JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2025

B.Tech - VIII Semester (BT/BI)

COURSE CODE (CREDITS): 18B1WBI834 (3) **MAX. MARKS: 15**

COURSE NAME: NGS Data Analysis & Applications

COURSE INSTRUCTORS: Dr. Shikha Mittal **MAX. TIME: 1 Hour**

Note: (a) All questions are compulsory.

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

<table>
<tr><th>Q.No</th><th>Question</th><th>CO</th><th>Marks</th></tr>
<tr><td>Q1</td><td>You are given a sequence of base calls from a DNA sequencing experiment, and you need to calculate the Phred score for each base call. The following table contains the error probabilities for each base call in a DNA sequence:
<table>
<tr><th>Base Call</th><th>Error Probability (P)</th></tr>
<tr><td>A</td><td>0.01</td></tr>
<tr><td>T</td><td>0.05</td></tr>
<tr><td>C</td><td>0.002</td></tr>
<tr><td>G</td><td>0.03</td></tr>
</table>
a. Calculate the Phred score for each base.
b. If the average Phred score for a sequencing read is 30, what is the error probability associated with that score?</td><td>[CO-1]</td><td>(5)</td></tr>
<tr><td>Q2</td><td>a. Difference between de novo and reference-based sequencing?
b. Difference between Sanger sequencing and next-generation sequencing (NGS)?</td><td>[CO-3]</td><td>(4)</td></tr>
<tr><td>Q3</td><td>What are the key steps in Illumina sequencing?</td><td>[CO-2]</td><td>(4)</td></tr>
<tr><td>Q4</td><td>Explain the following –
a. FASTQ format
b. Data quality</td><td>[CO-1, CO-3]</td><td>(2)</td></tr>
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