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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-1 EXAMINATION- September -2017

B. Tech (5th Semester) Bioinformatics

COURSE CODE: 15B11BI512

MAX. MARKS: 15

COURSE NAME: Computational Genomics

COURSE CREDITS: 04

MAX. TIME: 1 HR

Note: All questions are compulsory. Carrying of mobile phone during examination will be treated as case of unfair means. Marks are indicated below each question

1. Define multicontig model for fragment assembly. Discuss 4 crucial parameters for primer designing. [1+1]
2. Why Bioinformatics is called a tool? Discuss evolution of genomics through the eyes of Bioinformatics. [2]
3. Which kind of sequence data is better or preferred for bioinformatic analyses? Discuss various flavors of BLAST. [2]
4. What are four major problems in fragment assembly? Discuss each with a real sequence example. [1*4=4]
5. What are various kind of repeats in genomic sequences? Explain their role in the structure of genomes. [1+1]
6. Elucidate computational steps for FASTA method by aligning following sequences using FASTA method:
Seq. A = ARNDCEPN
Seq. B = NDCEP [3]

BI-2 . BT