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

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

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| **Code :** | **NEXT GENERATION SEQUENCING** | **Duration :** | **3hrs** |
| **Sub. Name :** | **14BI2020** | **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. | Describe workflow of Next Generation Sequencing in step wise. | CO1 | 10 |
| b. | Explain the Illumina Sequencing method with example. | CO1 | 10 |
| **(OR)** | | | | |
| 2. | a. | Write note on various DNA Sequencing technologies. | CO1 | 10 |
| b. | Justify the statement “Sequence alignment is central to most genomic research” with example. | CO1 | 10 |
|  |  |  |  |  |
| 3. |  | Define Genome Annotation. Write in detail about the web resources of Genome annotation with example. | CO2 | 20 |
| **(OR)** | | | | |
| 4. | a. | Explain features of Integrated Genomics Viewer (IGV). | CO2 | 15 |
| b. | Give an Illustration of FASTAQ format. | CO2 | 05 |
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| 5. | a. | Justify the statement “SNP and INDEL discovery find inherited genetic variations by sequencing”. | CO1 | 10 |
| b. | Mention the uses of bedtools for fiding the least genetic variations. Give an example. | CO3 | 10 |
| **(OR)** | | | | |
| 6. | a. | Define and explain Metagenomics. | CO1 | 5 |
|  | b. | Write notes on GPU server. | CO2 | 5 |
|  | c. | Describe in detail about High Performance Computers in NGS. | CO3 | 10 |
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| 7. | a. | Explain ChIP-Seq data analysis based on statistical approach. | CO2 | 10 |
| b. | Descirbe ChIP-Seq applications in computational genomics. | CO3 | 10 |
| **(OR)** | | | | |
| 8. |  | Write Galaxy server uses for enabling the genomic reproducible research. | CO2 | 20 |
|  | | **Compulsory:** |  |  |
| 9. |  | Explain RNA-Seq Analysis based on statistical approach and their application in computational genomics. | CO3 | 20 |