# COMPUTATIONAL BIOLOGY
## (BIOT 4221)

**Time Allotted : 2½ hrs** **Full Marks : 60**

***Figures out of the right margin indicate full marks.***

***Candidates are required to answer Group A and any 4 (four) from Group B to E, taking one from each group.***

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

## Group – A

1. Answer any twelve: **12 × 1 = 12**

*Choose the correct alternative for the following*

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

(ii) The number of amino acid residues in a protein of molecular weight 58300 is
(a) 110 (b) 253 (c) 530 (d) 330

(iii) The repeating unit of starch is
(a) Glucose (b) Maltose (c) Sucrose (d) Fructose

(iv) In Computational Biology Margaret Dayhoff developed first data base named
(a) SWISSPROT (b) PDB
(c) Atlas of protein sequence and structure (d) Protein sequence databank.

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

(vi) _____ is the process of recognizing patterns by using machine learning algorithm.
(a) Processed Data (b) Literate Statistical Programming
(c) Pattern Recognition (d) Likelihood

(vii) Where does the Hidden MarkovModel is used?
(a) Speech recognition
(b) Understand in go freal world
(c) Both Speech recognition & Understand in go freal world
(d) None of the mentioned.

(viii) Molecular dynamics approaches use classical mechanics in the form of Newton's laws of motion because:
(a) Quantum mechanics only applies to light particles such as electrons.
(b) Scientists have not yet developed any methods able to describe motion of atoms using quantum mechanics.
(c) Vibrational frequencies of proteins are so incredibly small that it would be dangerous to attempt a quantum mechanical description of them.
(d) Given the relatively high mass of atoms, it is often an acceptable approximation to neglect quantum mechanical effects when describing their motion.

(ix) Which of the following approach is considered under the 'Ligand based drug designing'?
(a) Molecular docking (b) QSAR Modeling
(c) Pharmacophore modelling (d) (b) and (c) both

(x) Which of the following is used to grow bacterial cultures continuously?
(a) Chemostat (b) Thermostat
(c) Haemostat (d) Coulter counter

*Fill in the blanks with the correct word*

(xi) In a protein, the amino acids are joined by _____ bonds.

(xii) _____ is an example of a secondary structure of a protein.

(xiii) In a polysaccharides, the monosaccharides are joined by _____ bonds.

(xiv) _____ is used to define a block of code in Python language.

(xv) _____ tool is used to predict the three-dimensional structure of a protein.

## Group - B

2. (a) Define amino acids. Classify amino acids based on polarity of amino acids. *[(CO1)(Remember/LOCQ)]*
(b) Calculate the ATP produced per mole of glucose consumption. *[(CO2)(Calculate/HOCQ)]*
**(2 + 4) + 6 = 12**

3. (a) Enumerate the types and function of the protein. *[(CO1)(Analyse/IOCQ)]*
(b) Derive the relation between number of amino acids and molecular weight of protein. *[(CO1)(Derive/IOCQ)]*
(c) Amino acids are known as Ampholytes-explain. *[(CO1)(Apply/IOCQ)]*
**6 + 3 + 3 = 12**

## Group - C

4. (a) Write short notes on PDB citing structure, function of it. *[(CO3)(Analyse/HOCQ)]*
(b) Describe in detail about SCOP and CATH. *[(CO3)(Remember/LOCQ)]*

(c) Mention two names of each of the following:
(i) Secondary database of nucleotide sequence
(ii) Secondary database of protein sequence. *[(CO3)(Remember/IOCQ)]*

**4 + 3 + (3 + 2) = 12**

5. (a) Define primary database and secondary database. *[(CO3)(Understand/LOCQ]*
(b) Discuss the two main functions of biological database.
*[(CO3)(Understand-knowledge/LOCQ)]*
(c) What type of data are available in biological databases? Write down the manes of two primary sequence databases and secondary databases.
*[(CO4)(Understand-apply/IOCQ)]*

**(2 + 2) + (2 + 2) + (2 + 2) = 12**

## Group - D

6. (a) What is Hidden Marcov Model? Discuss the application of HMM in computational biology. *[(CO3)(Analyse/HOCQ)]*
(b) What are the advantages and disadvantages of use Artificial Neural Network in computational biology? *[(CO4)(Remember/LOCQ)]*
(c) Mention one important application of ANN in computational biology.
*[(CO2)(Apply/IOCQ)]*

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

7. (a) Mention the characteristics of Python. *[(CO6)(Understand/LOCQ)]*
(b) Mention how Python can be used to for parsing of biological data. *[(CO6)(Analyse/IOCQ)]*
(c) Mention with example how representation of sequences can be done using Biopython. *[(CO6)(Remember/LOCQ)]*

**3 + 5 + 4 = 12**

## Group - E

8. Some mathematical models are used for studying bacterial growth kinetics These models are divided in to structured, unstructured and segregated models mention the characteristics of one each microbial growth kinetics model based on the above mentioned models. *[(CO6)(Remember-evaluate/HOCQ)]*

**(3 × 4) = 12**

9. (a) Describe the basic steps of drug discovery. *[(CO6)(Describe/HOCQ)]*
(b) Mention the trials which are needed to be followed in drug discovery process.
*[(CO6)(Examine/IOCQ)]*
(c) Briefly describe any one method used in computational drug design.
*[(CO6)(Analyse/IOCQ)]*

**5 + 3 + 4 = 12**

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| Cognition Level | LOCQ | IOCQ | HOCQ |
|---|---|---|---|
| Percentage distribution | 34.37 | 31.25 | 34.37 |