

# BIKALI COLLEGE LIBRARY

Total number of printed pages-4

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

**2022**

**ZOOLOGY**

(Honours Elective)

Paper : ZOO-HE-5016

(DSE(H)-1)

**(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 : **(any seven)** 1×7=7
  - (a) SWISPROT protein sequence database began in the year \_\_\_\_\_ .
  - (b) Bioinformatics database was first created by \_\_\_\_\_ .
  - (c) The human genome contains approximately \_\_\_\_\_ base pairs.

Contd.

# BIKALI COLLEGE LIBRARY

- (d) COPIA is used for identification of \_\_\_\_\_ .
- (e) STAG is maintained by \_\_\_\_\_ .
- (f) The information retrieval tool of NCBI Gene Bank is \_\_\_\_\_ .
- (g) Proteomics refers to the study of \_\_\_\_\_ .
- (h) EMBL is a \_\_\_\_\_ sequence database.
- (i) Phylogenetic relation can be shown by \_\_\_\_\_ .
- (j) The first molecular biology server expasy was used in the year \_\_\_\_\_ .
- (k) \_\_\_\_\_ is the first completed and published gene sequence.
- (l) The identification of drugs through the genome study is called \_\_\_\_\_ .

2. Answer the following : **(any four)**

2×4=8

- (a) EMBL
- (b) Global alignment
- (c) Standard error

- (d) Phylogram
- (e) DNA database of Japan
- (f) Goodness-of-fit
- (g) OMIM
- (h) Genetic Code

3. Answer the following questions : **(any three)**  
5×3=15

- (a) Explain the hierarchial method of multiple sequence alignment.
- (b) Discuss the database that contain the information of protein sequences.
- (c) Explain the secondary database.
- (d) What is dendrogram ?
- (e) What are biological databases based on data type and database design ?
- (f) Explain co-efficient of variance and its importance.
- (g) How standard deviation is differed from standard error ?
- (h) Application of Chi-square tests.

4. Answer the following questions : (*any three*)  
10×3=30

(a) What is phylogeny ? Discuss the various method for phylogenetic analysis.

(b) Elaborate different file formats in biological resources with the help of an arbitrary example each.

(c) Give various types of BLAST. Explain briefly the algorithm of BLAST.

(d) Discuss STRING database. Describe its various features.

(e) How can you predict the structure of a protein sequence ? Explain in detail one of the knowledge-based method to predict the protein structure.

(f) Explain the various apparatus used in pairwise sequence alignment.

(g) What is Biostatistics ? How biostatistics help in biological sequence analysis ?

(h) Calculate the standard deviation from the following data :

X :	20-30	30-40	40-50	50-60	60-70	70-80	80-90	90-100
Y :	30	58	62	85	112	70	57	26