COMPUTATIONAL BIOLOGY
(BIOT 4221)

Time Allotted : 3 hrs **Full Marks : 70**

Figures out of the right margin indicate full marks.

Candidates are required to answer Group A and any 5 (five) from Group B to E, taking at least one from each group.

Candidates are required to give answer in their own words as far as practicable.

Group – A
(Multiple Choice Type Questions)

1. Choose the correct alternative for the following: **10 × 1 = 10**

(i) Examples of basic amino acids are
(a) Glutamic acid and Aspartic acid (b) Glycine and Leucine
(c) Histidine and Lysine (d) Methionine and Lysine.

(ii) A comprehensive database for the study of human genetics and molecular biology is
(a) PDB (b) STAG (c) OMIM (d) PSD.

(iii) SCOP is
(a) primary database
(b) nucleotide sequence database
(c) based on architectural classification of protein
(d) structural database.

(iv) Which of the following is a nucleotide sequence database?
(a) EMBL (b) SWISS PROT (c) PROSITE (d) TrEMBL.

(v) Which of the following is protein structure database?
(a) GenBank (b) SWISS PROT (c) DDBJ (d) PDB.

(vi) PDB is
(a) Primary sequence database for macromolecule
(b) Composite database
(c) Database for three dimensional structure of biological macromolecule
(d) Secondary database for macromolecule.

(vii) Molecular modeling and simulation tools are written in a variety of languages find the odd one out
(a) C (b) fortran (c) python (d) arabic.

(viii) In the design of the OpenMM the API must support
(a) efficient implementations on a variety of architectures
(b) non implementations on a variety of architectures
(c) formation of a variety of architectures
(d) Efficient implementations on a variety of variables.

(ix) Joining of two monosaccharides take place through
(a) glycosidic bond (b) condensation
(c) oxidation (d) cellular respiration.

(x) Philosophy of development of Biopython is to
(a) ready to run programs (b) focus on the running of programs
(c) focus on the development of libraries (d) focus on debugging.

Group- B

2. (a) Derive the Henderson-Hasselbalch Equation for an amino acid. [(CO1)(Derive/HOCQ)]
(b) Enumerate the mechanism of DNA replication. [(CO2)(Enumerate/IOCQ)]
5 + 7 = 12

3. (a) Give a comparative analysis of a fibrous protein and a globular protein. [(CO1)(Compare/IOCQ)]
(b) Comment on the functions of carbohydrates. [(CO1)(Comment/IOCQ)]
(c) Analyze the structure and function of steroids. [(CO1)(Analyze/IOCQ)]
4 + 4 + 4 = 12

Group - C

4. (a) Describe what do you mean by computational Biology. [(CO3)(Understand-knowledge/LOCQ)]
(b) Define the following terms: Pfam, BLOCKS and Profiles. [(CO3)(Understand-knowledge/LOCQ)]
(c) What type of data are available in biological databases? Write down the names of two primary sequence databases and two secondary databases. [(CO4)(Understand-apply/IOCQ)]
2 + (2 × 3) + (2 + 1 + 1) = 12

5. (a) Define motif. Name 2 databases which contains this type of data. [(CO3)(Remember-understand/LOCQ)]
(b) Mention two secondary databases that can classify protein according to their structure and describe about them. [(CO4)(Remember-understand/LOCQ)]
(c) Analyse the significance of PRINT and PROSITE databases. [(CO4)(Analyse/HOCQ)]
(2 + 2) + (2 × 2) + 4 = 12

Group - D

6. (a) Define pattern. [(CO6)(Remember/LOCQ)]
   (b) Classify pattern and analyse the areas briefly where pattern recognition technique is used. [(CO6)(Remember-analysis/IOCQ)]
   (c) Mention two tools which are based on this pattern analysis. [(CO6)(Remember-analysis/IOCQ)]

2 + (4 + 4) + 2 = 12

7. (a) Justify with reasons why LINUX is used in computational Biology [(CO5)(Remember-evaluate/HOCQ)]
   (b) Evaluate the areas where BioLinux can be used. [(CO5)(Remember-analysis/IOCQ)]

6 + 6 = 12

Group - E

8. (a) Write the full form of CADD. Evaluate the role of CADD in drug discovery. [(CO6)(Remember-analysis/IOCQ)]
   (b) Classify the categories of CADD and briefly describe them with suitable example. [(CO6)(Remember-analysis/IOCQ)]

(2 + 2) + (4 + 4) = 12

9. (a) Describe briefly the following methods - steepest descent method and conjugate gradient method. [(CO6)(Describe/IOCQ)]
   (b) Critically analyse the steps followed in comparative modelling for the prediction of 3D structure of target proteins. [(CO6)(Analyze/IOCQ)]
   (c) Name any one software which is followed for this case. [(CO6)(Remember/LOCQ)]

(3 × 2) + 4 + 2 = 12

Cognition Level	LOCQ	IOCQ	HOCQ
Percentage distribution	20.83	63.54	15.63

Course Outcomes (CO):

At the end of this course students will be able to:

1. Acquire basic understanding of structures and functions of different biomolecules.
2. Obtain knowledge about the different metabolic pathways.
3. Explain different biological data and biological databases.
4. Understand classification of databases and how the biological data are stored in those databases.

5. Obtain the knowledge of different algorithms and programming languages to manage biological data. 6. Apply different tools and software for analysis of biological data.

*LOCQ: Lower Order Cognitive Question; IOCQ: Intermediate Order Cognitive Question; HOCQ: Higher Order Cognitive Question