

Dr. Trinath Raj

**JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT**

**TEST-1 EXAMINATION - Summer Semester June-2018**

**B.Tech (Bioinformatics)**

**Course Code: 10B11BI311**

**MAX. MARKS: 50**

**Course Name: Biological Computations**

**COURSE CREDITS: 04**

**MAX. TIME: 2 HR**

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

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Q.1. Describe biological sequence analysis with all parameters. Also explain the applications of sequence analysis. [5]

Q.2. What is BLAST? What are its various types? Explain its internal working with an example. [5]

Q.3. Align following amino acid sequences using FASTA method: [7]

Seq.1. ARNDCACT; Seq.2. NDCACG

Q.4. How dynamic programming is being used in sequence alignment? Discuss global and local alignment algorithms for the same. [7]

Q.5. What is MSA? Discuss its applications. Also discuss sum of pairs method with any 5 sequences of your choice. [8]

Q.6. How we measure distance between biological sequences? Differentiate between Edit and Hamming distances with a suitable example. [6]

Q.7. Discuss classification of phylogenetic methods. Describe any distance based method with a suitable example. [8]

Q.8. What is gap penalty? Explain its significance in sequence alignment procedure. [4]