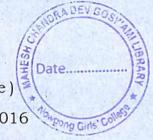
### 3 (Sem-5/CBCS) ZOO HE 1

# 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.

į., v.	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			

- (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) 5×3=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:

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