

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 : 1×7=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 : 2×4=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 :  $10 \times 3 = 30$

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.

**OR**

(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

---