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**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 :  $2 \times 4 = 8$

(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)**

$5 \times 3 = 15$

(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

OR