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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- Oct 2017

B.Tech (Biotechnology) VI Semester

COURSE CODE: 10B11BT511 MAX. MARKS:25

COURSE NAME: Introduction to Bioinformatics

COURSE CREDITS: 4 MAX. TIME: One Hour Thirty Minutes

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

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1. Answer the following with respect to the BLST program:
   (a) How is PSI-BLAST different from the normal BLAST and PHI-BLAST programs? Which one is the best of the three and why? (2)
   (b) tBLASTx is more time-consuming than BLASTN. Why? (2)
   (c) Distinguish between BLAST and BLAST2. How do we incorporate gaps in the alignment? Explain. (2)
   (d) Why do we ignore low complexity and repetitive regions in BLAST? (2)
   (e) How and why do we convert raw score to bit score? (2)
   (f) Which sequence filters are used in the BLAST program and why? (2)

2. With reference to multiple sequence alignment (MSA), answer the following:
   (a) How do we use MSA for designing degenerate primers and genome sequencing? (2)
   (b) Explain the SP measure method of scoring the alignment using your own hypothetical example. (2)
   (c) What is the qualitative meaning of δ and ε parameters in MSA? Explain. (2)
   (d) Discuss the difference between CLUSTALW and PILEUP methods of MSA. Explain the inherent weakness of progressive methods for MSA. (3)
   (e) What are sequence logos and why do we use them? (1)
   (f) How do we convert an MSA into a profile. Explain the two methods. (3)