

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- APRIL-2023

COURSE CODE(CREDITS): 18B1WBI834

MAX. MARKS: 25

COURSE NAME: NGS Data Analysis & Applications

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 1 Hour 30 Minutes

*Note: All questions are compulsory. Marks are indicated against each question in square brackets.*

- Q1. What do understand by Phred score in a fastq file? What is the minimum requirement of Phred score to start further downstream analysis? For a sequence, if Phred score is 30, what will be the percentage inaccuracy? [3 marks] (CO-3)
- Q2. Suppose, the sequencing of Covid-19 patient was performed and paired end data have been received by RNA sequencing. What will be the further steps used for RNA-Seq data analysis. What are the pipelines used for *denovo* and reference based assembly. [5 marks] (CO-1 & CO-3)
- Q3. Explain sequence formats and feature formats commonly used in different steps of next generation sequencing. [4 marks] (CO-2 & CO-3)
- Q4. Describe the principle of Illumina sequencing technology in detail? [3 marks] (CO-1 & CO-2)
- Q5. How does NGS differ from traditional DNA sequencing techniques? [3 marks] (CO-1)
- Q6. What challenges do you think a researcher might face while working with large volumes of NGS data? [3 marks] (CO-1 & CO-2)
- Q7. [4 marks] (CO-1 & CO-2)
- (a) Can you explain what FASTQ format files are?
- (b) Difference between chain termination method and chemical degradation method.