



MBH-1603220001020300 Seat No. _____

B. Sc. (Bioinformatics) (Sem. II) (CBCS) Examination

March / April - 2018

BI - 203 : Introduction to Bioinformatics

(New Course)

Time : $2\frac{1}{2}$ Hours]

[Total Marks : 70

- Instructions :** (1) All questions are compulsory.
(2) The right side figure indicates total marks of the question.

- 1 Attempt the following : **14**
- (A) Answer the following short questions : **4**
(ALL COMPULSORY)
- (1) Full form of NHGRI is _____.
- (2) In which year was NCBI founded?
- (3) What is the full form of NCBI?
- (4) The Smallest known vertebrate genome is _____.
- (B) Answer Any **One** of the following short questions : **2**
- (1) What is SRS?
- (2) Define cheminformatics.
- (C) Answer Any **One** of the following short question : **3**
- (1) Explain Applications of Information theory.
- (2) Use of database in Biological discovery.
- (D) Explain Any **One** of the following questions in details **5**
- (1) What are the ways biological data being heterogeneous?
- (2) What are the different branches of Bioinformatics and its applications?

- 2** Attempt the following : **14**
- (A) Answer the following short questions : **4**
(ALL COMPULSORY)
- (1) Who first set up the PDB at Brookhaven?
 - (2) What are the online submission tools for GenBank?
 - (3) What is the full form of INSDC?
 - (4) Give examples for protein visualization Tools?
- (B) Answer Any **One** of the following short questions : **2**
- (1) Describe open-source model visualization tool
 - (2) Define EST
- (C) Answer Any **One** of the following short questions : **3**
- (1) Write in detail about literature database?
 - (2) Define orthologous, paralogous, and xenologous.
- (D) Explain Any One of the following questions in detail : **5**
- (1) Explain any five latest bioinformatics tools
 - (2) ENA
- 3** Attempt the following : **14**
- (A) Answer the following short questions : **4**
(ALL COMPULSORY)
- (1) Different protein or gene in similar or relative function presents in same organism it call?
 - (2) BLOSUM matrix is developed from _____ database
 - (3) What is TPA?
 - (4) _____ is process of identification of similarity present in the entire length of sequences.
- (B) Answer Any **One** of the following short questions : **2**
- (1) Pairwise alignment
 - (2) How to creating sub problems in dynamic programming ?

- (C) Answer Any One of the following short questions : **3**
- (1) NCBI Genome Database
 - (2) Difference between PAM and BLOSUM Matrix.
- (D) Explain Any **One** of the following questions **5**
in detail :
- (1) Write in detail about literature database
 - (2) What are the sequence comparison methods available?
- 4** Attempt following : **14**
- (A) Answer the following short questions : **4**
(ALL COMPULSORY)
- (1) What is the full form of MAFFT?
 - (2) UniProt KB consist of _____ and _____.
 - (3) BLAST developed by Stephen Altschul, Warren Gish, Webb Miller, Eugene Myers and David J. Lipman.
(True / False)
 - (4) _____ search the sequence against the genome of specific organism.
- (B) Answer Any **One** of the following short questions : **2**
- (1) Consensus sequences
 - (2) Score
- (C) Answer Any One of the following short questions : **3**
- (1) Substantiate EB-Eye is a sequence retrieval Tool
 - (2) Database similarity search
- (D) Explain Any One of the following questions in detail: **5**
- (1) Multiple Sequence Alignment
 - (2) Methods for protein secondary structure prediction.

- 5 Attempt the following : 14
- (A) Answer the following short questions : 4
(ALL COMPULSORY)
- (1) _____ is a way to judge the reliability of the branches in a tree.
 - (2) Definition: Node
 - (3) Full form of UPGMA _____.
 - (4) TreeFam is a database composed of _____.
- (B) Answer Any **One** of the following short questions : 2
- (1) Unit of Phylogenetic tree construction
 - (2) What are nodes? Types of nodes?
- (C) Answer Any **One** of the following short questions : 3
- (1) Why Smith-Waterman algorithm cannot have used for BLAST search?
 - (2) List out a few Phylogenetic tree construction software.
- (D) Explain Any **One** of the following questions in details : 5
- (1) Explain distance based methods to construct phylogenetic tree.
 - (2) Phylogenetic tree topology and branch length.
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