4/12/18/(M)

Sl. No. of Ques. Paper	: 645	**IC**
Unique Paper Code	: 32237905	
Name of Paper	: **Computational Biology**	
Name of Course	: B.Sc. (H) Zoology : DSE–1	
Semester	: V	
Duration	: 3 hours	
Maximum Marks	: 75	

*(Write your Roll No. on the top immediately
on receipt of this question paper.)*

Attempt **five** questions in all including
Question No. **1**, which is compulsory.

1. (a) Define the following :

   (i)   Bioinformatics

   (ii) Metabolomics

   (iii) Composite database

   (iv) Molecular phylogeny

   (v)   Webin.   5

   (b) Explain the following symbols :

   (i) Σ

   (ii) SE_M

   (iii) μ

   (iv) β 4

   (c) Expand the following abbreviations :

   (i)   NDB

P.T.O.

(ii) ADMET

(iii) ZINC

(iv) OMIM   2

(d) Differentiate between :

(i) Linear and affine gap penalty

(ii) Local and global alignment

(iii) Paralogous and xenologous sequence

(iv) Type I and type II error

(v) Homology and similarity.   10

(e) Mention the major contribution of the following scientists in the field of computational biology :

(i) Saul B. Needleman and Christian D. Wunsch

(ii) Margaret Dayhoff

(iii) William Sealy Gosset   3

(f) Match the following :

Column A	Column B
(i) Database for structural classification	(a) SAGE map
(ii) Primary database	(b) SWISS-Prot
(iii) Gene expression database	(c) SCOP
	(d) DDBJ 3

2. (a) What is functional genomics? Elaborate the methods used to study forward genomics.

(b) Name few protein secondary structure prediction software. What is the significance of open access software?

6+6=12

3. (a) Define PAM matrix and discuss its principle of working.

(c) Enumerate the merits and demerits of PAM matrix in sequence alignment.

(d) A combination of PAM40 and PAM250 matrix will be used for what type of sequence? Justify your answer.

5+4+3=12

4. (a) Describe the principle and applications of Microarray.

(b) Briefly discuss sequence annotation methods.   6+6=12

5. Calculate the Dynamic Programming Matrix and an optimal alignment of the DNA sequence GAA TTC and GATT A, Score +2 for match, −1 for mismatch, and +2 for gap.   12

6. (a) Define χ^2 (*Chi-square*) test. Write down the formula of chi-square and describe the hypothesis on which it is based.

(b) RBC count lac/mm³ and Hb % g/100 ml of 500 persons of test locality was recorded as follows. Is there any significant relation between RBC count and Hb%? Find it by χ^2 method.   4+8=12

RBCs Count	Hb%		Total
	Above normal	Below normal	
Above normal	85	75	160
Below normal	165	175	340
Total	250	250	500

7. Write short notes on the following (any *three*) :

(a) Molecular docking

(b) MetaCyc

(c) T-test

(d) Multiple Sequence Alignment.   4+4+4=12

645   4   500