# 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
<u>any 5 (five)</u> from Group B to E, taking <u>at least one</u> 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)     The repeating unit of proteins are
            (a) glucose units                          (b) amino acids
            (c) fatty acids                            (d) peptides

    (ii)    Amino acids are joined by
            (a) peptide bond                           (b) hydrogen bond
            (c) ionic bond                             (d) glycosidic bond

    (iii)   The most abundant biomolecule on the earth
            (a) nucleic acid                           (b) protein
            (d) lipids                                 (d) carbohydrates

    (iv)    The major functions of carbohydrates include
            (a) structural framework                   (b) storage
            (c) both (a) and (b)                       (d) none of these

    (v)     Sucrose is a
            (a) monosaccharide                         (b) disaccharide
            (c) polysaccharide                         (d) triose

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

    (vii)   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.

(viii)   The procedure of aligning many sequences simultaneously is called
(a) multiple sequence alignment      (b) pairwise alignment
(c) global alignment      (d) local alignment

(ix)   Choose how can we generate random numbers in python using methods from the following options
(a) random.uniform ()      (b) random.randint()
(c) random.random()      (d) All of the above

(x)   The dmesg command
(a) Shows user login logoff attempts
(b) Shows the syslog file for info messages
(c) kernel log messages
(d) Shows the daemon log messages

# Group – B

2.   (a)   What are carbohydrates? What are the different types of carbohydrates exist?

(b)   Write down and justify the energy yield after completion of glycolysis and TCA cycle of one molecule of glucose? Where glycolysis and TCA cycle occurs in the cell?

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

3.   (a)   Classify proteins according to their chemical composition and function.

(b)   What is saturated and unsaturated fatty acid?

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

# Group – C

4.   (a)   How can you categorise biological database? What type of data are submitted in those database?

(b)   What is profile and pattern?

(c)   Mention atleast two names of each of the following databases
(i)  Primary nucleotide sequence database
(ii) Primary protein sequence database.

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

5.   (a)   Write down the significance of PAM and BLOSUM in computational biology.

(b)   What are the different types of sequence alignment? Explain in detail.

**(3 + 3) + 6 = 12**

# Group – D

6.   (a)   What is Hidden Marcov Model (HMM)? What are the applications of HMM in biotechnology?

(b)     What are the features of Artificial Neural Network (ANN)? Write down the merits and demerits of ANN

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

7.   (a)     Write short notes on steepest descent method and conjugate gradient method.

     (b)     Mention the steps followed in comparative modeling for the prediction of 3D structure of target proteins. Name any one software which are followed for this case.

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

# Group – E

8.   (a)     Write short notes on Open MM Library

     (b)     Describe the architecture of Open MM Library with suitable diagram

     (c)     Discuss any two platform specific prpperties of CUDA Platform

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

9.   (a)     Mention the approaches followed to compute energy of a molecule. Write characteristics of those approaches.

     (b)     Define force fields. write the equation for calculation of total energy of the molecule, mention briefly the parameters

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

| Department & Section | Submission Link |
|---|---|
| **AEIE** | https://classroom.google.com/c/MzIzNzM4MDQ1MTcw/a/MzA0NDY4Mzk2Mzkz/details |
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