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CHAPTER 1: INTRODUCTION TO BIOINFORMATICS **13-102**

- Introduction, definition, scope and importance of Bioinformatics
- Emerging fields: Genomics, Transcriptomics, Proteomics, Systems Biology, Functional Genomics, Metabolomics, and Molecular Phylogeny.
- Applications and limitations of Bioinformatics.
- Biological Databases:
 - Introduction, types, and classification: primary, secondary, and composite databases.
 - National Centre for Biotechnology Information (NCBI)
 - Nucleic Acid Databases: GenBank, DDBJ and data submission process, EMBL, and NDB, Gene Expression Database
 - Protein Databases: PIR, SWISS-PROT, TrEMBL, and PDB.
 - Metabolic Pathway Databases: KEGG, EcoCyc, and MetaCyc.
 - Small Molecule Databases: PubChem, DrugBank, ZINC, and CSD.
- Biological Database Retrieval Systems
 - Data Retrieval Systems:
 - Sequence Retrieval System (SRS) and Entrez.
 - Concepts of similarity, identity, and homology.
- Functional Genomics: genome-wide and high-throughput approaches to study gene and protein function.
- Drug Discovery Methods: basic concepts and applications in computational drug design.
- Data Generation and Submission:
 - Methods of data generation: gene sequencing, protein sequencing, mass spectrometry, microarray.
 - Sequence submission tools: BankIt, Sequin, Webin.
 - Sequence file formats: flat file, FASTA, GCG, EMBL, Clustal, Phylip, Swiss-Prot.
 - Sequence annotation principles.

CHAPTER 2: SEQUENCE ALIGNMENT AND MOLECULAR PHYLOGENY **103-142**

- Basic concepts of sequence alignment:
 - Concept and types of sequence alignment
 - Types: Local vs. Global alignment;
 - Pairwise and Multiple alignments.
 - Multiple Sequence Alignment (MSA) by CLUSTALW
- Global and local alignment algorithms:
 - Needleman-Wunsch method (Global Alignment)
 - Smith-Waterman method (Local Alignment)
- Scoring matrices: PAM (Percent Accepted Mutation), BLOSUM

(Blocks Substitution Matrix)

- Sequence analysis tools - BLAST: principles and applications.
- Concepts of similarity, identity, and homology.
- **Phylogenetic Analysis:**
 - Properties and types of phylogenetic trees.
 - Tree-Building Methods:
 - Distance-based approaches: UPGMA (Unweighted Pair Group Method using Arithmetic Mean), Neighbour Joining, Minimum Evolution, and Least Squares methods.
 - Character-based approaches: Maximum Parsimony and Maximum Likelihood methods.
- Methods of phylogeny and software used for phylogenetic analysis
- Consistency and validation of molecular phylogenetic predictions

CHAPTER 3: PROTEIN STRUCTURE AND HOMOLOGY MODELLING 143-164

- Amino Acids and Protein Structure:
 - Classification and structure of amino acids.
 - Levels of protein structure: primary, secondary, tertiary, and quaternary.
 - Ramachandran plot: concept, interpretation, and applications in protein modelling.
- Homology Modelling of Proteins:
 - Concept, methodology, and applications in structure prediction.
 - Template identification, alignment, model building, and validation.
- Protein Interactions:
 - Overview of protein-protein and protein-ligand interactions.
 - Significance of interaction on networks in biological systems.

CHAPTER 4: INTRODUCTION TO BIOSTATISTICS AND STATISTICAL DATA 165-184

- Concept and applications of statistics in biological sciences
- Importance of Biostatistics in biological research
- Sampling methods
- Types of data: primary and secondary
- Nature of data: qualitative vs. quantitative; discrete vs. continuous
- Collection, tabulation, and graphical representation (Pie chart, Bar diagram, Histogram, Frequency polygon).

CHAPTER 5: DESCRIPTIVE STATISTICS, PROBABILITY, AND STATISTICAL TESTS 185-272

- Measures of central tendency: Mean, Median, Mode
- Measures of dispersion: Variance, Standard Deviation, Standard Error, Coefficient of Variation
- Analysis of Variation (ANOVA): One-way and Two-way ANOVA.
- Distribution on patterns: Binomial, Poisson, and Normal distributions. Normal, Binomial and Poisson distributions,
- Skewness, and Kurtosis

- Probability concepts and applications.
- Hypothesis testing: Null and Alternative hypotheses
- Tests of significance: t-test, F-test, and Chi-square test, Correlation Coefficient, Correlation and Regression Analysis.
- Confidence intervals and confidence levels

CHAPTER 6: TECHNIQUES IN BIOLOGY

273-375

- Microscopy:
 - Working principle and uses of optical microscopy (resolving power, brightfield, darkfield)
 - Electron microscopy (SEM, TEM)
 - Phase-contrast microscopy
 - Fluorescence Microscopy
 - Confocal Microscopy
- Tracer Techniques:
- Principles and applications of:
 - Autoradiography
 - Radioimmunoassay (RIA)
- Immunological Techniques:
- Immunodiffusion and Immunoelectrophoresis
- Enzyme Linked Immunosorbent Assay (ELISA)
- Chromatographic Techniques:
 - Paper, Thin-Layer (TLC), Ion Exchange, Adsorption, Partition, Gel Filtration, Affinity Chromatography, High-Performance Liquid Chromatography (HPLC) and Column chromatography
- Centrifugation:
- Principles and types
- Density gradient and unit gravity methods
- Tissue processing and sub-cellular organelle separation
- Cryopreservation: methods and applications
- Colorimetry and Spectrophotometry:
 - Colorimeter, UV-Vis spectrophotometer (components, principle, applications, precautions)
- Electrophoresis and Blotting:
 - Gel electrophoresis,
 - Blotting techniques: Southern, Northern, and Western blotting
- DNA Sequencing:
 - Sanger's method and principle

CHAPTER 7: PRACTICALS

376-442

1. Compute Coefficient of Variance (CV) from collected data and measure variability.
2. Collect data on biological parameters (e.g., height/weight of plant or animal samples) and test the significance between mean, median, and mode.
3. Performing a two-sample t-test for a given dataset.

4. Creating graphical representations of statistical data using computer tools.
5. Accessing various biological databases.
6. Retrieval of nucleotide and protein sequences from online databases.
7. Performing pairwise sequence alignment using BLAST and interpreting the results.
8. Predicting protein structure from its amino acid sequence.
9. Construction of phylogenetic tree using MEGA software.
10. Retrieve DNA, RNA, and protein sequences and structures from biological databases to create datasets.
11. Perform pairwise and multiple sequence alignments using online/offline tools.
12. Demonstrate the working of the microscope, colorimeter, spectrophotometer, pH meter, and autoclave.
13. Visualise DNA through agarose gel electrophoresis.
14. Fractionate cellular components using centrifugation.
15. Separate amino acids through paper chromatography.

Suggested Readings

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