

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION-2022

M.Tech-I Semester (BT)

COURSE CODE (CREDITS): 13M11BT112 (3)

MAX. MARKS: 25

COURSE NAME: Advanced Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar

MAX. TIME: 1 Hour

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

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- Q1. If you have several DNA sequence reads from a NGS experiments, how will you proceed with computational analysis in a step-wise manner? [5]
- Q2. A Sanger sequence output must be processed before conducting database similarity search. What should be the guidelines to help with DNA sequencing troubleshooting and analysis? [5]
- Q3. Conventional approaches for DNA sequencing were more expensive and time consuming. How the introduction of NGS technologies has affected the feasibility of DNA sequencing? [4]
- Q4. A Sanger sequencing output is obtained in the form of a chromatogram. What does amplitude of peaks and colors indicate? [4]
- Q5. What does a score of Q(30) corresponds for in a FASTQ file? Discuss importance of quality scores in a FASTQ file. [4]
- Q6. In a general NGS data analysis procedure several types of files are produced. Briefly explain the file types and type of data they may store? [3]