



**AAQ-003-006203**      Seat No. \_\_\_\_\_

**B. Sc. (Bioinformatic) (Sem. II) (CBCS) Examination**

**April / May - 2016**

**B. Sc. BI-203 : Bioinformatics**

*(Introduction to Bioinformatics)*

**Faculty Code : 003**

**Subject Code : 006203**

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

[ Total Marks : 70

### **PART-A**

**1      Attempt MCQ :      20**

- (1) Methods such as \_\_\_\_\_ and \_\_\_\_\_ can achieve up to 80% overall accuracy in globular proteins.  
(A) Neural networks and Support vector machines  
(B) GOR and Chou-Fasman  
(C) HMM and GOR  
(D) Neural networks and Chou-Fasman
- (2) What is full form of GOR?  
(A) Genome Organization Research  
(B) Garnier Osguthorpe and Robson  
(C) Garnier Organization Research  
(D) Global Organization Research
- (3) Which is the method is used in Structure Comparison?  
(A) X-ray crystallography  
(B) DALI  
(C) CE  
(D) Both (A) and (C)
- (4) Which of the following is the protein sequence analysis tools?  
(A) ExPASy molecular biology server  
(B) Tools for Biochemistry and Molecular Biology  
(C) Cyber Genome Tools Analysis  
(D) All the above
- (5) The Smallest known vertebrate genome  
(A) Yeast      (B) C. elegans  
(C) Pufferfish      (D) A. thaliana

- (6) The study of relationships between the genomes of different species is known as
  - (A) Structural Genomics
  - (B) Comparative Genomics
  - (C) Metagenomics
  - (D) Systems Biology
- (7) Post transcriptional modification occurs in
  - (A) Cytoplasm
  - (B) Mitochondria
  - (C) Golgi complex
  - (D) all
- (8) What is computational chemistry?
  - (A) Knowing function of genes
  - (B) Solving neurological problem via information technology
  - (C) Solving chemical problems via computational technology
  - (D) Solving pharmacology problem via information technology
- (9) Method for retrieving the GenBank data
  - (A) QUICK
  - (B) BLAST
  - (C) SAGE
  - (D) FASTA
- (10) After what duration, every database in INSDC shares their database?
  - (A) Within 24 hrs
  - (B) Within 48 hrs
  - (C) Every 24 hrs
  - (D) Every 48 hrs
- (11) Full form for UniMES
  - (A) UniProt Metagenomics Energetic Sample Sequence
  - (B) UniProt Metaphylogenetic Energetic Sample Sequence
  - (C) UniProt Metagenomic Environmental Sample Sequence
  - (D) UniProt Metagenesis Environmental Sample Sequence
- (12) Referring any previous article having source of information is called?
  - (A) Simulation
  - (B) Citation
  - (C) Assimilation
- (13) Who is the scientist to introduce the concept of impact factor?
  - (A) Thomson Reuters
  - (B) T.K Attwood
  - (C) Eugene Garfield
  - (D) David Mount

- (14) Which method is used to produce multiple sequence alignment?
- (A) Dynamic programming
  - (B) Word based method
  - (C) Dot matrix
  - (D) Progressive method
- (15) Which method can give optimal alignment out of many sub-optimal alignment?
- (A) Dot matrix
  - (B) Dynamic programming
  - (C) BLAST
  - (D) All
- (16) One of the standard method of scoring MSA is?
- (A) Dynamic
  - (B) Accurate
  - (C) Sum of Pair
  - (D) Sum of Sequence
- (17) Which among the following is also a scoring method of MSA?
- (A) K-coffee
  - (B) T-cafe
  - (C) Gene algorithm
  - (D) Genetic algorithm
- (18) Which among the following is/are the application of MSA?
- (A) Gene Identification
  - (B) Identification of protein family
  - (C) Pattern identification
  - (D) All of the above
- (19) Protein with different gene and same organism is known as?
- (A) Orthologous
  - (B) Paralogous
  - (C) Xenologous
  - (D) None of these
- (20) If the scale of the phylogenetic tree is mentioned then it is called Scaled, Dendogram or \_\_\_\_\_ tree.
- (A) Xenogram
  - (B) Hectogram
  - (C) Xelogram
  - (D) Phylogram

## PART-B

- 2** (a) Explain any **three** : **6**
- (1) Systems biology
  - (2) PAM
  - (3) List out the secondary database of protein
  - (4) Sequence Alignment
  - (5) What are the skills required to become a Bioinformatics expert?
  - (6) Gene and Genome

- (b) Explain any **three** : **9**
- (1) What is Gene, Genome and Genomics?
  - (2) What Subject knowledge needed to the Computer Scientist, who want to become Bioinformatician?
  - (3) Classification of Biological databases
  - (4) How can you retrieve GenBank data
  - (5) Applications of Information theory
  - (6) Motif V/s Fingerprint
- (c) Attempt any **two** : **10**
- (1) What are the challenges of Bioinformatics and what is the Solution for that?
  - (2) Various disciplines in Bioinformatics
  - (3) Summarize Uniprot
  - (4) Swiss PDB Viewer
  - (5) Difference between MEDLINE, PubMed and PMC.
- 3** (a) Explain any **three** : **6**
- (1) Global vs local alignment
  - (2) Local vs Global Alignment
  - (3) Profile
  - (4) Scoring Matrix
  - (5) Metabolomics
  - (6) Topology and Branch length
- (b) Explain any **three** : **9**
- (1) Topology and Branch length in Phylogenetic tree
  - (2) Human Genome Project
  - (3) Dot Matrix
  - (4) Multiple sequence alignment method
  - (5) Scores for sequence
  - (6) Significance of pairwise sequence alignment
- (c) Attempt any **two** : **10**
- (1) Information theory
  - (2) Phylogenetic analysis
  - (3) BLAST
  - (4) Methods for protein secondary structure prediction
  - (5) What are the activities fall under the Plagiarism?