BHARATHIAR UNIVERSITY: COIMBATORE – 641046
M.Sc. BIOINFORMATICS
CBCS Syllabus (University Department)
Effective From the Academic year 2016-2017

Sem	Code No.	Subjects	University Examination			
			Internal	External	Total	Credit
I	16BIIA13A	Cell & Molecular Biology	25	75	100	4
	16BIIA13B	Computational Methods for Sequence Analysis	25	75	100	4
	16BIIA13C	Programming in C And C++	25	75	100	4
	16BIIA13D	Recombinant DNA Technology	25	75	100	4
	16BIIA1EA 16BIIA1EB	Basics of Mathematics & Statistics (or) Biostatistics	25	75	100	4
	16BIIA13P	Practical – I. Wet lab – Protein and Pharmacology	40	60	100	4
		Supportive I	12	38	50	2
II	16BIIA23A	Perl for Bioinformatics	25	75	100	4
	16BIIA23B	Molecular Interactions	25	75	100	4
	16BIIA23C	Biophysics &Crystallography	25	75	100	4
	16BIIA23D	Pharmacogenomics and Drug Design	25	75	100	4
	16BIIA2EC 16BIIA2ED	Biodiversity Informatics (or) Basics of Cheminformatics	25	75	100	4
	16BIIA23P	Practical II- Computer Programming	40	60	100	4
		Supportive - II	12	38	50	2
III	16BIIA33A	Genomics	25	75	100	4
	16BIIA33B	Proteomics	25	75	100	4
	16BIIA33C	Programming in Visual Basic with RDBMS	25	75	100	4
	16BIIA33D	Molecular Modeling	25	75	100	4
	16BIIA3EE 16BIIA3EF	Systems Biology (or) Introduction to Next Generation Sequencing	25	75	100	4
		Supportive - III	12	38	50	2
	16BIIA33P	Practical III -Molecular techniques	40	60	100	4
	16BIIA33Q	Practical IV- Biological Sequence Analysis and Computer Aided Drug Design	40	60	100	4
IV	16BIIA47V	Project Work, Viva-Voce			200	8

Total Marks: 2250 Credit: 90

Supportive offered to other Department

Sem	Code No.	Subjects	University Examination			
			Internal	External	Total	Credit
I&III	16BIIA1GS	Supportive-I Database & Sequence Analysis	12	38	50	2
II	16BIIA2GS	Supportive-II Basics of Bioinformatics	12	38	50	2

__Industrial visit becomes optional without any credits__
__Eligibility for admission to M.Sc., Bioinformatics:__ A pass in any of the following degree courses of UGC recognized universities
__B.Sc.,/B.Tech. In all Science disciplines, B.V.Sc , B.Pharm, M.B.B.S.and B.D.S..__

16BIIA13A   **SEM I**

CELL AND MOLECULAR BIOLOGY

Objective: To understand the basics of organization, biology and functions of the basic unit of life - Cell.

Unit I:

Biology of cell: Cells as a unit of life, structure of prokayotic and eukaryotic cells. An overview of organells (Mitochondria, chloroplasts, ER, Golgi, ribosomes, lysosomes and peroxysomes, nucleus and nucleolus). Differences and similarities in plant and animal cells. Cellular membrane: structure, transport, channels, carriers, receptors, endocytosis, membrane potentials.

Unit II:

Central Dogma of Life: DNA replication, Transcription and Translation. Cell-cell interactions and signal transductions: Intercellular junctions, signaling by hormones and neurotransmitters; receptors, G-proteins, protein kinases and second messangers.Protein traffic in cells.

Unit III:

Cell Cycle: Mitosis, Meiosis, Regulation. Mutation – Types of mutations, types of mutagenic agents and their molecular mechanism; DNA repair; Chromosomal types and structure; Mechanism by which genome undergoes changes, recombination, mutation, inversion, duplication, and transposition.

Unit-IV

Molecules of Life: Introduction to carbohydrates-Monosacharides and their derivatives, Disacharides, Polysacharides. Proteins –Structure of aminoacids, Different levels of organization-Primary, secondary tertiary and Quarternary structures. Nucleic acids – Purines, pyrimidines, Nucleosides and Nucleotides, Different structural form of DNA, denaturation and renaturation of DNA. Lipids-Structure and function of Fatty acids, Triacylglycerols, sphingolipids, steroids and glycerophospholipids. Water, small molecules-Alkaloids, glycosides, phenols, oligopeptides, Flavonoids, and terpenoids

Unit-V

Enzymes: Units of Activity, coenzymes and metal cofactors, temperature and pH effects, Michaelis – Menten kinetics, inhibitors and activators, active site and mechanism of enzyme action, Isoenzymes, allosteric enzymes.

References:

1. Lehninger, A. L. 1984. **Principles of Biochemistry.** CBS publishers and distributors, New Delhi, India

2. Horton, Moran, Ochs, Rawn, Scrimgeour **Principles of Biochemistry** Prentice Hall Publishers.

3. David. E. Sadava **Cell Biology: Organelle Structure and Feunction** Jones & Bartlett publishers.

4. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.

16 BIIA13B   **SEM I**

COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS

Objectives: To understand various computational techniques employed to analyze biological data with the use of sequence information.

Unit-I

Introduction to bioinformatics, Classification of biological databases, Biological data formats, Introduction to single letter code of amino acids, symbols used in nucleotides, data retrieval-Entrez and SRS.

Unit-II

Introduction to Sequence alignment. Substitution matrices, Scoring matrices – PAM and BLOSUM. Local and Global alignment concepts, Dot plot. Dynamic programming methodology: Needleman and Wunsch algorithm. Smith–Waterman algorithm. Statistics of alignment score. Multiple sequence alignment. Progressive alignment. Database search for similar sequences using FASTA and BLAST Programs.

Unit-III

Evolutionary analysis: distances, Cladistic and Phenetic methods. Clustering Methods. Rooted and unrooted tree representation. Bootstrapping strategies, Use of Clustal and PHYLIP.

Unit-IV

Gene finding methods. Gene prediction: Analysis and prediction of regulatory regions. Fragment assembly. Genome sequence assembly, Restriction Mapping, Repeat Sequence finder.

Unit-V

Concepts of secondary structure prediction of RNA and Protein. Probabilistic models: Markov chain, Hidden Markov Models-other applications.

References:

1. S.C. Rastogi, Namita Mendiratta, Parag Rastogi. **Bioinformatics – Concepts, Skills, Applications".**

2. Andréa's D. Baxevanis, B.F. Francis Ouellette. **Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.**

16BIIA13C   **SEM I**
PROGRAMMING IN C AND C++

Unit-I

Introduction to programming languages: Introduction –Programming languages – Problem solving Technique: Algorithm, Flowchart, Compiling, Testing and Debugging, Documentation – Data structures – Array, Stack, Queue, Linked List concepts.

Unit-II

Programming in C: C language Introduction – Tokens – Keywords, Identifier , Variables, Constants, Operators – Expression – Data types –Operator precedence - Statement: Input statement, Output statement, Conditional and Unconditional Control Statement – Looping Statement: while, do-while, for – nested loop – Arrays.

Unit-III

C - Procedural Concepts: Structured Programming – Built-in library function – User defined functions – Pointerintroduction – Passing pointer in a function – Structure – Union – File handle: Read and Write character from a file.

Unit-IV

Object Oriented Programming and C++: Basic concepts of OOPS- Data hiding-Encapsulation-Inheritance, Polymorphism – Introduction to C++, C vs C++ – data types, variables, constants, operators and statements in C++ – Conditional and looping statements.

Unit-V

Programming and C++: C++ classes - Classes & Objects – Functions in C++ – function prototype-definition-Different forms of Constructor – Destructor – Copy constructor – Inheritance –Single, Multiple and Multi level inheritance – Function & operator overloading - inline functions – Friend and virtual functions – Overloaded functions.

References:

1. **The C Programming Language**, B.W.Kernighan and D.M. Ritchie 2nd Edition. Prientice Hall of India.

2. Byron Gottfried, - **"Programming with C"** (Schaum's Outline Series) - Tata McGrawHill Publishing Company – 1998

3. E. Balagurusamy - **"Programming in C++ "** **-** Tata Mc. Graw Hill Edition

4. **Object oriented programming with C**++ -Robert Laffore -Waite series.

16BIIA13D   **SEM I**
RECOMBINANT DNA TECHNOLOGY

Subject Description: This paper provides the student the knowledge in genetic engineering, vectors in gene cloning, transformation in higher organisms and the applications of rDNA technology.

Objective: The objective of the paper is to introduce the Bioinformatians to application of rDNA technology. **Goal:** This paper will help the student to understand the techniques in recombinant DNA technology.

Unit -I

Introduction to cloning and rDNA technology, Cloning vectors: Plasmids (pUC 18 and Ti plasmids), Bacteriophages ($\Box\Box$ phage), Plasmids, Cosmids (pJB8), SV40, retrovirus and Artificial Chromosomes (BAC, YAC).

Unit-II

Strategies in gene cloning: restriction, ligase, insertion into vector, cloning, transformation into host cell, Enzymology of Recombinant DNA. Screening for recombinant (Insertional inactivation, Colony/in situ hybridization, radioactive antibody test, Xgal, complementation and physical methods).

Unit-III

Methods of gene transfer and genome sequencing:CaPO4 mediated gene transfer, liposomes, electroporation, electro fusion, micro-injection, particle bombardment. DNA sequencing (Sanger and Coulson method; Maxam and Gilbert method and Automated method) - Chromosomal walking, transposons, construction of genomic and cDNA libraries; molecular markers- RAPD, RFLP.

Unit- IV

Transgenic plants – high yielding, salt, draught, herbicide, disease resistant. Transgenic animals - for improved livestock production.

Unit-V

rDNA in medicine: Vaccines, enzymes, blood factors, interferon, gene therapy, DNA fingerprinting and its applications in forensic sciences.

References:

1. Principles of genetic manipulation; Ed. Old and Primrose, 6th Edition. Blackwell Science publication

2. Gene Cloning, a introduction – T. A. Brown, Chapman and Hall publications, 3rd Edition, 1995.

16BIIA1EA   **SEM I**

BASICS OF MATHEMATICS AND STATISTICS

Objectives: To understand the basics of mathematical and statistical techniques.

Unit-I

Basic Mathematics Matrix Algebra – Types – Determinants – Transpose – Conjugate – Inverse – Eigen values of matrices – Rank – Solving Simultaneous equations in three variables using matrices, Cayley – Hamilton theorem without proof – Verification and Computation of Inverse of a Matrix – Consistency of linear equations. **Vector** – Addition, subtraction – Dot product – Cross product (up to 3 vectors) – Scalar triple product – Gradient – Divergence and Curl.

Unit-II

Calculus Differentiation – Standard results – Derivatives of simple functions – Product Rule – Quotient Rule. **Partial Differentiation** – Partial derivative of simple functions (3 variables case only) - Euler's Theorem. **Integration** – Standard results – Integrals of simple functions – Definite Integrals – Indefinite Integrals – Integration by parts – Integration by substitution – Integration by partial fractions.

Unit-III

Basic Statistics Ungrouped Data and Frequency Distribution: Collection – Classification – Tabulation – graphical and diagrammatic representation of numerical data – Graphs – Histogram, Frequency curve. **Statistical Averages:** Mean, Median, Mode, SD, Variance and Coefficient of variation. **Correlation and regression analysis:** Types of correlation, Methods of studying correlation – Rank correlation – Simple linear regression – Regression Equations.

Unit-IV

Probability: Random experiment – Definitions of probability – Theorems of Probability: Addition rule –Multiplication Rule – Properties of probability – Conditional probability - Bayes Theorem – Simple Problems. Random variables – Discrete and Continuous – Probability mass functions – Probability density functions – Cumulative density function and its properties – Distributions Function. **Theoretical distributions** – Binomial, Poisson and Normal distributions – Basic ideas and their applications.

Unit-V

Test of Hypothesis Sampling: Population – Sample – Parameter – Statistic – Standard error - Hypothesis-Null Hypothesis – Alternative Hypothesis – Critical Region – Level of Significance – Errors in Sampling – One tailed and two test statistic-test of significance and its test procedure.

Test of significance for small samples: Tests based on normal distribution for Single mean, difference of two means - Tests based on t-distribution for single mean, difference of two means, paired test and observed correlation coefficient – F Test – Parametric and Non parametric tests - Chi-square ($\chi2$) test for goodness of fit. **Analysis of variance:** One way and two way classifications.

References:

1. T.K.Manickavachagam Pillai et al., **Calculus** - Volume I &II .

2. Raymond A.Barnett and Michael R.Ziegler **, Applied Mathematics** .

3. V.K.Kapoor and S.C.Gupta, **Fundamentals of Mathematical Statistics.**

 4. S.P.Gupta**, Statistical Methods.**

5. P. R. Vittal, **Allied Mathematics**, Margham Publishers.

(OR)

16BIIA1EB   **SEM I**

ELECTIVE PAPER: BIOSTATISTICS

UNIT – I

Statistics – Definition – Statistical methods – Basic principles – Variables – Measurements, functions- Collection of Data – Primary and Secondary – Types and methods of data collection – Procedure – Merits and Demerits – Classification and tabulation of data – Diagrams and graphs.

UNIT – II

Measures of Central tendency – Mean, Median, Mode, Geometric Mean – Merits and Demerits – Dispersion and measure of dispersion – Range, Standard deviation, quartile deviation – Merits and Demerits – Co-efficient of variations.

UNIT – III

Skewness and Kurtosis – Correlation – Types and method of correlation – Regression – Simple regression equation fitting – Prediction, similarities and dissimilarities of correlation and regression -

UNIT – IV

Distribution – Binomial, Poisson, Normal – Statistical inference – Sampling methods – Simple hypothesis testing – Students "t"- test – Chi square test.

UNIT – V

Sign test, Wilcoxon signed rank test, one sample Run Test, Median test, Kruskal Wallis H test, Kolmogorov Smirnov test, Mann Whitney U test.

TEXT BOOK:

1. Schaum's Outline Statistics by Murray.R, Spiegel, Larry.J.Stephens, 4th edition, McGraw Hill Companies.

2. Zar, J. - Bio-statistical Analysis, Prentice Hall of India.

3. An introduction to Bio-Statistics by N.Gurumani.2009 – MJP Publications.

16BIIA13P   **SEM I**

PRACTICAL – I

WET LAB – PROTEIN and PHARMACOLOGY

PROTEIN LAB

1. Isolation of bacteria from soil – serial dilution technique

2. Using serial dilution technique isolating fungi from soil

3. Isolation of actinomycetes from soil – serial dilution technique

4. Screening microbes for antibiotic production

5. Extraction of proteins from microbes, plant and blood

6. Separation of protein and molecular weight determination using SDS-PAGE

7. Staining the gel – CBB and Silver staining

PHARMACOLOGY LAB

8. Extraction of secondary metabolites from medicinal plants - Cold percolation method

9. Extraction of secondary metabolites from medicinal plants - Soxhlet method

10. Preliminary Phytochemical analysis of plant extracts

11. Antibiotic bioassay-inhibitory activity (Disc Diffusion)

12. Tissue culture - callus induction

13. Tissue culture - cell suspension culture

16BIIA23A   **SEM II**

PERL FOR BIOINFORMATICS

Unit-I

PERL BASICS: History of Perl —Data types – Operators – variables –Variable Interpolation- If, If-else, else if, For loops ,While loops , Until loop–Scalars, Lists, Hashs - Arrays – Array functions – Push and Pop , Shift and unshift – Hashes.

Unit-II

SUBROUTINES and MODULES: Subroutines for calculation, Reference to subroutine, Passing arrays and hashes to subroutines. Modules-Perl standard modules-Library.

Unit-III

OBJECT PERL, RE, and FILES: Object oriented Perl – Working with objects. Perl and Databases – Perl and DBM. Regular Expression – Working with regular expression. File Handling – Writing to Files.

Unit-IV

BioPERL: General Bioperl classes, Sequences (Bio::Seq Class, Sequence Manipulation), Features and Location Classes (Extracting CDS), Alignments (AlignIO), Analysis (Blast, Genscan), Databases (Database Classes, Accessing a local Database).

Unit-V

PERL FOR BIOINFORMATICS: Sequences and Strings – Representing Sequence data, store a DNA sequence, concatenating DNA fragments, Transcription. Motifs – Finding motifs, counting nucleotides. Genbank – Files and libraries. Protein Data Bank – files and folders, PDB files. Blast – String matching and homology, blast output files.

REFERENCES:

1. Simon Cozens and Peter Wainwright, **" Beginning Perl"** *,* Shroff publishers, Mumbai,2005.

2. James Tisdall, **"Beginning Perl for Bioinformatics",** Fourth Indian reprint, O'Reilly Publications, USA, 2005.

16BIIA23B   **SEM II**
MOLECULAR INTERACTIONS

Objective: to understand the basic concepts of interaction, how biological molecules interact with each other and the experimental techniques to study these molecules.

UNIT-I

Fundamentals of atomic and molecular orbitals: Theory of atomic and molecular orbitals; Linear combination of atomic orbitals; Quantitative treatment of valency bond theory and molecular orbital theory; Resonance structures; -bonds and -bonds.

UNIT-II

Fundamentals of chemical bonding and non-bonding interactions: Electrovalent bond, stability of electrovalent bond. Co- valent bond – partial ionic character of co-valent bonds. Shape of orbitals and hybridization. Co-ordination bond, Vander Waals forces; Metallic bond. Molecular geometry- VSEPR Theory.

UNIT-III

Folding pathways: Principles of protein folding, role of chaperons, hydrophobic interactions, electrostatic interactions, non-bonded interactions. Beta turns, gamma turns, types of helices, disulphide bridge.

UNIT –IV

Molecular interactions: protein-protein, protein-DNA, DNA-Drug, Protein-Lipid, Protein-Ligand, Protein-Carbohydrate interaction, Metalloprotein. Pi … Pi interactions, C-H…Pi interactions.

UNIT-V

Spectroscopy: Principles, Theory, Instrumentation and Application of UV, IR, NMR and Circular dichroism (CD) to macro molecules. Stereochemistry of proteins and nucleic acids.

References:

1. Albert cotton, F. 1971. **Chemical Application of Group Theory**. John Wiley and Sons, Inc. New York. 386 pp.

2. Spice, J. E. 1964. **Chemical Bonding and Structure**. Pergamon Press Ltd., Headington Hill Hall, Oxford. 395 pp.

3. Winter, m. j. 1996. **Chemical Bonding**. Oxford University Press, Inc., New York. 91 pp.

4. Ernest Eliel, 1996. **Stereochemistry of carbon compounds**, Prentice Hall

5. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.

16BIIA23C   **SEM II**

BIOPHYSICS AND CRYSTALLOGRAPHY

Objective: To get an insight into the biophysical techniques and introduction of X-ray crystallography to analyze protein molecular structures.

Unit – I

Introduction to protein structure: Physical and chemical properties of amino acids and polypeptides. Secondary, Super Secondary, tertiary and quaternary structure of proteins. Theoretical and experimental methods for determination of size of proteins. Physical nature of non covalent interactions. Conformational properties of proteins, Ramachandarn Plot.

Unit – II

Structural Bioinformatics: Homology modeling, Threading, Fold recognition, Model refinement and validation. Vector based method, neural network. Structural databases- PDB, CATH (Classification by Class, Architecture, Topology), SCOP - Structural Classification of Protein, FSSP – Fold classification based on structure – structure alignment, MMDB – Molecular Modeling Database, SARF – Spatial arrangement of backbone fragments. mmCIF formats used for archiving structures. Comparison of structures by tools – PyMOL, Chimera

Unit - III

Functional Bioinformatics: Cell surface receptors, GPCR's, Kinases, Channel proteins, Ubiquitin. Biophysical Techniques: Principles, Process and Applications of Thin layer chromatography, Column chromatography (ion exchange and affinity only), HPLC; Low Resolution Techniques: CD spectroscopy and DLS. 1 Directional and 2 D Electrophoresis, UV Visible spectroscopy. High Resolution Techniques: NMR, X-ray crystallography

Unit – IV

X-ray crystallography Introduction: x-ray generation; its application; unit cell lattices, Bragg's Law; synchrotron radiation and its uses; Symmetry, Atomic scattering factor and structure factor; phase problem; intensity data collection and reduction; hydrogen bonding.

Unit – V

X-ray crystallography of macromolecules: Isolation and purification of protein, crystallization (sitting and hanging drop method). Protein structure determination-molecular replacement technique; multiple isomorphous replacement method, multi wavelength anomalous diffraction method and x-ray anomalous scattering; Calculation of electron density map, interpretation of electron density map. Refinement of structure. Structure validation methods.

References:

1. Thomas. E. Creighton **Proteins Structures and Molecular Properties** Freeman and Company

2. Cantor and Schimmel **Biophysical Chemistry Part II Techniques for the study of biological structure and function** Freeman and Company

3. Thomas M Devlin **Textbook of Biochemistry** Wiley LISS Fifth edition

4. Stephen Neidle **Nucleic Acid Structure and Recognition**

5. Leonard Banaszak **Foundations of Structural Biology**

6. Philip E. Bourne **Structural Bioinformatics** John Wiley & sons

7. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.

8. J. Drenth: **Principles of protein x-ray crystallography**. Springer, New York (1994)

9. C. Brandén & J. Tooze: **Introduction to Protein Structure**. Second Edition, Garland, New York (1998).

16BIIA23D   **SEM II**

PHARMACOGENOMICS AND DRUG DESIGN

Unit – I

Introduction to pharmacogenomics, pharmacodynamics, pharmacokinetics, toxicokinetics and ADME properties, process of drug development-clinical trials phase I, II and III. Physiological drug distribution of protein binding: physiological factors, drug distribution, clinical pharmacodynamics, clinical pharmacokinetics and toxicokinetics.

Unit – II

Drug concentration, nature of cell membrane, physiological factors related to drug absorption – drugs across cell membrane, route of drug administration, oral absorbtion and gastro intestinal tract absorption. Metabolic changes of drugs and related organic compounds: General pathways, sites of drug biotransformation, oxidative biotransformation, reductive reactions, hydrolytic reactions, conjugation reactions, factors affecting drug metabolism.

Unit – III

Factors affecting variability in drug response, drug metabolism, Ayugenomics (integration of Ayurveda & genomics), genetic analysis of human variation, Microsatellite for studying genetic variation, Ayugenomics for human population. Microarray in herbal drug research, Pharmacodynamics, Pharmacogenomics and Pharmacognosy.

Unit – IV

Pharmacogenomics in the treatment of cancer, neurodegenerative diseases, cardiovascular diseases. Pharmacogenomics in pharmaceutical industry, Ethical issues related to Pharmacogenomics, Pharmacogenomics and ethanopharmacology, Benefits of Pharmacogenomics.

Unit – V

Macromolecular modeling, design of ligands for known macro molecular target sites, Drug-receptor interaction, classical SAR/QSAR studies and their implications to the 3-D modeler, 2-D and 3-D database searching, pharmacophore identification and novel drug design, molecular docking, Structure-based drug design for all classes of targets.

References:

1. J.H. Block and J.M. Beale Jr. 2004. Organic medicinal and Pharmaceutical chemistry. Lippincott Williams and Wilkins, New York.

2. B.Patwaradhan.2007. Drug discovery and development. New India publishing agency, New Delhi.

3. L.Shargel and A.B.C.Yu.1999. Applied Biopharmaceutics and Pharmacology. McGraw-Hill, New York.

4. D.M. Brown.2004. Drug delivery systems in Cancer therapy. Humana press, Totowa, New Jersey.

5. Rothstein, Pharmacogenomics: Social, ethical and clinical dimensions, Wiley Less.

6. Jin Xiong. Essential Bioinformatics. Cambridge University Press.

7. Andrew R. Leach Molecular Modeling: Principles and Applications.

16BIIA2EC   **SEM II**

BIODIVERSITY INFORMATICS

Objective To aware of digitized biodiversity data resource available nationally and internationally and to utilize the same effectively to conserve biodiversity.

Unit-I

Biological diversity of life- Methods for species identification & classification- Information needs in biodiversity assessments and inventorying programmes- Role of information technology in distributing biodiversity information.

Unit-II

Introduction to biodiversity informatics-Assessing, analyzing and documenting biodiversity- Morphological and molecular characterization of biodiversity- Introduction to biodiversity database: endangered animals, endemism and Red data books- Biodiversity registers.

Unit-III

Designing information systems to support biodiversity conservation- Networks for distributing information- Distributed Databases and Web- Accessible Resources

Unit-IV

Software for identification of Assessing existing biodiversity databases on the world- wide web- Probabilistic and deterministic identification, Delta, MicroIS, AVIS, ICTV.

Unit-V

Global biodiversity information system-Overview of the UNEP/GEF biodiversity data management project (BDM) – CBD and bioethics- General agreement on trade and traffics.

 References:

1. Global Biodiversity: Status of the Earth's Living Resources. Water Conservation Monitoring Centre (1992), Chapman & Hall, London.
2. Systematics and Conservation Evaluation- Forey, P.L., C.J. Humphries and R.I Vane-Wright (eds) (1994), Clarendon press, Oxford.
3. Biodiversity: Measurement & Estimation –Hawkswoth, D.I. (Ed.) (1995), Chapman & Hall, London.
4. Alice, 1990. A Biodiversity database system. Alice software partnership. Cnhos, D.A.L. Canhos, V.P and Kirsop, B.E (eds) 1994. Linking Mechanisms for biodiversity information, Tropical foundation, Tropical Foundation, Campinas, Brazil.

5. Uhlir, P.F, 1980. The public international law of Civilian remote sensing: an overview. In: Mink, P.D. (ed), American Enter price, the law, and the commercial use of spece, Vol II. National Legal Center for the public interest, Washington, Dc.

6. Heywood, V.H., Watson, R.T.1995. Global Biodiversity Assessment. Published for the United Nations Environment programme, Cambridge University press, Cambridge.

7. P.Shanmughavel (2010) Bioinformatics Applications in Forestry, VDM Verlag, Germany.

Web Resource:

1. www.Biodiv.org

2. www.wri.org/wri/biodiv/

3. www.wcmc.org.uk

(OR)

16BIIA2ED   **SEM II**
BASICS OF CHEMINFORMATICS

UNIT I:

Graph theory and molecular numerology; Logic, sets and functions; Algorithms, integers and matrices; Mathematical reasoning, induction and recursion; Counting; graphs, trees and sets, basic probability and statistics; Markov processes

UNIT II:

Basic Stereochemistry, Amino acids and Proteins and Properties; pKa, pH and ionization of acids and bases; Protein structure - Primary structure, Secondary structure - helix & sheet; Tertiary structure; Quaternary structure; covalent and non-covalent forces that maintain structures. Introduction to drug action, pro drug design and applications

UNIT III:

History of scientific information communication-chemical literature-chemical information-chemical information search-chemical information sources-chemical name and formula searching-analytical chemistry-chemical history-biography-directories and industry sources

UNIT IV:

Introduction; Experimental sources of biological data; Publicly available databases; Gene expression monitoring; Genomics and Proteomics; Metabolomics; Visualisation of sequence

data; Visualization of structures using Rasmol or SPDB Viewer or CHIME;   Genetic basis of disease; Personalised medicine and gene-based diagnostics.

UNIT V:

Introduction to drugs, structure-based drug design. QSAR and 3D-QSAR Methods. Pharmacophore Design, Ligand-Based Design and *De Novo* Drug Design Virtual screening/docking of ligands. Protein structure, Drug action & enzymes. Drug action & receptors. Prediction of Binding Modes, Protein–Ligand binding free energies, Fragment-Based Drug Design, ADMET prediction.

REFERENCES:

1.Mathematical Methods for Physicists. Arfken, Academic Press 1985

2. Schaum's Outline of Probability and Statistics, Murray R Spiegel, John J. Schiller, R. Alu Srinivasan

3. Stereochemistry, by David G. Morris, Eddie Abel

4. Introduction to Protein Structure: Second Edition, Carl Branden , John Tooze

5. Combinatorial Chemistry and Molecular Diversity in Drug Discovery, Eric M. Gordon, James F. Kerwin

6. Computer-Aided Drug Design: Methods and Applications, T.J. Perun C.L. Propst

7. Chemical Information Sources (Mcgraw-Hill Series in Advanced Chemistry) ,Gary Wiggins

8. Introduction to Bioinformatics, Teresa K. Attwood, David Parry-Smith

9. Molecular Modeling: Basic Principles and Applications, 3rd Edition,Hans-Dieter Höltje, Wolfgang Sippl, Didier Rognan, Gerd Folkers

10. Trends in Bioinformatics. by Dr. P. Shanmughavel. 2006 Pointer publishers, Jaipur, India.

11. Principles of Bioinformatics. by Dr. P. Shanmughavel. 2005 Pointer publishers, Jaipur, India.

16BIIA23P   **SEM II**

PRACTICAL - II

COMPUTER PROGRAMMING

Programming in C

I. Character array manipulations

1) Read and Display a character array

2) Reverse print the array (Sting Reverse)

3) Length of the array

4) Copying the contents of one array to another (String Copy)

5) Copy the Uppercase character of one array as Lowercase character to another array

6) Checking whether a string is a palindrome or not

7) Copy the left 'n' characters of one array to another

8) Copy the last 'n' characters of one array to another

9) Copy the middle 'n' characters of one array to another

10) Concatenate two character arrays (String Concatenate)

11) Counting the numbers of Words, Lines and characters in an array

12) Counting the numbers of Uppercase and Lowercase Alphabets, Digits and special characters in an array

13) Check the number of occurrences of a pattern

14) Check the occurrences of a pattern and skip the same.

15) Check the occurrences of a pattern and replace it with a different pattern

II. Pointers and Character Array

16) Pattern Counting

17) Pattern Skipping

18) Pattern Replacing

III. Files and Command Line Arguments

19) Read data from the keyboard and write it in the file(char by char)

20) Read data from the file and display it on the screen(char by char)

21) Display the content of all the files(Cat all the files)

22) Copy data from one file to another

23) Pattern Count

24) Line in which the pattern occurs with line number

25) Grep all files (Pattern match all the files)

Programming in PERL Programming

1. Program to store a DNA sequence

2. Program to concatenate DNA fragments

3. Program to convert DNA to RNA.

4. Program to calculate reverse compliment of DNA sequence

5. Program to read protein sequence data from a file

6. Program to print the elements of a array

7. Program to take an element off the end of an array

8. Program to take an element off the beginning of an array

9. Program to put an element at the beginning of an array

10. Program to put an element at the end of an array

11. Program to reverse an array

12. Program to get the length of an array

13. Program to insert an element at a random position in an array

14. Program to find motifs in a protein sequence

15. Program to count nucleotides in a sequence

16 Program to find the percentage of hydrophobic amino acids in a sequence

17 Program to find the percentage of G and C in a DNA sequence

18. Program to append ATGC to a DNA sequence using subroutines

19. Program to concatenate two strings using subroutines

20. Program to count the number of given motifs

21. Program to convert DNAto RNA using subroutines

22. Program to find if a DNA is stable or not

16BIIA33A   **SEM III**
GENOMICS

Objectives: To understand the genome architecture and to extract information like gene function, gene regulation, protein evolution and targets for drug designing.

Unit – I

Introduction to Genomics: Definition of Genome, Genome sequencing, Genome map: Types of Genome maps and their uses, High and low-resolution map, Map elements, Polymorphic markers, Types of maps: Cytogenetic, Linkage map, Transcript map, Physical map, Comparative map, Integrated map, STS content maps, Map repositories: NCBI – Entrez Human genome map viewer, OMIM – Online Mendelian Inheritance in Man, Linkage map resources: CEPH reference pedigree, CHLC – Cooperative human linkage center, Radiation hybrid map resources. Practical uses of genome maps: Locating genomic regions, Target identification, Arrangement of genes,

SNP diagnosis, Positional specific cloning, M.Sc. Bioinformatics (Uni.Dept) 2010-11 Annexure : 59 B Page 18 of 28 SCAA Dt. 28.05.2010

Unit – II

Genome Anatomy: The anatomy of the Eukaryotic Genome –The special features of metaphase chromosomes, where are the genes in the genome? Families of genes, pseudogenes – Eukaryotic organelle genomes, Repetitive DNA content of the human genome. **Transcriptomes and Proteomes** Genome Expression in outline; The RNA content of the Cell– the Transcriptome – yeast and human; The Protein content of the cell - the link between the Transcriptome and the Proteome.

Unit – III

Annotation of the Genome: Structural annotation (Locating coding regions and other structural elements of the gene). Various approaches in gene prediction: ORF prediction, Gene prediction in prokaryotes and eukaryotes, Hidden Markov Model, Pattern discrimination, Evaluation of gene prediction methods, Prediction of promoter sequences, Functional annotation: (Prediction of gene function), Employing the similarity in the sequence, gene family and metabolic pathway. Employing the conserved domain, Profile and motif comparison, EST Comparison. Analysis of Human Genome.

Unit – IV

Comparative Genomics: Purpose and Methods of comparison, Tools for genomic comparison: Applications of Comparative Genomics, Reconstruction of metabolic pathway, Predicting regulatory elements, Identifying targets, examination of domain function, analysis of conserved strings. Genome projects and Model Organism research -Yeast; Drosophila; C. elegans; and Mouse – a comparative analysis. Comparative genomics as an aid to gene mapping and in the study of human diseases.

Unit – V

Functional Genomics: Gene expression analysis by cDNA micro arrays, SAGE, Strategies for generating ESTs and full length inserts; EST clustering and assembly; EST databases (DBEST, UNIGENE); Expression and regulation of entire set of genes, Sporulation Vs Vegetative condition in yeast and Bacillus.

References:

1. Inna Dubchak et al. 2000. **Active Conversation of Non-coding Sequences revealed by three way species comparisons.** Genome Research. 10, 1305–1306.

2. Andreas D. Baxevanis and B.F. Francis Ouellette. A, **Bioinformatics A Practical Guide to the Analysis of Genes and Proteins**. Ed. John Wiley & Sons, Inc., Publications (For mapping and comparative Genomics and COG and other database repositories).

3. David W. Mount, 2001. **Bioinformatics Sequence and Genome Analysis,** Cold Spring Harbor Laboratory Press.

4. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.

5. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.

6. Ann Gibbons, 1998. **Comparative genetics.** Science. 281: 1432 – 1434.

7. Peter D. Karp et al. 1996. **Encyclopedia or *Escherchia coli* genes and Metabolism.** Eco-Cyc: Nucleic Acids Research. 10: 86-90.

8. Jeffrey et al. 2000. **Structural Genomics and its importance for Gene Function Analysis.** Nature Biotechnology. 18:283 – 287.

9. Roman Tatusov et al. 2001. **The COG database: New developments in phylogenetic classification of Proteins from complete genomes.** Nucleic Acids Research. 29:22-28.

10. Jeremy D. Peterson et.al. 2001. **The Comprehensive Microbial Resource.** Nucleic Acids Research. 29: 123 – 125.

11. Baxevanis A.D. 2001. **The Molecular Biology Database Collection: Updated Compilations of Biological Database Resources.** Nucleic Acids Research. 29 p 1-10.

12. T.A. Brown, 2001. **Genomes.** Taylor and Francis Group

16BIIA33B   **SEM III**

PROTEOMICS

Objectives : Structure - function relationship and functional aspects of the entire cellular proteins.

Unit – I

Protein classification: Structural elements and terminology: Helix, Sheet, Strand, Loop and coil, Active site, Architecture, Blocks, Class and Domains, Fold, Motif, PSSM. Principles of classification: Based on structural features, Phylogenetic relationship. Properties of protein in solution and in membranes. Interaction with other molecules like lipids, carbohydrates, metal Ions.

Unit – II

Protein structure prediction: Use of sequence pattern, leucine zipper, coiled coil, transmembrane, signal peptide, cleavage site. Secondary structure prediction: Chou – Fasman / GOR method, Neural network, nearest neighbor method, tertiary structure prediction, threading profile, contact potential, modeling

Unit – III

Bioanalysis of protein and peptides: Complex protein and peptide mixtures, Extracting proteins from biological samples, Protein separation before digestion: 1D and 2 D Electrophoresis, Immobilized pH gradient, Sample preparation, First dimension criteria, second dimension criteria, Stabilization, Detecting protein on gel: Electro blot, Image analysis, Digital imaging, Spot detection and quantification, Gel matching. Data Analysis – Database for 2D gel.

Unit – IV

Tool of Proteomics: Mass Spectrometry for protein and peptide analysis: MALDI-TOF Analyzers, ESI Tandem MS instrument, Tandem Mass Analyzers, The Triple Quadrupole Mass Analyzer, The Ion Trap Mass Analyzer, Q-TOF & Fourier Transform–Ion Cyclotron Resonance, MS Instrument

Unit – V

Functional Proteome Analysis: Integrated Proteome Analysis - Phage antibody as tool, Protein expression analysis, High throughput analysis for proteomics. Automation of proteomic analysis. Proteomics in plant breeding: Objectives, principles and methods, Genetic diversity analysis, Distribution of varieties, lines and cultivars, Mutant characteristics, Variability between organ and developmental stage, Identification of abiotic stress, Genetic mapping of protein markers.

References:

1. Daniel C. Leibler, (2002), **Introduction to Proteomics: Tools for New Biology**, Humana Press, Totowa, NJ.
2. Branden, Carl and Tooze John. 1999. **Introduction to Protein Structure** (2nd. Ed.),Garland Publishing, NY, USA.
3. Mount, David, W., (2001); **Bioinformatics: Sequence and Genome Analysis**, Cold Spring Harbor Lab. NY, USA
4. Pennington, S, (Editor), M. J. Dunn (Editor); (2001); **Proteomics: From Proteins Sequence to Function,** Springer Publications
5. Palzkill, Timothy; (2002); **Proteomics,** Kluwer Academic Publishers
6. Suhai, Sandor, (ed).,(2000); **Genomics and Proteomics : Functional and Computational Aspects,** Plenum Pub. Corp.
7. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
8. Proteins - **Structure and molecular properties** by Thomas E Creighton

16BIIA33C   **SEM III**

PROGRAMMING IN VISUAL BASIC WITH RDBMS

Unit-I

Introduction: Data abstraction, Data models, Instances & schemes E-R Model: Entity and entity sets, Relations and relationship sets, E-R diagrams, Reducing E-R diagrams to tables. Network Data Model: Basic concepts, Hierarchical Data Model: Basic concepts. Introduction to distributed database processing.

Unit-II

Data definition languages – Data Manipulation language, Data Control language, Data and String Functions, Union and intersect operator, Sub queries, Normal Form, Introduction to PL/SQL , Data types in SQL, Simple PL/SQL programs.

Unit-III

Visual Basic: Introduction to Client / Server technology, Introduction to Visual Basic features, Data types, Strings, Variant, Constant, Data Arrays, looping and iterative statements.

Unit-IV

Simple controls, Command buttons, text boxes, labels, list box, drive list box, directory list box, file list box, combo box, check box, timer control, functions in Visual Basic. Introduction to data connectivity, different database connectivity approaches, simple connectivity program using data control.

Unit-V

Menu creation, MDI forms, VB scripting, Introduction to ASP.

REFERENCES:

1. **Database System Concepts**. Silberschatz, Tata Mac-Graw Hill Publications.
2. **Database system organization**. J.M.Martin, Princeton-Hall.
3. **Introduction to Database Systems**. C.J.Date
4. **Introduction to Database Systems**. J.M.Martin, Princeton-Hall.
5. **Parallel and Distributed Databases**. Wilteach et.al.
6. **Using Visual Basic**. Que Series. 2001.

7. **Visual Basic 6 From the Ground Up**. Gary Cornell Tata Mc-Graw Hill.

16BIIA33D   **SEM III**

MOLECULAR MODELING

Unit-I

Introduction to the concept of molecular modeling, molecular structure and internal energy, applications of molecular graphics, coordinate systems,

Unit-II

Introduction to computational quantum mechanics: one electron atom, poly electronic atoms and molecules, Hartree Fock equations; calculating molecular properties using ab initio and semi empirical methods

Unit-III

Molecular mechanics: general features of molecular mechanics force field, bond stretching, angle bending, torsional terms, non-bonded interactions; force field parametrisation and transferability;

Unit-IV

Potential energy surfaces, discussion of local and global energy minima, energy minimization: derivative and non-derivative methods, applications of energy minimization.

Unit-V

Molecular dynamics simulation methods: molecular dynamics using simple models, molecular dynamics with continuous potential, setting up and running a molecular dynamic simulation, constraint dynamics; Monte carlo simulation method: Monte Carlo simulation of molecules.

REFERENCES

1. **Molecular Modeling: Principles and Applications.** Andrew R. Leach
2. Basic principles and applications Hans-x
3. Yvonne C. Martin. **Designing bioactive molecules three-dimensional techniques and applications.**
4. **Exploring QSAR.** Leo, Albert, Hockma, D.H.– Hansch, Corwin.
5. **Principles of Bioinformatics,** Shanmughavel, P. 2005 , Pointer Publishers, Jaipur, India.
6. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.

16BIIA3EE   **SEM III**

SYSTEMS BIOLOGY

Objectives: Insilico. Convergence of Genomics, Proteomics, Transcriptomics and Metabolomics into Phenomics.

Unit – I

Introduction to Systems Biology: What is Systems Biology? Integrating Networks. Methods of study: Micro array – definition, types of array, Micro array analysis: Hierarchical clustering, Self-organizing maps. Applications of Micro Array in systems biology.

Unit – II

Metabolomics: Digestion of proteins and protein metabolism, Urea Cycle, Transport metabolism, Carbohydrate metabolism – metabolism of glucose – glycolysis, TCA cycle, glycogenesis, Pentose phosphate shunt, Electron transport. Lipid metabolism: beta oxidation. Interconnection of pathways, metabolic regulations. Interconnection of pathways, metabolic regulation, Phylogeny, RNA secondary Structure, Gene Prediction.

Unit – III

Computational Cell Biology: Principle and levels of simulation – Virtual Erythrocytes, Pathological analysis. Flux Balance Analysis; Graphical Biological Network Editor and Simulator (Cell Designer).

Unit-IV

Location Proteomics: Protein subcellular location- Pattern Recognition. Predicting ligand-binding function, Use of gene cluster, detecting protein – protein interaction. Methods for Protein-Protein Interaction Analysis- Yeat Two Hybrid System (Y2H); Peptide Mass Fingerprinting (PMF).

Unit –V

Creative Bioinformatics: Novel use for database. Use of EST database – Unigene, gene discovery, Primer design, Restriction mapping, Position specific cloning, KEGG, SNP database, Target identification, Epitope identification. Spatial Signalling Dynamics – Methods and Quantification of receptor signaling.

REFERENCES

1. Foundation of Systems Biology – Hi Roaki Kitano
2. Introduction to Systems Biology – Sangdun Choi
3. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
4. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.
5. **The underlying pathway structure of biochemical reaction networks.** Christopher H. Schilling *et. al*. 1998. PNAS. **95**:4193-8
6. **Towards metabolic phenomics: Analysis of Genomics Data Using Flux Balances**. Christopher H. Schilling *et. al*. 1999. *Biotechnology. Prog.* **15**: 288-295.
7. **The Minimal Gene Complement of *Mycoplasma genitalium.*** Claire M. Fraser *et. al*. 1995. *Science*, **270**: 397- 403.
8. **Molecular Classification of Cancer: Class Discovery and Class prediction by Gene Expression Monitoring.** Golub TR. *et. al*. 1999. . *Science*, **286**: 531 – 537.
9. **The *Escherichia coli* MG. 1655 *in silico* metabolic genotype: its definition, characteristics and capabilities.** Jeremy S. Edwards et. al. 2000. PNAS. **97**:5528-33.
10. **Whole cell simulation: a grand challenge of the 21st Century.** Masaru Tomita, 2001. *Trends in Biotechnology.* **19**: 205-210
11. **Cluster Analysis and Display of Genome – wide expression patterns.** Michael B.Eisen *et. al*. 1998, *Proc. Natl. Acad. Sci. USA*. **95**: 14863 – 14868.
12. **A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks.** Stephen Schuster *et. al*. 1999. *Nature Biotechnology*. **18**: 326-332.
13. **Of micro array and meandering data points.** Steven R. Gullans, 2000. . *Nature Genomics*. **26**: 4-5.
14. **A gene expression database for the molecular pharmacology of cancer.** Uwe Scherf *et. al*. 2000. *Nature genetics*, **24**: 236-244

15. **The transcriptional program in the response of Human Fibroblast to Serum** Viswanth R. Iyer 1999. *Science.* **283**: 83-87.
16. : Mount, David, W., (2001)**; Bioinformatics**: Sequence and Genome

(OR)

16BIIA3EF   **SEM III**

Elective – Introduction to Next Generation Sequencing

Unit 1

What is Next Generation Sequencing, and how is it different from traditional sequencing/Microarrays -Various NGS technologies/platforms, experiment types and applications -Workflows for various NGS experiments

Unit 2

Steps involved in implementing various NGS workflows (variant discovery, expression profiling, etc.) - working with reads, alignments, quality scores, etc. - Algorithms and tools for NGS read alignment, SNP calling, etc. - Various file formats such as SAM, VCF, BED, WIG, PILEUP, etc.

Unit 3

DNA-seq - genetic variations -NGS and personal genome sequencing, whole genome sequencing, target sequencing - Sequencing mappability - Refined alignment - Base quality recalibration -Variants identification - Four different workflows for mutation discovery (CrossBow, Bowtie, BWA, MAQ)

Unit 4

RNA-seq I- Biological theories on RNA-seq experiments - Major scientific advance using RNA-seq – Alignment - Gene expression analysis, Differential expression analysis - Alternative splicing - TopHat and Cufflinks for RNA-seq

Unit 5

ChIP-seq - Introduction and biological theories on ChIP-seq analysis - •   DNA   frament evaluation - Peak identification - Two condition comparison - Saturation analysis - Motif finding and related theories

Reference

1. Next-Generation DNA Sequencing Informatics, Second Edition Edited by Stuart M. Brown, New York University School of Medicine (ISBN-13: 978-1621821236)
2. NextGeneration Sequencing Data Analysis, by Xinkun Wang, CRC Press (ISBN13: 9781482217889)

16BIIA33P   **SEM III**

PRACTICAL – III
MOLECULAR TECHNIQUES

Isolation Techniques

1. Pure culture techniques

2. Preparing competent culture

3. Microbial genomic DNA isolation

4. Microbial plasmid isolation

5. Plant genomic DNA isolation

6. Animal genomic DNA isolation

Recombinant DNA Techniques

7. Restriction mapping with Lambda DNA

8. Ligation

9. PCR (Polymerase Chain Reaction)

10. Blotting techniques

ImmunoTechniques

11. Counting of blood cells- Haemocytometer count

12. Preparation of serum from blood

13. Blood grouping – Haemoagglutination

14. ELISA

16BIIA33Q   **SEM III**

PRACTICAL – IV

BIOLOGICAL SEQUENCE ANALYSIS & COMPUTER AIDED DRUG DESIGN

1. Biological Databanks Sequence Databases, Structure Databases, Specialized Databases

2. Data retrieval tools and methods

3. Database file formats

4. Molecular visualization

5. Gene structure and function prediction (using GenScan, GeneMark)

6. Sequence similarity searching (NCBI BLAST)

7. Protein sequence analysis (ExPASy proteomics tools)

8. Multiple sequence alignment (Clustal)

9. Molecular phylogeny (PHYLIP)

10. Analysis of protein and nucleic acids sequences,

11. Sequence analysis using EMBOSS or GCG Wisconsin Package
12. Small molecule building, using ISIS DRAW and CHEM SKETCH
13. Homology Modeling using SPDBV
14. Model structure refinement using SPDBV
15. Model validation using What Check and Pro Check
16. Docking using DOCK or AUTODOCK or AMBER

Reference:

1**.** K. Mani and N. Vijayaraj , **Bioinformatics a Practical Approach**, Aparna Publications, Coimbatore.

SUPPORTIVE PAPER I

16BIIA1GS   **SEM- I & III**

DATABASES AND SEQUENCE ANALYSIS

Unit-I

Introduction to Bioinformatics, Biological Databases and Data formats, Nomenclature of nucleotides and amino acids, Application of Bioinformatics.

Unit-II

Introduction to sequence alignment, PAM - BLOSUM, Local and Global alignment, Needleman-wunsch algorithm, Smith-waterman algorithm, Multiple sequence alignment, FASTA, BLAST.

Unit-III

Evolutionary analysis, Cladistic, and Phenetic methods, Clustering methods, Rooted and Unrooted tree representation.

Unit-IV

Gene finding methods, Gene prediction methods, Repeat sequence finder.

Unit-V

Structure prediction methods: Chou-Fasman/GOR method,Neural Network, Threading and Fold recognition, Modeling.

References:

1. David. W. Mount (2001): Bioinformatics Sequence and Genome Analysis, Cold spring Harbor Lab. NY.USA

2. Comparative Genomics Ann Gibbons, 1998, Science.

3. Genomes T.A Brown,2001, Taylor and Francis Group.

<u>**SUPPORTIVE PAPER-II**</u>

16BIIA2GS   **SEM II**

BASICS OF BIOINFORMATICS

Objectives: To understand the gradual maturation of Genomics and Proteomics into Biology

Unit-I

Definition of Genome, NCBI, OMIM, Practical uses of genome maps, Locating enomic regions, Target identification, Arrangement of genes, SNP Diagnosis.

Unit -II

Protein Classification – Helix, Sheet, Strand, Loop and Coil, Active site, Class and Domains, Fold, Motif, PSSM, Profile.

Unit-III

Comparative Genomics- Profile Comparison, Motive Comparison, EST Comparison, human genome Project.

Unit-IV

Annotation of Genome- structural annotation by Genscan and Genmark and functional annotation by pattern searching, TMPred

Unit-V

CATH- Classification by Class, Architecture, Topology, Homology, SCOP- Structure Classification of Proteins.FSSP- Fold Classification based on Structure- Structure alignment, MMDB – Molecular Modeling Database,SARF-Special arrangement.

References:

1. Mount David W. (2001); Bioinformatics: Sequence and Genome Analysis, Cold spring Harbor Lab. NY.USA.

2. Introduction to Protein Structure (2nd Ed) Brander, Carl and Tooze John. 1999.

3. Bioinformatics : A Practical Guide to analysis of Gene and Proteins. Ed. Andreas D.Barevanii and B.F. Francis Ouellette.