JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
T-1 EXAMINATION, Sep 2019
Ph.D. I Semester

COURSE CODE: 13M11BT112
COURSE NAME: Advanced 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.

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1. Explain why RNA-seq has superseded the traditional technologies for studying gene expression profile. (2 Marks) (CO2,CO3)

2. Distinguish between alpha and beta diversity, outlining the relevance of each to microbiome profiling. (2 marks) (CO2, CO3)

3. Discuss the application of fastQC program in contemporary biomedical research. (1) (CO2,3)

4. Discuss the following terms in the context of evolution of biological sequences: (3 marks) (CO1)

   a) Homologues
   b) Paralogues
   c) Orthologues

5. Explain global and local sequence alignment. Discuss similarities and differences and the cases where each type of alignment is relevant. (4 marks) (CO1)

6. Discuss substitution matrices used in sequence alignment programs. (3 marks) (CO1)