4. (a) How is dynamic programming different from heuristic approach? Explain different heuristic methods using well labelled diagrams.

(b) Differentiate between the Needleman-Wunschand and Smith-Waterman algorithm. (8,4)

5. Explain various RNA based approaches used in functional genomics. (12)

6. (a) Define t-Test and discuss about its types. (4,8)

(b) 10 fishes from Tank I and 10 fishes from Tank II of a species of fish were procured and measured in cm.

Tank I	20	24	20	28	22	20	24	32	24	26
Tank II	12	10	8	10	6	4	14	20	10	6

Calculate the mean difference in body length between the two ponds of fishes is significant or not. (5% level of significance).

7. Write short note on **ANY THREE** (3×4=12)

(i) Chi-square test

(ii) Dot plot

(iii) Machine learning

(iv) Sequence annotation

[This question paper contains 4 printed pages.]

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

05.01.2024(M)

Sr. No. of Question Paper : 4616 G

Unique Paper Code : 32237905

Name of the Paper : DSE Computational Biology

Name of the Course : **B.Sc. (H) Zoology Examination, 2023 – 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.

P.T.O.

1. (a) Define the following : (7)
   - (i) Functional Genomics
   - (ii) Metabolomics
   - (iii) Clustal
   - (iv) BLAST
   - (v) Dot matrix
   - (vi) flat file
   - (vii) standard deviation

   (b) Expand the following terms : (6)
   - (i) PDB
   - (ii) PAM
   - (iii) PIR
   - (iv) GWAS
   - (v) EMBL
   - (vi) KEGG

   (c) Explain the following symbols : (0.5×6=3)
   - (i) α
   - (ii) χ^2
   - (iii) d.f.
   - (iv) C.V.

   - (v) H_a or H_1
   - (vi) S^2

   (d) Write the contribution of following scientists (3)
   - (i) Mark Schena
   - (ii) Stephen Altschul
   - (iii) Margaret Dayhoff

   (e) Differentiate between the following : (2×4=8)
   - (i) Primary Database and Secondary Database
   - (ii) BLAST and FASTA
   - (iii) t-test and z-test
   - (iv) Local Alignment and Global alignment

2. (a) What are the various steps of Drug discovery. How bioinformatics has 8,4 revolutionized the process of drug designing?

   (b) Describe Sanger method of DNA sequencing. (8,4)

3. (a) Differentiate between PAM and BLOSUM scoring matrices.

   (b) Classify biological databases based upon data types. (6,6)