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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-2 EXAMINATIONS-2022

B. Tech.-IV Semester (BI)

COURSE CODE: 18B1WBI834 MAX. MARKS: 25

COURSE NAME: NGS Data Analysis and Application

COURSE CREDITS: 03 MAX. TIME: 1 Hour 30 Min

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

Q1. Write the major differences between the Sanger sequencing (Fist Generation sequencing) and next generation sequencing (Pyrosequencing and Illumina Sequencing)? 3 marks (COI & COII)

Q2. Highlight the basic areas where Sanger sequencing finds difficulty and next sequencing such as pyrosequencing is applicable? 3 marls (COI)

Q3 Exome comprises of approximately what % of the human genome? Complex diseases result from a combination of genetic and environmental factors, many of which are not understood. State the advantage associated with exome sequencing in the case complex diseases? 3 marks (COII)

Q4 Explain the term 'alignment' and 'contig', applicable in NGS analysis? 2 marks (CO II)

Q5 Illumina sequencing has emerged as an importance tool for the whole genome or transcriptomic studies, write the mechanism of illumina sequencing and if you have been provided with NGS facility how do approach to identify the genes that are associated cancerous vs normal tissue? 3 marks (COIII)

Q 6 Sanger sequencing output is obtained in the form of a chromatogram. What does amplitude of peaks and colors indicate? (2 Marks)

Q7 What does a score of Q(30) corresponds for in a FASTQ file? Discuss importance of quality scores in a FASTQ file. (3 Marks) (CO I & II)

Q8 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? (3 Marks) (COIII)

Q9 Which of the following figures represent Hamiltonian path and/or circuit? Justify your answer. (3 Marks) (CO II)

A B C