Total number of printed pages-4

3 (Sem - 5/CBCS) ZOO HE 1

2023

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 $1 \times 7 = 7$
 - (a) Gold biotechnology is also known as
 - (b) DDBJ is a ______sequence database.
 - (c) _____ is a computer-annotated protein sequence database.
 - (d) The information retrieval tool of NCBI GenBank is _____.
 - (e) Proteomics refers to the study of

Contd.

- (f) _____ has been referred to as the mother and father of Bioinformatics.
- (g) The identification of drugs through the genomic study is called _____
- 2. Answer the following : $2 \times 4 = 8$
 - (a) Write the differences between local alignment and global alignment.
 - (b) Write about the different branches of bioinformatics.
 - (c) What is systems biology ?
 - (d) Write about the ddNTP structure and its use.
- 3. Answer the following questions : (any three) 5×3=15
 - (a) Describe the different sequence submission tools available at NCBI.
 - (b) Describe the Sanger's di-deoxy method of DNA sequencing.
 - (c) Briefly explain essential aspects of primary and secondary database.
 - (d) Write the differences between PAM and BLOSUM matrices.

(e) Explain co-efficient of variance and its importance.

Answer the following questions : 10×3=30

4. (a) Describe the scope and applications of bioinformatics in frontier areas of biology.

OR

- (b) What is phylogeny ? Discuss the various methods of phylogenetic analysis.
- 5. (a) Describe various types of BLAST with their applications. Briefly explain the algorithm of BLAST.

OR

- (b) What is sequence alignment ? Explain the various parameters used for optimum sequence alignment.
- 6. (a) How can you predict the structure of protein sequence ? Explain in detail one of the knowledge-based method to predict the protein structure.

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(b) Calculate the standard deviation and standard error from the following data:

X:	10 - 20	20-30	30 - 40	40-50	50-60	60-70	70-80
Y:	4	6	10	18	15	12	5

4

3500