

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
T-1 EXAMINATION, Sep 2018
B.Tech. (Bioinformatics) III Semester

COURSE CODE : 10B11BI311
COURSE NAME: Biological Computation

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. Write a note on the dot matrix plot for biological sequence analysis. Discuss how its constructed and interpreted. (3 Marks)
2. Write a brief note on the following in the context of biological sequence alignment with a suitable hypothetical example. (3 Marks)
 - a) Percentage Similarity
 - b) Percentage Identity
 - c) e-value
3. What are substitution matrices? Describe BLOSUM and PAM substitution matrices and how they differ from each other. (3 Marks)
4. Similar biological sequences can be thought to be derived from the common ancestral sequences. How do related sequences differ from each other during the course of evolution? Briefly describe homologous, orthologous and paralogous sequences. (4 Marks)
5. You want to detect distantly related proteins by sequence alignment. Which one is a better choice between PAM250 and PAM120 matrices and why? (2 Marks)