Syllabus Prescribed for 2024 Year   **UG. Programme**

B.Sc. Bioinformatics

Semester V

Course Subject Title of the Couse/ Subject   **No. of periods/ week**

DSC V   **Methods in Bioinformatics**   **03**

Cos:

1. To use & develop tools to curate (compare &analyze) biological data.
2. 2. To utilized skill of databases for bioinformatics

UNIT I: Introduction to Bioinformatics and Databases: Introduction to Bioinformatics; Different definitions of Bioinformatics, Bioinformatics – A. multidisciplinary Approach, History of Bioinformatics; Application and Scope of Bioinformatics.Importance of Database, Types of Databases, Data Models, Data Abstraction, Database Design (DBMS & RDBMS), Data Security, Data Warehousing, capture and Analysis, Data Management and Architecture. Microarray Database, Enzyme Database, Biodiversity Database,Nucleic Acid Sequence databanks, Genomic Databases.

UNIT II:**Biology and Computer Science:** Structural Organization of genome. In silico analysis of primary structures of nucleic acid sequences. Representing sequence Data, a program to store a DNA sequence, DNA Fragments, Transcription: DNA to RNA.Translating DNA into proteins.Random number generators. A program using randomization. A program to simulate DNA mutation generating random DNA analyzing DNA.

UNITIII: Sequence Similarity Searches: Sequence similarity searches methods (Pairwise and Multiple Sequence alignment); Significance of sequence alignment; Sequence alignment – global, & local and freespace; Alignment scores and gap penalties; Measurement of sequence similarity; Similarity and homology. Database Similarity Searches: BLAST, FASTA, PSI-BLAST, PHI-BLAST,Reading DNA from files in FASTA format reading frames,BLAST output files, parsing BLAST output presenting data.

UNIT IV: Restriction Maps and Regular Expression: Regular expression restriction maps and restriction enzymes GenBank, GenBank files, GenBank libraries, separating sequence and annotation, parsing annotations indexing GenBank with DBM. Biological Databanks; Introduction to Biological databanks (NCBI, Uniprot, EMBL, PIR, MMDB, Pfam) Protein Sequence databanks: PDB, SRS, SWISSPROT.

UNIT V: Protein Data Bank: The Organization of proteins. Basic principles on which the protein prediction methods of first, second and third generation are based; algorithms of Chou Fasman, GOR methods; Protein Tertiary structure prediction methods: Homology modeling, fold recognition, Abintio Method. Comparison between and tertiary structure. Files and Folders PDB files parsing PDB files controlling other programs.

UNIT VI: HMM (Hidden Markov Model): Introduction to HMM, its application in sequence alignment and structure prediction, based Software's (HMMER and HMMSTR) obtaining BLAST String Matching andHomology, Introduction to bioperl (Installation, uses features and application).

Suggested Reading:
1. D.W. Mount Bioinformatics: Genome and Sequence Analysis: (2001) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.
2. Ian Korf, Mark &Josaph: BLAST, Oreilly Publisher, 2003
3. R. Durbin, S. Eddy, A. Krogh and G. Mitchison, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Cambridge University Press.
4. A.D. Baxevanis& B.F.F. OuletteBioinformatics – A practical guide to the Analysis of Genes and Proteins,2002, Willey International publishers.
5. M.J. Bishop and C.J. Rawlings (editors), DNA and Protein Sequence Analysis---A Practical Approach IRL Press at Oxford University Press, ISBN 0 19 963464 7 (Pbk) 6.
6. J. Pevsner (2002) Bioinformatics and Functional Genomics; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York
7. Peakman M, and Vergani D. (2009). Basic and Clinical Immunology. 2nd edition Churchill Livingstone Publishers, Edinberg.
8. Richard Coico, Geoffrey Sunshine 2008 Immunology: A Short Course, 6th Edition Wiley- Blackwell
9. Sudha Gangal 2013 Textbook of Basic and Clinical Immunology Orient Blackswan Private Limited - New Delhi
10. J. Setubal and J. Meidanis(1997) Introduction to Computational Molecular Biology, PWS Publishing Co
11. . 11. J. Pevsner (2002) Bioinformatics and Functional Genomics; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.

Learning Outcome:
1. To gain knowledge about various biological databases that provide information about nucleic acids and protein.
2. Introduction to Biological databases and database systems.
3. Overview about types and biological data and database search tools

Syllabus Prescribed for 2024 Year UG. Programme
Programme   **B.Sc. Bioinformatics**
Semester V
Code of the Course Subject Title of the Couse/ Subject No. of periods/ week
AEC V Advanced Techniques01

Cos: Student would be able to use and understanddifferent tools/software and techniques used in Bioinformatics.

Unit I
Advanced Techniques: Algorithms for searching sequence patterns: MeMe, PHI-BLAST, SCanProsite and PRATT; Algorithms for generation of sequence profiles: Profile Analysis method of Gribskov, HMMER, PSI-BLAST; Basic concepts on identification of disease genes, role of bioinformatics in OMIM database, reference genome sequence, integrated genomic maps, gene expression profiling; identification of SNPs, SNP database (DbSNP). Role of SNP in Pharmacogenomics, SNP arrays.

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~~B.Sc.~~ **Programme**   **B.Sc. Bioinformatics**

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**Practical V   (Laboratory/Practical's/   06
                                hands on Activity)**

Practical's:

1. Primary structure database-GENBANK, PIR, PDB, MMDB.
2. Protein Sequence comparison and analysis- PDB, SCOP, CATH
3. Properties of primary structure of proteins using online tools.
4. Prediction of secondary structure of proteins-GOR-IV
5. Visualization of tertiary structure of proteins in Rasmol or Cn3d.
6. Prediction of Tertiary structure of protein- SWISS-MODEL
7. Database Searches: NCBI, DDBI, EMBL, Uniprot, Swissport
8. Pairwise sequence alignment – BLAST, FASTA, PSI-BLAST, PHI-BLAST.
9. Multiple Sequence alignment – CLUSTAL-W, CLUSTAL Omega.
10. Different File Format- FASTA, GENBANK.

Suggested Readings:
1. Myers E.W. (1997), Computational Methods in genomic research Plenum Press, New York.
2. NCBI: National Centre for Biotechnology Information (1993), Manual for NCBI software development

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