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Total Number of Pages: 02

M.TECH
BTPE 202

2nd Semester Regular/ Back Examination – 2015-16
COMPUTATIONAL BIOLOGY

Time: 3 Hours

Max marks: 70

Q.CODE:W757

Answer Question No.1 which is compulsory and any five from the rest.
The figures in the right hand margin indicate marks.

- Q1 Answer the following questions: (2 x 10)
- a) Explain TIGR.
 - b) What is PDB?
 - c) Explain pharmacophore.
 - d) What are pattern databases?
 - e) How to choose the PAM matrix in accordance to sequence similarity?
 - f) What is PlasmoDB?
 - g) What do you mean by Entrez?
 - h) Name two wet lab techniques for macromolecular structure prediction.
 - i) Name sequence deposit tools in ENA database.
 - j) What is the significance of R value in a PDB file?
- Q2 What is dynamic programming? Explain methods of dynamic programming used for pairwise sequence alignment. (10)
- Q3 a) What is substitution matrix? Describe different amino acid substitution matrices. How they differ from each other (5)
- b) What is substitution matrix? Describe different amino acid substitution matrices. How they differ from each other (5)
- Q4 a) Explain Markov chain and Markov model. How they can be used in bioinformatics applications? (5)
- b) Explain Difference between primary and secondary databases with example. (5)
- Q5 a) Explain the process of molecular dynamics simulation with suitable flow chart. How MD simulation is different from MC simulation? (5)
- b) Explain molecular descriptors and their types? Differentiate between 2D and 3D QSAR. (5)
- Q6 a) Explain different approaches in drug design process. Explain the rules and parameters to describe basic nature of a drug candidate. (5)
- b) How FASTA is different from BLAST? (5)
- Q7 a) Explain in brief Force field (5)
- b) Describe Baum-Welch algorithm. (5)

Q8 Write short notes on any two

(5 x 2)

- a) NMR spectroscopy
- b) Uniprot
- c) Energy minimization
- d) Threading