# 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.

•	Fill	in the blanks : (all seven) $1 \times 7 = 7$
	(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)  $5\times 3=15$ 
  - (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:  $10\times3=30$ 
  - (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