | |
| 6. |  | Describe protein identification using Peptide fingerprinting data. | CO2 | 20 |
|  |  |  |  |  |
| 7. |  | Explain the working of Melanie software for 2DPAGE image analysis. | CO3 | 20 |
| (OR) | | | | |
| 8. |  | Discuss motif detection, domain prediction, and protein structure analysis. | CO3 | 20 |
|  | |  |  |  |
|  | | **Compulsory**: |  |  |
| 9. |  | Describe the topological properties of biological networks. | CO3 | 20 |

ALL THE BEST