Total No. of printed pages = 3

63/2 (SEM-2) BIT 204

2022

BIOTECHNOLOGY

(Theory Paper)

Paper Code : BIT 204

(Biostatistics and Bioinformatics)

Full Marks – 80

Time – Three hours

The figures in the margin indicate full marks for the questions.

1. State whether the following statements are True or False : 1×6=6

(a) Orthologous genes are related through gene duplication events.

(b) WHATIF is a software to verify structure of the protein molecule.

(c) TIGR is a protein database.

(d) The branch lengths in Cladogram are constant.

(e) Micro-array technique is used in functional genomics.

(f) BLOSUM62 is not a scoring matrix.

2. Define the following : 2×5=10

(a) Systems Biology

(b) Metabolomics

(c) Genome Annotation

(d) Paralog

(e) PubMed

3. Write short notes on any *six* from the following : 5×6=30

(a) E Value

(b) Uses of Chi Square Test

(c) FASTA Format

(d) NCBI

(e) Types of BLAST

(f) PAM Matrix

(g) Primary Database

(h) ANOVA

(i) TCP/IP

4. Answer any *two* from the following questions : 10×2=20

(a) Discuss the importance of biological databases in bioinformatics.

(b) What is meant by secondary database ? What are the major secondary databases ?

(c) Describe PHI-BLAST.

5. Answer any *one* from the following questions : 14×1=14

(a) Describe the method of structure based Drug Designing. 14

(b) Name the protein structure predictive methods. Describe any two methods with a note on their advantages and disadvantages. 4+5+5=14