

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)** $1 \times 7 = 7$

(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.

- (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 hierarchical 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