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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 : $2 \times 4 = 8$

- (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)**
 $5 \times 3 = 15$

- (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 : $10 \times 3 = 30$

- (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