

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
T-1 EXAMINATION, Feb 2020
B. Tech. (Bioinformatics) II Semester

COURSE CODE: 18MS1BI214
COURSE NAME: Basic Bioinformatics

MAX MARKS: 15
MAX. TIME: 1 Hr.

*Note: All questions are compulsory. Attempt all questions of a particular section at one place.
Answer each question to the point.*

1. Explain the following terms with respect to biological sequences: (3 marks) (CO1, CO2)
 - a) Homologues
 - b) Paralogues
 - c) Orthologues
2. What is a biological sequence alignment? Why do we need it? What are the parameters used to assess the goodness of an alignment? Discuss sequence similarity, sequence identity, length of an alignments, and gaps in alignment. (3 marks) (CO1) (CO2)
3. Differential between “local” and “global” protein sequence alignments. Discuss the merits of each one with respect to the biological function. (3 marks) (CO1, CO2)
4. What are substitution matrices? What do the scores in the matrices represent? Discuss PAM matrices. (3 marks) (CO2)
5. What is 62 in BLOSUM62 matrix? In this matrix a histidine-histidine substitution has a score of 8 while Leucine to Aspartic acid substitution has a score of -4. Interpret and discuss. (3 marks) (CO2)