(ii) Biocyc database

(iii) Mass Spectrometry

(iv) Measures of variability

[This question paper contains 8 printed pages.]

03.01.24(M)

Your Roll No..............

Sr. No. of Question Paper : 4499 **G**

Unique Paper Code : 32237905

Name of the Paper : DSE : Computational Biology

Name of the Course : **B.Sc. (H) Zoology**
Examination – LOCF

Semester : V

Duration : 3 Hours Maximum Marks : 75

Instructions for Candidates

1. Write your Roll No. on the top immediately on receipt of this question paper.
2. Use of simple calculator is allowed.
3. Statistical tables should be provided,
4. Attempt five questions in all, including Question No. **1** which is compulsory.

1. (a) Expand the following abbreviations : (3)

(i) EMBL

(ii) PDB

(iii) PAM

(iv) OMIM

(v) ORF

(vi) BLAST

(b) Match the terms in column A with those given in column B : (3)

A	B
Multiple Sequence Alignment	BLAST
Margaret Dayhoff	Chi Square
Visualizing 3-D protein	CLUSTAL X
Stephen Altschul	Rasmol
Test of Independence	PubMed
Literature Database	PAM

(c) In a dihybrid cross with two traits (9:3:3:1), the following data (with respect to the number of offspring with different genotypes) was obtained:

1. Dominant for both traits: 576,
2. Dominant for trait 1 and Recessive for trait 2: 191
3. Dominant for trait 2 and Recessive for trait 1:181
4. Recessive for both traits: 57

Perform a chi-square analysis to see if the data given above agrees with the predicted outcome of this cross. State the null and alternate hypothesis as well as degrees of freedom used and explain your results in detail ($\alpha = 0.05$) (2+4+6)

7. Write short notes on **(any three)** : (4×3=12)

(i) Molecular Docking

4. (a) Discuss in detail about Dynamic programming method of sequence alignment with suitable example.

   (b) Define BLAST and discuss about basic types of BLAST. (8+4)

5. (a) What are scoring matrices? How does PAM differ from BLOSUM?

   (b) Explain with a suitable example how PAM matrix is generated? (4+8)

6. (a) Define Null hypothesis. Why is it called 'Null' hypothesis?

   (b) Calculate the Standard Deviation (S.D.) and Co-efficient of variance of following data collected on number of seeds present in different pods of *Cajanuscajan* (pigeonpea):

   Number of seeds in different pods- 6, 7, 3, 4, 6, 7, 6, 4

(c) Define the following : (5)

- (i) E-value
- (ii) Open Reading Frame
- (iii) BankIT
- (iv) K-tuple method
- (v) Standard Deviation

(d) Differentiate between the following : (8)

- (i) Local and Global Alignment
- (ii) Bits score and e-value
- (iii) Genomics and Proteomics
- (iv) Similarity and Homolgy

(e) Explain the following symbols : (3)

- (i) H_o

(ii) S^2

(iii) Σ

(iv) x_i

(v) $1 - \alpha$

(vi) df

(f) Write the contribution of following scientists : (2)

(i) Steve Henikoff

(ii) Frederick Sanger

(iii) David J Lipman

(iv) Smith and Watermann

(g) State whether the following statements are *true* or *false*. Give reasons for your answer. (3)

(i) The term 'Bioinformatics' was coined by J. D. Watson

(ii) The computational methodology used for best matching between two molecules, a receptor and a ligand, is called molecular docking

(iii) Confidence interval at 99% significance level is narrower than at 95%.

2. (a) Describe the importance of Biological Databases and classify the different databases based on the type of data.

(b) What is Structural bioinformatics and discuss about PDB database. (8+4)

3. (a) Discuss in detail about Chain termination method of DNA sequencing.

(b) Discuss about DNA microarray technique and its applications. (6+6)