

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-1

B.Tech (BT and BTDD) V Semester

COURSE CODE: 10B11BT511

MAX. MARKS: 15

COURSE NAME: Introduction to Bioinformatics

COURSE CREDITS: 4

MAX. TIME: 1 hour

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

1. Elucidate the role of bioinformatics in the field of drug discovery, illustrating with examples. (2)
2. Explain the different classes of biological databases on the basis of data source and data access with examples of each kind. (2+2)
3. Show the differences between FASTA and PIR formats used for storing sequences. (2)
4. How can we use dotplots for obtaining sequence alignments? (Describe both the methods). Is it better than using dynamic programming based methods? Why or why not? Justify in terms of pros and cons of both. (4)
5. Compare the score of the following alignments when we use linear and affine gap penalty systems. Given that match=10, mismatch=-2, gap_extension=-7, gap_start=-15. What do you conclude about the two systems on the basis of these scores? (3)

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