

Instructions

- Subject: ABIN (2022 class)
- Answer all questions
- Plagiarism or misconduct is punishable as per IIIT-D rules
- Total points: 32
- Total Time: 75 minutes
- Type of quiz: Graded & closed book

Questions

1. Answer the following
 - a. What are the key expectations from a compression technique such as BWT? **(4 points)**
 - b. Why does BWT work in the case of the human genome? Will it work for a random nucleotide sequence? **(4 points)**

Or,

 - c. Given a DNA string A and its BWT, A' can you come up with a measurement of compressibility? **(8 points)**
2. Answer the following
 - a. Write the pseudo code for alignment backtracking using SW algorithm **(4 points)**
 - b. Find the best global alignment of these two sequences: ACTGATTCA
ACGCATCA Using -2 as a gap penalty, -3 as a mismatch penalty, and 2 as the score for a match. **(4 points)**
3. Answer the following
 - a. How do we compute Phred score in sequencing? Illustrate with an example. **(4 points)**
 - b. Analyze pattern branching algorithm complexity. **(4 points)**