



MBD-003-006305

Seat No. _____

**B. Sc. (Bioinformatics) (Sem. III) (CBCS)
Examination**

November / December – 2016

**BI - 303 : Principles of Sequence Analysis
(Old Course)**

Faculty Code : 003

Subject Code : 006305

Time : $2\frac{1}{2}$ Hours]

[Total Marks : 70

- Instructions :** (1) All questions are compulsory.
(2) The right side figure indicates total marks of the question.

SECTION — I

- 1 Answer the short answer questions : **20**
1. What is Specificity ?
 2. Inserting some number of "-" symbols which is called a..... ?
 3. Which is the amount of characters which match exactly between two different sequences ?
 4. The three primary, methods of producing pairwise alignments are _____, _____ and _____.
 5. Local alignments never have terminal gaps, because a higher score could be obtained by deleting the gaps. (True or False)
 6. The guide tree can be established using a pairwise distance-based approach or by choosing from many guide trees in a parsimony framework. (True or False)
 7. Needleman-Wunsch algorithm is a general global alignment technique based on _____.
 8. Is an expression commonly used to measure computational complexity
 9. Hidden Markov Model (HMM) can produce both global and local alignment (True / False)
 10. What is the use of phylogenetic, reconstruction ?

11. A _____ is a broad term for the diagrammatic representation of a phylogenetic tree.
12. Phylogenetic trees can also be built using T-Theory (True/false)
13. Abbreviation of UPGMA
14. PSI-BLAST produces _____ alignments.
15. Name any one tool to construct MSA
16. Name any one tool to construct Phylogenetic tree
17. Motif finding, also known as _____ analysis, is a method of locating sequence motifs in global MSAs
18. _____ is a method to find protein-coding genes.
19. Which motifs appears to lack secondary structure ?
20. Which motif describes the connectivity between secondary structural elements ?

SECTION - II

- | | | |
|----------|---|-----------|
| 2 | Answer the following questions : | 25 |
| | (A) Explain any Three : | 6 |
| | 1. Global Alignment | |
| | 2. GenBank | |
| | 3. Bit score | |
| | 4. PHI BLAST | |
| | 5. Blocks | |
| | 6. SP Score. | |
| | (B) Explain any Three : | 9 |
| | 1. Application of MSA | |
| | 2. Properties and types of phylogenetic tree | |
| | 3. How to retrieve sequence data from NCBI Gene ? | |
| | 4. Dot matrix | |
| | 5. Application of sequence alignment | |
| | 6. FASTA algorithm. | |

- (C) Attempt any Two : 10
1. Make brief note on PAM matrices
 2. Explain Needleman Waunsch algorithm for pairwise alignment
 3. Explain Hidden Markov Model in MSA
 4. Describe Progressive method of MSA
 5. Describe PSI BLAST.
- 3** Answer the following questions : 25
- (A) Explain any Three : 6
1. Distance matrix
 2. Gap penalty
 3. Cladogram vs. Phylogram
 4. E-value
 5. Hamming Distance
 6. Regular expression.
- (B) Explain any Three : 9
1. Maximum parsimony
 2. Types of BLAST
 3. BLOSUM
 4. Relationship of phylogenetic analysis with MSA
 5. Motifs and Domains
 6. Maximum likelihood.
- (C) Attempt any Two : 10
1. How local MSA is performed ?
 2. BLAST algorithm
 3. Make note on pattern searching
 4. Distance based method for phylogenetic analysis
 5. Phylogenetic analysis steps.
-