

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -1 EXAMINATION- Sept.2017
B.Tech V Semester (Biotechnology)

COURSE CODE: 10B11BT511

MAX. MARKS: 15

COURSE NAME: Introduction to Bioinformatics

COURSE CREDITS: 04

MAX. TIME: 1Hour

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

1. Which of the following sequence formats is preferred for most sequence analysis programs-GenBank, FASTA, XML, EMBL and why? (2)
2. Distinguish between: (10)
 - (a) Smith-waterman and BLAST
 - (b) Primary and secondary database
 - (c) UniGene and UniParc
 - (d) Linear and Affine scoring system
 - (e) Dynamic Programming and heuristic methods
3. Find Smith-Waterman alignment for the following two sequences: ATCAGAGTC and GTCAGTCA. Gap penalty=-2 (3)

Scoring matrix:

	A	C	G	T
A	1	-1	-1	-1
C	-1	1	-1	-1
G	-1	-1	1	-1
T	-1	-1	-1	1