



**JAY-003-1133003**      Seat No. \_\_\_\_\_

**M. Sc. (Biotechnology) (Sem. III) (CBCS)  
(W.E.F. 2016) Examination**

December - 2019

**BT - 313 : Bioinformatics**

Faculty Code : 003  
Subject Code : 1133003

Time :  $2\frac{1}{2}$  Hours] [Total Marks : 70]

1 Answer the following : (Any Seven)  $2 \times 7 = 14$

- (a) Define the terms identity and similarity.
- (b) What is proteome and genome?
- (c) What is artificial intelligence?
- (d) Describe the types of alignment.
- (e) What is annotation?
- (f) Distinguish primary and secondary database.
- (g) Give the full form - HTTP, EBI, SCOP, BLAST
- (h) Name microarray methods used for the genome analysis.
- (i) Define the term analogy and paralogy.
- (j) Give the names of different software used for sequence alignment.

2 Answer the following : (Any Two)  $2 \times 7 = 14$

- (a) Write a note on multiple sequence alignment and its applications.
- (b) Exemplify how BLAST works.
- (c) What are the current perspectives and emergence of bioinformatics?

**3 Answer the following : 2×7=14**

- (a) Write a short note on PAM & BLOSUM Matrix
- (b) Explain the principle of DNA microarrays. Describe the procedure involved in detail.

**OR**

- (a) Describe ORF prediction.
- (b) What are the different approaches used for gene finding?

**4 Answer the following : 2×7=14**

- (a) Give a detailed account on functional genomics.
- (b) What is homology modeling? Describe the procedure of homology modeling and advantages.

**5 Answer the following : (Any Two) 2×7=14**

- (a) Give an overview of protein sequences databases used in bioinformatics.
- (b) Explain the various levels at which structures are classified in SCOP and CATH databases.
- (c) Write a detailed account on commercial use of bioinformatics.
- (d) Briefly describe DBMS & RDBMS.

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