

Tirna Raj Singh

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- October 2017

B.Tech (Bioinformatics) V<sup>th</sup> Semester

COURSE CODE: 15B11BI512

MAX. MARKS: 25

COURSE NAME: Computational Genomics

COURSE CREDITS: 4

MAX. TIME: 1.5 Hrs

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

Q.1. Define following with an exclusive explanation towards computational genomics:

(a) BruteForcePDP (b) Homometric Stes (c) Rebase [2\*3=6]

Q.2. Define the parameters for reconstruction model for fragment assembly. Implement the model for a set of you fragment sequences of your choice. [3]

Q.3. What is partial digest problem? How it is different from double digest problem? Solve the following DDP for the given set of enzymes. Fragments data is given below as:

For first Enzyme A = 2, 3, 4; for second enzyme B = 1, 3, 5; As for DDP A+B is required which is A+B = 1, 1, 2, 2, 3. [6]

Q.4. For the given X {0, 1, 3, 4, 5, 7, 12, 13, 15}, find out L. Also prove that the answer obtained is correct through reverse processing and formulations separately. [4]

Q.5. What are various kind of mapping? Explain the functional and evolutionary role of restriction enzymes in Genomics. [3]

Q.6. Explain each with an example:

(a) A Graph where Greedy algorithm fails (b) PSI-BLAST (c) Overlap Multigraph [1\*3=3]