

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST 3 EXAMINATIONS - DECEMBER 2017

B.Tech V Semester (BI)

COURSE CODE: 15B11BI512

MAX. MARKS: 35

COURSE NAME: Computational genomics

COURSE CREDITS: 04

MAX. TIME: 2.0 HRS

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.

Q.1. Describe the following with reference to functional genomics: [1*10=10]

- (a) Motifs and domains (b) Ontology (c) Fragment assembly (d) Orthologs (e) SNMP
(f) Splicing (g) Homologs (h) Restriction mapping (i) Primer designing (j) PSI-BLAST

Q.2. What do you understand by microarray data analysis? Discuss its all steps in detail. [6]

Q.3. What are various NGS techniques? Explain complexities of fragment assembly and how new techniques can overcome these difficulties [4]

Q.4. Given $A = 1, 2, 4, 5, 6$; $B = 1, 3, 5, 6$, and $AB = 1, 1, 1, 1, 2, 2, 2, 3, 5$. Solve the PDP for this given data set for two enzymes. [4]

Q.5. Differentiate between Reconstruction and Multicontig model through a real example data set. [2+2]

Q.6. Discuss following with their specific role in microarray data analysis:

- (a) Euclidean distance (b) Pearson correlation coefficient (PCC) [2+2]

Q.7. Solve the PDP for the given data: $X = \{0, 4, 5, 6, 7, 10, 16\}$. [3]