Total number of printed pages–3

3 (Sem–5/CBCS) ZOO HE 1

2024

ZOOLOGY

(Honours Elective)

Paper : ZOO–HE–5016

(Computational Biology and Biostatistics)

Full Marks : 60

Time : Three hours

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

1. Fill in the blanks : ***(all seven)*** 1×7=7

   (a) RDBMS stands for _____.

   (b) GenBank is a _____ sequence database.

   (c) _____ is regarded as father of Biostatistics.

   (d) The information retrieval tool of NCBI GenBank is _____.

   (e) Genomics refers to the study of _____.

Contd.

(f) DNA microarray is a technique to study _____.

(g) Edman degradation is the method of sequencing _____.

2. Answer the following questions : 2×4=8

(a) Write the differences between primary database and secondary database.

(b) What is FASTA format ? Give an example of nucleotide sequence in FASTA format.

(c) What is Pharmacogenomics ?

(d) Write the applications of Chi-square tests.

3. Answer the following questions : ***(any three)*** 5×3=15

(a) Briefly describe the different branches of Genomics.

(b) Describe the chain termination method of DNA sequencing.

(c) Briefly explain essential aspects of local and global sequence alignment.

(d) Write the similarities and differences between BLAST and FASTA.

(e) Explain the methods of optimizing sequence alignments.

4. Answer the following questions : 10×3=30

(a) Describe the role of a bioinformatician in present biological research and development area.

OR

What are the different components of a phylogenetic tree ? Describe the different methods of molecular phylogenetic analysis. 3+7=10

(b) What is BLAST ? Describe the different variants of BLAST. 2+8=10

OR

Describe the major categories of biological database with examples.

(c) Describe the different methods of protein tertiary structure prediction.

OR

Calculate the standard deviation and standard error from the following data :

X:	20 – 30	30 – 40	40 – 50	50 – 60	60 – 70	70 – 80	80 – 90
Y:	26	70	65	58	15	45	30