



JAO-1603220001030100 Seat No. _____

B. Sc. (Sem. III) (CBCS) Examination

November - 2019

**BI 301 : Bioinformatics Databases &
Sequence Analysis**

(New Course)

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

[Total Marks : **70**

- 1 Attempt the following : **14**
- (a) Answer the following short questions : **4**
(All Compulsory)
- (1) What is ELIXIR ?
 - (2) What is TGCA project ?
 - (3) An advantage of the _____ is that it permits more complex, hierarchical (tree-like) structures to be represented.
 - (4) _____ is a model for integrating data where the data from different sources reside on a central repository.
- (b) Answer any one of the following questions : **2**
- (1) What are Data, Metadata and Application Flow ?
 - (2) What is Data management ?
- (c) Answer any one of the following questions : **3**
- (1) Explain data standardization ?
 - (2) Big Biological data, its challenges and opportunities.
- (d) Answer any one of the following questions : **5**
- (1) Data exploitation and data heterogeneity.
 - (2) Data integration and its challenges ?

- 2** Attempt the following : **14**
- (a) Answer the following short questions : **4**
(All Compulsory)
- (1) _____ is a database of protein families that includes their annotations and multiple sequence alignments generated using hidden Markov models.
 - (2) JASPAR is a database for protein families.
(True or false)
 - (3) Define Exons.
 - (4) Define transcription factor.
- (b) Answer any one of the following questions **2**
- (1) Explain about PFam database ?
 - (2) Explain Nucleic acids structure database.
- (c) Answer any one of the following questions : **3**
- (1) Give a brief note on sequence motifs and active sites database.
 - (2) Explain protein localisation and targeting database.
- (d) Answer any one of the following questions : **5**
- (1) Explain in detail protein sequence database.
 - (2) Explain in detail about nucleotide sequence databases.
- 3** Attempt the following : **14**
- (a) Answer the following short questions : **4**
(All Compulsory)
- (1) Expand HAMAP.
 - (2) The _____ was developed to disseminate the results of transposon-based forward genetic screens in mice.
 - (3) Name the database for Enzymes and enzyme nomenclature.
 - (4) List the database for human ORF's.

- (b) Answer any one of the following questions : **2**
- (1) EBI metagenomics
 - (2) What is protein interaction and its importance ?
- (c) Answer any one of the following questions : **3**
- (1) Explain HMDB.
 - (2) Explain BRENDA.
- (d) Answer any one of the following questions : **5**
- (1) Explain a Hamap.
 - (2) Explain Ensemble database ?
- 4 Attempt the following : **14**
- (a) Answer the following short questions : **4**
- (All Compulsory)
- (1) Give full form of RAP.
 - (2) _____ is a Chromosome-based genome encompassing primary sequence data from Arabidopsis thalianaTAIR9.
 - (3) _____ is a database containing quantitative binding data for peptides binding to MHC Ligand, TCR-MHC Complexes, T Cell Epitope, TAP, B Cell Epitope molecules and immunological Protein-Protein interactions.
 - (4) _____ is part of the Swedish biobanking infrastructure of Sweden (BBMRI.se) and is developed and managed at the Department of Immunology Genetics and Pathology, Uppsala University, Sweden.
- (b) Answer any one of the following questions : **2**
- (1) What is TAIR ?
 - (2) What do you mean by GEO ?
- (c) Answer any one of the following questions : **3**
- (1) Mitochondrial gene and protein database. Explain.
 - (2) Explain Immunological Database.

- (d) Answer any one of the following questions : **5**
- (1) Explain Microarray database.
 - (2) DrugBank : Explain in detail.
- 5** Attempt the following : **14**
- (a) Answer the following short questions : **4**
(All Compulsory)
- (1) _____ are heuristic methods that are significantly more efficient than dynamic programming.
 - (2) _____ have been used to produce probability scores for a family of possible multiple sequence alignments for given query set.
 - (3) Evolutionary pathways describe a phylogeny. (True/False)
 - (4) Common software tools used for general sequence alignment tasks include.
- (b) Answer any one of the following questions : **2**
- (1) What is log odd score ?
 - (2) Define pairwise alignment.
- (c) Answer any one of the following questions : **3**
- (1) What is sequence alignment and its importance ?
 - (2) Explain BLAST.
- (d) Answer any one of the following questions : **5**
- (1) Explain PAM and BLOSUM.
 - (2) Multiple sequence alignment and Progressive methods of multiple sequence alignment, Iterative methods of multiple sequence alignment.
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