

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST – 1 EXAMINATION, SEPTEMBER 2016

B.TECH V SEMESTER

COURSE CODE: 15B11BI512

MAX. MARKS: 15

COURSE NAME: Computational Genomics

COURSE CREDITS: 04

MAX. TIME: 1 HRS

*Note: All questions are compulsory. Carrying of mobile phone during examination will be treated as case of unfair means. Make your own assumptions, if required.*

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Q.1. Define computational genomics. Describe its association with comparative and functional genomics. [1.5]

Q.2. Discuss various parameters for statistical analysis of genomic sequence data. [1.5]

Q.3. What is annotation? Discuss the role of genomic era through annotation. Explain the significance of substitution matrices in sequence alignment and annotation. [3]

Q.4. How FASTA works? Solve the alignment problem for the given set of sequences:

A = "FAMLGFIYKLGPCM" and B = "TGFIYKLGPACT" using FASTA method. [1.5+3]

Q.5. What is restriction mapping? Solve the following problem of restriction maps:

Restriction map = {0, 1, 3, 4, 5, 7, 12, 13, 15}, identify all possible multiset options. [1.5+3]

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