

B.TECH/AEIE/CHE/CSE/IT/8TH SEM/BIOT 4281/2019
COMPUTATIONAL BIOLOGY
(BIOT 4281)

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) A comprehensive database for the study of human genetics and molecular biology is
(a) PDB (b) STAG (c) OMIM (d) PSD.
- (ii) 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.
- (iii) Which of the following is a nucleotide sequence database?
(a) EMBL (b) SWISS PROT (c) PROSITE (d) TrEMBL.
- (iv) 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.
- (v) 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.
- (vi) The alignment method that tries to align the entire sequence is
(a) multiple sequence alignment (b) pairwise alignment
(c) global alignment (d) local alignment.

B.TECH/AEIE/CHE/CSE/IT/8TH SEM/BIOT 4281/2019

- (vii) Adenosine Triphosphate (ATP) is formed by the
(a) ADP (b) Phosphate (c) Monosaccharides (d) all of the above.
- (viii) Each record in a database is called an
(a) entry (b) file (c) record (d) ticket.
- (ix) Which of the following is an E.coli model organism database?
(a) EcoGene (b) EcoBase (c) EcoSeq (d) ColGene.
- (x) The most abundant biomolecule on the earth
(a) nucleic acid (b) protein
(c) lipids (d) carbohydrates

Group – B

2. (a) Classify proteins according to chemical composition, shape and solubility.
(b) What is starch?
(c) What are the differences between amylose and amylopectin?
(d) Write down the importance of highly branched structure of glycogen.
- 6 + 2 + 2 + 2 = 12**
3. (a) What are glycosidic bond and peptide bond? Classify simple protein.
(b) What are hormones? Discuss about the three most important types of hormones.
- (3 + 4) + (1 + 4) = 12**

Group – C

4. (a) What are the two main functions of biological database?
(b) What type of data are available in biological databases?
(c) Write down the names of three primary sequence databases.
(d) What is sequence motif?
(e) Name two databases which contain this type of data
- 2 + 3 + 3 + 2 + 2 = 12**
5. (a) Write down at least two examples of primary, secondary and composite structure databases.
(b) What is sequence alignment? Write down the importance of scoring matrix. Define global alignment and local alignment.
- 6 + (2 + 2 + 2) = 12**

Group - D

6. (a) What is Hidden Markov Model (HMM)?
(b) Discuss the application of HMM in computational biology.
(c) What are the advantages and disadvantages of using Artificial Neural Network (ANN) in computational biology?
(d) Mention one important application of ANN in computational biology.

$$2 + 4 + 4 + 2 = 12$$

7. (a) Write with reason the basic of formation of Biopython.
(b) Mention how Python can be used to for parsing of biological data.
(c) Mention the advantages and disadvantages of Biopython

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

Group - E

8. (a) Write the construction and design principles of Open MM Library.
(b) Discuss with the help of diagram about Open MM architecture.
(c) Describe any two platform-specific properties of CUDA Platform.

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

- 9.(a) Mention the any four aspects of computer in biomolecular study.
(b) Mention the steps of in silico drug design.
(c) Mention the trials needed to be followed after in silico drug designing.

$$4 + 6 + 2 = 12$$