JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2024

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 30 Minutes

Note: *(a) All questions are compulsory.*

(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

Q.No	Question	Marks
Q1	Analyze the roles of different SRA accession types in the context of NGS data analysis.	3
Q2	Highlight some important outcomes of the Human Genome Project.	2
Q3	Outline the workflow of a typical next-generation sequencing (NGS) data analysis pipeline.	3
Q4	Sanger sequencing is a method of DNA sequencing that involves electrophoresis and is based on the random incorporation of chain-terminating dideoxynucleotides by DNA polymerase during in vitro DNA replication. How would you analyze and interpret the data obtained from a Sanger sequencing experiment? What bioinformatics tools could assist in this process?	5
Q5	Can you illustrate how the detection of pyrophosphate is applied in pyrosequencing to determine DNA sequences? Analyze the types of errors that are commonly associated with pyrosequencing. How do these errors impact the reliability of sequencing results.	5
Q6	If a base has a Phred score of 30, what is the probability that this base is called incorrectly? Calculate the accuracy of the result.	4
Q7	Analyze the structure of a FASTQ file. What are the four lines associated with each read, and what information does each line provide?	3

JUIT TEST-2 EXAMINATION-OCT-2024