ADDITIONAL NEW SUBJECTS

Code	Subject Name	Credits
BI216	Bioinformatics Networks and Applications	4:0:0
BI217	Molecular Modeling and Drug Design	4:0:0
BI218	PERL programming	4:0:0
BI219	Structural Bioinformatics	4:0:0
BI220	Biological Database Lab	0:0:2
BI221	Biological Sequence Analysis lab	0:0:2
BI222	PERL Lab	0:0:2
BI223	Biocomputing	3:0:0
BI224	Biopharmaceutical Technology	3:0:0
BI322	Research Methodology	4:0:0

BI216 BIOINFORMATICS NETWORKS AND APPLICATIONS

Credit: 4:0:0

Unit I Introduction to Bioinformatics

Scope of Bioinformatics – Elementary commands and Protocols, ftp, telnet, http. Printer on information theory. Databanks – nucleotide databanks – Genbank, NCBI, EMBL, DDBJ – protein databanks – sequence databanks – PIR, SWISSPROT, TrEMBL _ structural databases – PDB, SCOP, CATH, SSEP, CADB, Pfam and GDB.

Unit II : Sequence Alignment and Dynamic Programming

Introduction – Strings – Edit distance two strings – string similarity local alignment -gaps – Parametric sequence alignments – suboptimal alignments – multiple alignment – common multiple alignment methods.

Unit III : Sequence Databases and Their Uses

Introduction to databases – database search – Algorithms issues in database search – sequence database search – FASTA – BLAST – Amino acid substitution matrices PAM250 and BLOSUM62. GCG Sequence Analysis(Basic concepts only)

Unit IV : Evolutionary Trees and Phylogeny

Ultrasonic trees – parsimony – Ultrametric problem – Perfect phylogeny – Phylogenetic alignment – connection between multiple alignment and tree construction.

Unit V : Special Topics in Bioinformatics

DNA Mapping and sequencing – Map alignment – Large scale sequencing and alignment – Shotgun – DNA sequencing – Sequence assembly – Gene predictions – Molecular predictions with DNA strings.

Text Book

1. T.K.Attwood & D.Parry-Smith, *Introduction to Bioinformatics*, Pearson Education, 2001.
2. R.Durbin, R.Eddy, K.Anders and M.Graeme, *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids*, Cambridge University Press, 1997

Reference Books

1. Dan Gusfield, *Algorithms On Strings Trees And Sequences,* Cambridge University Press, *1997*.
2. Lesk, *Introduction to Bioinformatics,* Oxford University Press, 2002.
3. Pennington, *Proteomics from Protein Sequence to Function*
4. Campell, *Discovering Genomics, Proteomics and Bioinformatics*
5. Baxevenis, B*ioinformatics, John Wiley & Sons*

BI217 MOLECULAR MODELLING AND DRUG DESIGN

Credit : 4:0:0

Unit I: Introduction to Molecular Modelling

Introduction - Useful Concepts in Molecular Modelling : Coordinate Systems. Potential Energy Surfaces. Molecular Graphics. Surfaces. Computer Hardware and Software. The Molecular Modelling Literature.

Unit II: Force Fields

Force Fields. Bond Stretching. Angle Bending. Introduction to Non-bonded Interactions. Electrostatic Interactions. Van der Waals Interactions. Hydrogen Bonding in Molecular Mechanics. Force Field Models for the Simulation of Liquid Water.

Unit III : Energy Minimisation and Computer Simulation

Energy Minimisation and Related Methods for Exploring the Energy Surface. Non-Derivative method, 1st and 2nd order minimisation methods. Computer Simulation Methods. Simple Thermodynamic Properties and Phase Space. Boundaries. Analyzing the Results of a Simulation and Estimating Errors. GROMACS and CNS.

Unit IV: Molecular Dynamics & Monte Carlo Simulation

Molecular Dynamics Simulation Methods. Molecular Dynamics Using Simple Models. Molecular Dynamics with Continuous Potentials. Molecular Dynamics at Constant Temperature and Pressure. Metropolis Method. Monte Carlo Simulation of Molecules. Models Used in Monte Carlo Simulations of Polymers. Molecular Modeling software: BIOSUITE

Unit V: Structure Prediction and Drug Design

Protein Structure Prediction - Introduction to Comparative Modeling. Sequence Alignment. Constructing and Evaluating a Comparative Model. Predicting Protein Structures by 'Threading', Molecular Docking, AUTODOCK and HEX. Structure based De Novo Ligand design, Drug Discovery – Chemoinformatics – QSAR.

Reference Books:

1. A.R.Leach, *Molecular Modelling Principles and Application*, Longman, 1996.
2. J.M.Haile, *Molecular Dynamics Simulation Elementary Methods*, John Wiley and Sons, 1997.
3. Satya Prakash Gupta, *QSAR and Molecular Modeling,* Springer - Anamaya Publishers, 2008.

BI 218 PERL PROGRAMMING

Credit : 4:0:0

Unit I: Introduction to Perl

Perl interpreter and its working. Variables and Data types: Perl variables, Scalar values, Calculations, Interpolation and Escapes. Arrays and Hashes: Arrays and Array manipulation, Push and Pop, Shift and Unshift, Splice and other array function.

Unit II: Control Structures

Comparisons, Choices, loops, Intermediate Loops and Loop exits. Subroutines: Creating a subroutine, Arguments, Return and Scope. String Manipulations: Array based character manipulations, Regular expressions Match, Substitue and Translate. Patterns.

Unit III: Input and Output

Program parameters, File I/O, File handles, working with file handles, Built-in file handles, file safety. Inter process communications, Processes, Process pipes, Creating and monitoring pipes. Perl modules and packages: modules, packages, CGI, Getopt, Io.

Unit IV: Advanced Perl

Creating references, ref( ), Object-Oriented programming: Introduction to Objects, OOP approach, Class design, inheritance. Perl objects: Rules, methods, constructors and Accessors, OOP versus Procedural, exercises.

Unit V: Bioperl

Sequences, Seqfeature, A class for Restriction enzymes, Perl in Bioinformatics, Perl and relational database, Perl and the web, Perl and the graphics. Installation of bioperl and its applications. Bioperl problems. bio-python.

Reference Books:

1. D. Curtis Jamison, *Perl Programming for Bioinformatics and Biologists,* Wiley-Dreamtech, 2004.
2. James D. Tisdall, *Mastering Perl for Bioinformatics*, O'Reilly & Associates, 2003.

BI219 STRUCTURAL BIOINFORMATICS

Credit : 4:0:0

Unit – I Structural features of biomolecules;

Techniques used to determine the structure of biomolecules; Methods for single crystal X-ray Diffraction of macromolecules; molecular replacement method and direct method – Fiber diffraction; analysis of structures and correctness of structures; submission of data to PDB; atomic coordinates and electron density maps

Unit – II Anatomy of proteins;

Ramachandran Plot; secondary structures; motifs; domains; tertiary and quaternary structures. Anatomy of DNA; A, B, Z-DNA, DNA bending. Structure prediction, Comparative protein modeling.

Unit – III Methods for prediction of secondary and tertiary structures of proteins
knowledge- based structure predication; fold recognition; ab initio methods for structure predication, Comparative protein modeling

Unit –IV Methods for comparison of 3D structures of proteins;
Methods to predict three dimensional structures of nucleic acids, rRNA; Electrostatic energy surface generation.

Unit – V Molecular Mechanics and Molecular dynamics of Oligopeptides,
Proteins Nucleotides and small molecules – Mechanism and dynamics of bio-macromolecules. Simulation of molecular mechanics and dynamics, Simulations of free energy changes; Force fields. Molecular interactions of protein-protein, protein – DNA, protein-carbohydrate and DNA-small molecules.

Recommended Texts:

1. Creighton,T.E. (1993) "*Proteins; structure and molecular properties*"; Second edition, W.H. Freeman and Company, New York, USA
2. Andrew R. Leach (2001) "*Molecular Modeling – Principle and Application*" ; Second Edition, Prentice Hall,USA

Reference Books:

1. Mount, D. (2004) "*Bioinformatics; Sequence and Genome Analysis*", Cold Spring Harbor Laboratory Press, New York.
2. Lesk,A.M.(2001) "*Introduction to Protein Architecture*", Oxford University Press UK.
3. Mcpherson, A. (2003) "*Introduction of Molecular Crystallography*", John Wiley Publication, USA.
4. Brandon and Tooze, (1999) *Introduction to protein structures,* Garland Publishing Company, New York.

BI220 BIOLOGICAL DATABASE LAB

Credit : 0:0:2

12 experiments will be notified by the HOD from time to time

BI221 BIOLOGICAL SEQUENCE ANALYSIS LAB

Credit : 0:0:2

12 experiments will be notified by the HOD from time to time

BI222 PERL LAB

Credit : 0:0:2

12 experiments will be notified by the HOD from time to time

BI223 BIOCOMPUTING

Credit : 3:0:0

Unit I: Types of Computing

Introduction to various Types of Computing: Parallel Computing, Distributed Computing, High Performance Computing, Mobile Computing, DNA Computing and GRID & Cluster computing – Key Characteristics, User requirements.

Unit II: Gene Mapping

Maximum Versus High Scoring Subsequences. Gene mapping- Restriction maps and interval graphs- Restriction fragment length measurements- Circular maps- Algorithms in MSD mapping Fragment identification problem- Physical mapping.

Unit III: Markov Chains and HMM

Probability, Introduction to Markov Chains, Biological Application of Markov Chains, Using Markov Chains to Find Genes, hidden markov model. Basic and learning algorithm, Rabiner's on tutorial on HMM, Application and profile of HMM software.

Unit IV: Gene Finding

Relative entropy site selection problem- Maximum subsequence problem- Interpolated markov Model -Start Codon Prediction- GPHMMS for cross-species gene finding -picking alignment from Steiner trees- Las vagas algorithms for gene recognition -Dictionary based approach for gene annotation- Knuth-Morris-Pratt string matching

Unit V: Artificial Neural Networks

Molecular Database management- Protein secondary structure-DAG-RANNS directed acyclic Graphs -Exon/Intron Discrimination using finite induction pattern matching technique -Sequence analysis by monitoring the learning process- Pattern Discovery and generation with respect to Data sequences- computational neural networks and quantum mechanical features of transition states and putative inhibitors.

Reference:

1. Peter Colty and Rolf Backofen, Wiley *series in Mathematical and Computational biology: Computational Molecular Biology: An Introduction,* (2000) John Wiley &Sons Ltd.
2. David W. Mount, *Bioinformatics sequence and genome analysis,* (2005) 2nd Ed. CBS pub.
3. Stephen Misener & Stephen A.Krawetz, Bioinformatics *methods and protocols* (2000) Humana press.

BI224 BIOPHARMACEUTICAL TECHNOLOGY

Credit : 3:0:0

Unit I: Introduction of drug action

History & Definition of Drugs- Sources of Drugs - Plant, Animals, Microbes and Minerals- Different dosage forms- Routes of drug administration- Pharmacodynamics- Physico-Chemical

Principles. Mechanism of drug action- drug receptors- and Physiological receptors- structural and functional families -Pharmacokinetics- Drug absorption- factors that affect the absorption of drugs-Distribution of drugs- Biotransformation of drugs- Bioavailability of drugs.

Unit II: Important Unit Processes and their Applications

Chemical conversion processes – Alkylation – Carboxylation – Condensation and Cyclization – Dehydration, Esterification (Alcoholysis) – Halogenation – Oxidation, Sulfonation – Complex Chemical Conversions – Fermentation

Unit III: Manufacturing Principles

Compressed tablets – wet granulation – Dry granulation or slugging – Direct compression – Tablet presses formulation – Coating – Pills – Capsules sustained action dosage forms – Parental solutions and injections – Oral liquids –ointments – standard of hygiene and good manufacturing practice.

Unit IV: Production & analysis of Biopharmaceuticals

Vitamins – Cold remedies – Laxatives – Analgesics – Non-steroidal contraceptives – External Antiseptics – Antacids and others. Antibiotics – Biological hormones – Vitamins – preservation- Analytical methods and tests for various drugs and pharmaceuticals- Packing – Packing Techniques – Quality Control - Recent advances in the manufacture of drugs using r-DNA technology.

Unit V: Drug delivery systems

Biomaterials and their applications-Controlled and sustained delivery of drugs- Biomaterial for the sustained drug delivery- Liposome mediated drug delivery- Drug delivery methods for therapeutic proteins- Drug development process- Drug discovery- Patenting- Delivery of pharmaceutical-Preclinical trials- Drug regulatory authorities.

Referance:

1. R.S.Sathoskar, S.D.Bhandrkar, S.S.Ainapure "*Pharmacology and pharmacotherapeutics* "17th edition, Popular Prakashan pub. (2001)
2. Remington, The Science and Practice of Pharmacy, Lippincot Williams & Wilkins pub.(2006)
3. Leon Lachman, Herbert A. Lieberman and Joseph L. Kanig, *Theory & Practice of Industrial Pharmacy*, (3rd ed.) Varghese Pub. (1987)

BI 322 RESEARCH METHODOLOGY

(For M.Phil/Ph.D in Bioinformatics)

Credit: 4:0:0

Unit –I

Research Methodology : Introduction; meaning of research; objectives of research; types of research; research approaches; significance of research; research methods vs. methodology; research and scientific method; importance of knowing how research is done; research process; criteria of good research; problem encountered by researchers in India. Defining the research problem; what is research problem? Selecting the problem; techniques involved in defining the problem; meaning of research design. Research design; Need for research design; features of good design; important concepts relating to design; different research designs; basic principles of experimental design.

Unit II
Hypothesis testing; what is the hypothesis? Basic concepts concerning testing of hypothesis; procedure for hypothesis testing; Probability: Markov models and Hidden Markov models; probability distribution; Binomial, Poisson, normal distribution, and multiple testing methods. ANOVA; Test of significance – t- test, F- test.

Unit – III
Interpretation and Report writing; Meaning of interpretations; techniques of interpretation; precaution in interpretations; significance of report writing; different steps in report writing; layout of the research project; types of report; oral presentation; mechanics of writing a research report; precautions for writing reports; conclusions

Unit –IV
Elements of C programming; Features of C, variables, constants, keywords, data types, operators statements, loops- simple programs using arrays. Introduction to Functions – simple program using functions- introduction to pointers, structures – string manipulations using pointers and arrays. Files: Defining & opening a file, closing a file, input/output operations on files.
PEARL: Basic Syntax- I/O- Variables, strings & array – control structures – regular expressions – simple programs.

Unit – V
Algorithms in computer sciences inspired by biology; genetic algorithms, neural networks and path optimization.

Reference:

1. S. Parthasarathy, *Essentials of Programming in C for Life science*, 2008, Ane Books India
2. N. Gurumani, *Research Methodology for Biological Science*, 2006, MJP Publishers.
3. Kithara, C.R. 2004. Research Methodology – Methods and Techniques, New age international (P) Ltd.
4. E. Balagurusamy, Programming in Ansi C Tata McGraw Hill.
5. Randal L. Schwartz, tom phoenix Learning Perl, third Edition.

ADDITIONAL SUBJECTS

Code	**Subject Name**	**Credit**
09BI201	Fundamentals of Biological Systems	3:0:0
09BI202	Cell Biology and Micro Biology Lab	0:0:1
09BI203	Introduction to Computer and Architecture	4:0:0
09BI204	Engineering Biochemistry	4:0:0
09BI205	Biochemical Thermodynamics & Engineering	4:0:0
09BI206	Instrumental Methods and Analysis	4:0:0
09BI207	Molecular Biology and Genetic Engineering	4:0:0
09BI208	Analytical Biochemistry Lab	0:0:2
09BI209	Bioinformatics Networks and Applications	4:0:0
09BI210	Biophysics	4:0:0
09BI211	Object Oriented Programming - C++ And Java	4:0:0
09BI212	Genomics	4:0:0
09BI214	Molecular Evolution and Phylogeny	4:0:0
09BI215	Molecular Modelling and Drug Design	4:0:0
09BI216	Machine Learning in Bioinformatics	4:0:0
09BI217	Perl Programming	4:0:0
09BI218	Structural Bioinformatics	4:0:0
09BI219	Biocomputing	4:0:0
09BI220	Introduction to Unix and Linux	4:0:0
09BI221	Datamining and Data Warehousing	4:0:0
09BI222	Introduction to Database Management Systems	4:0:0
09BI223	Biopharmaceutical Technology	3:0:0
09BI224	Introduction to Algorithm	4:0:0
09BI225	Biological Database Lab	0:0:2
09BI226	Biological Sequence Analysis Lab	0:0:2
09BI227	Molecular Modelling Lab	0:0:2
09BI228	Qsar & Drug Design Lab	0:0:2
09BI229	Perl Lab	0:0:2
09BI230	C++ And Java Lab	0:0:2
09BI231	Database Management System Lab	0:0:1
09BI232	Unix & Linux Lab	0:0:1
09BI233	Molecular Biology & Genetic Engineering Lab	0:0:1
09BI234	Bioorganic Chemistry	4:0:0
09BI235	Introduction to Systems Biology	4:0:0
09BI236	Protein Engineering	4:0:0
09BI237	Neurobiology and Cognitive Science	4:0:0
09BI238	Nanobiotechnology	4:0:0
09BI239	Neural Networks in Bioinformatics	4:0:0
09BI240	Advanced Immunology	4:0:0
09BI241	Bioethics, IPR And Biosafety	3:0:0
09BI242	Community Health and Social Awareness	3:0:0
09BI243	Bioinformatics	3:0:0

09BI244	Basics of Chemical Engineering	3:0:0
09BI245	Biological Databases	3:0:0
09BI322	Molecular Biology and Genetic Engineering	4:0:0
09BI323	Microarrays and Data Analysis	4:0:0
09BI324	biostatistics	3:1:0
09BI325	Biocomputing I	4:0:0
09BI327	Relational Database Management Systems	4:0:0
09BI328	Structural Bioinformatics	4:0:0
09BI329	Genomics And Proteomics	4:0:0
09BI330	Molecular Modeling and Drug Design	4:0:0
09BI331	Biocomputing – II	3:1:0
09BI332	Bioprogramming Lab	0:0:2
09BI333	Biocomputing Lab	0:0:2
09BI334	Molecular Modeling and Drug Design Lab	0:0:2
09BI335	Dbms Lab	0:0:2
09BI336	Computer Hardware & Networking	4:0:0
09BI337	Python Language	4:0:0
09BI338	Biophysical Chemistry	4:0:0
09BI339	Data Mining & Warehousing	4:0:0
09BI341	Server-Side Programming	3:0:0
09BI342	Perl and Xml	4:0:0
09BI343	Python Lab	0:0:2
09BI344	Cheminformatics Lab	0:0:2
09BI345	Relational Database Management Systems	4:0:0

09BI201 FUNDAMENTALS OF BIOLOGICAL SYSTEMS

Credit : 3:0:0

Objectives

- To develop the skills of the students in structure & organelles of cells & its regulation.
- To get familiarize with Biosignaling ,Microscopy & Staining techniques
- To acquire knowledge in Biodiversity

Outcomes

- Students may obtain interest in basics of Cells & its regulation.
- Students may acquire basic knowledge on microscopy & microorganisms.
- Students may acquire knowledge about the conservation of Biodiversity

Unit I Biology of cells

Structure of prokaryotic and eukaryotic cells overview of organelles (Mitochondria, Chloroplasts, ER, Golgi, nucleus). Difference between plant and animal cell. Cellular membrane

– Structure and functions- transport, endocytosis, role of membrane proteins as receptors. Cell cycle and regulation, cell division- mitosis and meiosis

Unit II Cell – cell interactions and signal transductions
Intercellular junctions, signaling by hormones and neurotransmitters, G protein receptors, protein kinesis, cAMP and inositol phosphates as second messengers.

Unit III Microbiology
Classification and nomenclature of micro organisms, light and electron microscopy, principle of different staining techniques- gram staining, acid fast and capsular staining Physical and chemical control of microorganisms, Microbial biosensors

Unit IV Microbial Nutrition, Growth And Metabolism
Nutritional requirements of bacteria and different media used for bacterial culture, growth curve and different methods to quantitate bacterial growth, aerobic and anaerobic bioenergetics, utilization of energy for biosynthesis of important molecules.

Unit V Biodiversity

Status of biodiversity, Uses of biodiversity, Community biodiversity conservation, Access and transfer of genetics resources, Mechanism of benefit sharing, Biodiversity conservation.

Text Books
- P.S. Verma, V.K. Agarwal, "Cell Biology, Genetics and molecular Biology", S. Chand and company ,2000.
- Pelzer. MJ, Chan ECS and Krein NR, "Microbiology", Tata Mc Graw Hill Publishers, New Delhi ,2000.

Reference Books
1. A.K. Ghosh , Biodiversity Conservation, APH Publications, New Delhi, 2007

09BI202 CELL BIOLOGY AND MICRO BIOLOGY LAB

Credit : 0:0:1

1. Study of Microscopes
2. Microscopical Identification of Cells in Permanent Fixed Slides
3. Differentiation of Blood Cells using Giemsa Staining
4. Separation of Peripheral Blood Mononuclear Cells and Trypan Blue Assay for Live Cells
5. Osmosis and Tonicity Studies using Red Blood Corpuscles
6. Staining for Various Stages of Mitosis in Allium cepa (Onion)
7. Culture Media – Types & Preparation of Agar medium and Nutrient Broth
8. Inoculation of micro- organisms
9. Isolation of pure culture by streak plate technique
10. Isolation of pure culture by pour plate technique
11. Gram staining
12. Hanging drop method

09BI203 INTRODUCTION TO COMPUTER AND ARCHITECTURE

Credits: 4: 0: 0

Objective:

- Introduce fundamentals of computers
- To give information about classification of computers.
- Basics of computer architecture.
- Enable students to understand network protocols.

Outcomes:

- Students will understand different protocols used in network communication.
- Know the different phases in software or program development.
- Understand the working principles of various Operating systems.

UNIT I

Introduction to computers- Types of computers, Characteristics of computers, Generations of modern computers, Classification of digital computer systems- micro computers, mini computers, mainframe, super computers, network computers, Anatomy of digital computer-Functions and components of a computer, central processing unit , memory.

UNIT II

Introduction to number system-Decimal number system, Binary number system, complements, Different types of codes and number systems, Boolean algebra and logic circuits, memory units.

UNIT III

Operating systems- function of an operating system, classification of operating system, MVS,UNIX, windows NT, windows 98, Mac OS, DOS, Linux, Programming languages-Machine languages, assembly languages, High-level languages, types of high level languages, compilers and interpreters, compilation process.

UNIT IV

Introduction to software development- Defining the problem-Program design-Coding-Testing the program-Documenting and Maintenance of programs. Data Processing: File processing- Database processing. Computer Networks: Overview-Communication processes-Media-Telecommunication software-Types of Networks-Network topologies-Network protocols-Network architecture-Distributed data processing

UNIT V

Compute architecture: Introduction –computer components and devices-Types of memory – CISC-RISC-Merits and Demerits of CISC and RISC -Speeding of pipeline machines- Issues in pipeline systems.

Text Book:

Alexis Leon and Mathews Leon "Introduction to computers" –Vikas publishing house pvt Ltd,2001

Reference Book:

V.Rajaraman "Fundamentals of Computers" Prentice Hall of India Fourth edition,2004.

09BI204 ENGINEERING BIOCHEMISTRY

Credit : 4:0:0

Objectives

- To learn the structure and properties of biomolecules
- To get advanced knowledge in the regulatory component of metabolic pathways
- To know the principle and kinetics of enzyme action
- Isolation, structural elucidation and the determination of mode of action of biomolecules.
- Study of in born errors of metabolism

Outcomes

- Get Knowledge in the chemistry of biomolecules and enzymes and their metabolism
- Will be able to understand how energy is generated, used, and stored by the various organs of the body

Unit - I : Structure and Properties of Carbohydrates and Lipids

Structure and properties of mono, di, oligo and polysaccharides, Structure and properties of fatty acids, phospholipids, sphingolipids, glycolipids and steroids.

Unit – II : Structure and Properties of Proteins and Nucleic Acids

Structure and properties of amino acids, peptides, proteins. Structure and properties of purines, pyrimidines, polynucleotides - rRNA, mRNA and tRNA, deoxy ribonucleic acids

Unit – III : Intermediary Metabolism And Bioenergetics

Bioenergetics: redox biochemistry, energy rich compounds, respiratory chain, oxidative phosphorylation and triose phosphate cycle. Carbohydrate Metabolism: Glycolysis, pentose phosphate pathway, TCA cycle, gluconeogenesis, glycogenesis and glycogenolysis.

Unit – IV : Metabolism Of Lipids, Proteins And Nucleic Acids

Lipid Metabolism: Biosynthesis and biodegradation of fatty acids. Biodegradation of proteins and nucleic acids. Biosynthesis and biodegradation of important amino acids- Leu, Tyr, Phe, Trp, and Cys- Urea Cycle, purines and pyrimidines, Inborn errors of their metabolism.

Unit-V : Mechanism of enzyme action

Enzyme – Introduction, substrate specificity, Coenzymes, Rate of enzymatic reactions- chemical kinetics, inhibition, effect of pH, bisubstrate reactions, Michaelis menton equation.

Text book:

Lehninger, A. L., Nelson, D. L. and Cox, M. M.. Principles of Biochemistry Third Edition (Freeman Publishers), New York. 2000

References:

1. Lubert Stryer, Biochemistry, 4th Edition, WH Freeman & Co., 2000.
2. Voet and Voet, Biochemistry, 2nd Edition, John Wiley & Sons Inc., 2000.
3. Murray, R.K., Granner, B.K., Mayes, P.A., Rodwell. V.W., Harper's Biochemistry, Prentice Hall International., 2000

09BI205 BIOCHEMICAL THERMODYNAMICS & ENGINEERING

Credit : 4:0:0

Objectives

- To learn the basic concepts of thermodynamics
- To know the principle of phase transformation
- Calculation of molecular properties and evaluating equilibrium constant

Outcomes

- To get knowledge in relating equations of state and calculating property changes.
- Theory and limitations for the applications of bio sensors.

Unit –I: **Basic Concepts in Engineering Thermodynamics**

First and Second law of Thermodynamics; Calculation of Work, energy and property changes in reversible process, Thermodynamics of flow process; Power cycle and refrigeration cycles.

Unit –II: **Thermodynamics Properties of Fluids**

Volumetric properties of gases exhibiting non-ideal behavior, Residual properties; Estimation of Thermodynamics properties using equations of state; Maxwell relationship and their applications; Calculation of flow based on actual properly changes.

Unit –III: **Phase and chemical reaction Equilibrium**

Criteria for phase equilibria; Vapour – liquid equilibrium calculations for binary mixtures, Liquid- Liquid equilibria and Solid – liquid equilibria , equilibrium criteria for homogeneous chemical reaction, Evaluation of equilibrium constant and effect of pressure and temperature on equilibrium constant, Calculation of equilibrium conversions and yields for single and multiple chemical reactions.

Unit – IV: **Biosensors**

Definitions, immobilization and membranes, transducer combinations; Biosensor development and diversification, Conductometric biosensors, Direct Electron transfer biosensors and Optic biosensors, Practical forms of Biosensors, specific applications of biosensors.

Unit – V: **Biochemical Thermodynamics**

Energetic of Metabolic path ways, Energy Coupling (ATP& NADH), Stoichiometry and energetic analysis of cell Growth and PRODUCT FORMATION, Elemental Balances, Degree of reduction concepts available – electron balances, yield coefficients, Oxygen consumption and heat evolution in aerobic cultures, Thermodynamics efficiency of growth.

Reference Books:

1. J.M.Smith, H.C. Van Ness and M.M.Abbott, Introduction to Chemical Engineering Thermodynamics, Sixth edition, McGraw Hill, 2002.
2. Y.V.C. Rao, Chemical Engg. Thermodynamics, University press, 1999.
3. J.A. Roels, Kinetic and Energetic in Biotechnology, Elsevier, 1983

09BI206 INSTRUMENTAL METHODS AND ANALYSIS

Credit : 4:0:0

Objectives

This course aims to study the definitions, preparations of buffering systems and its application. The course will explain the application of the following tools - Colorimeter, Flourimeter, Flame photometer and Spectrophotometer: types– UV – visible – IR – Raman spectroscopy. The course will also describe the principles, types of chromatography, immuno-electrophoresis, isotachophoresis, supporting materials-paper, starch, agarose, polyacrylamide, radioactive isotopes, radioactive decay and its applications in medicine & diagnosis

Outcomes

The student will learn about the definitions, preparations of buffering systems and its application. They will learn the function and application of Colorimeter, Flourimeter, Flame photometer and Spectrophotometer: types– UV – visible – IR – Raman spectroscopy. The principles and working condition of chromatography, immuno-electrophoresis, isotachophoresis for the supporting materials; paper, starch, agarose, polyacrylamide would be learned. They will also learn about the radioactive isotopes, radioactive decay their applications in medicine & diagnosis. The students would have an understanding about the are the thermo analytical techniques.

UNIT I Buffer Solutions

Definitions, preparations, derivation of Henderson-Hasselbalch equation and its application, buffering systems of blood, determination of pH using H2 electrode and glass electrode. calibration of instrumental methods, signal to noise ratio.

UNIT II Colorimeter, Flourimeter, Flame Photometer and Spectrophotometer

Beer - Lambert's law, Principle, description and application of Colorimeter, Flourimeter, Flame photometer and Spectrophotometer: types– UV – visible – IR – Raman spectroscopy.

UNIT III Chromatography and Electrophoresis

Chromatography- principles, types - paper, thin layer, adsorption, ion-exchange, affinity, gel filtration, gas and HPLC. Electrophoresis – principles, types – disc, Isoelectric focussing, immuno-electrophoresis, isotachophoresis, supporting materials-paper, starch, agarose, olyacrylamide.

UNIT IV Radio active techniques

Radioactive isotopes, radioactive decay and their types, radioactive techniques-RIA, GM counter, Scintillation counter, Autoradiography, Applications in Medicine & Diagnosis.

UNIT V Thermo Analytical Techniques

Theory of thermal analysis- thermo gravimetric- Basic theory, construction and working of Differential Thermal Analysis (DTA) and Differential Scanning Calorimeter (DSC)

Text Book

1. Willard and Merrit, Instrumental Methods and Analysis. VI Edition, CBS Publishers & Distributors; 1992.
2. D. Skoog, Instrumental Methods of Analysis, 2000.

Reference Books:

1. Ewing GW, Instrumental methods of Chemical Analysis, McGraw Hill BookCompany, 1989.
2. Braun. H, Introduction to Chemical Analysis, McGraw Hill, 1987.

09BI207 MOLECULAR BIOLOGY AND GENETIC ENGINEERING

Credits: 4:0:0

Objectives

- To develop skills of the students in understanding the basics of Molecular Biology and Genetic engineering.
- To provide basic knowledge on replication. Transcription and Translation
- To provide knowledge on methods of cloning, construction of DNA libraries and applications of rDNA technology.

Outcome

- Students may obtain interest in Molecular biology research
- Students may acquire knowledge about the methods of rDNA technology.

Unit I Molecular Genetics

DNA as genetic material, classical experiments – Hershey and chase; Avery McLeod & McCarty. Bacterial conjugation, transduction and transformation, prokaryotic and eukaryotic genome organization.

Unit II Replication and Transcription

Replication in prokaryotes and eukaryotes - D-loop and rolling circle mode of replication, replication of linear viral DNA. Transcription- initiation, elongation, termination, features of promoters and enhancers, transcription factors, inhibitors, post-transcriptional modification - RNA splicing, ribozyme. RNA editing.

Unit III Translation

Elucidation of genetic code, Process of translation in prokaryotes and eukaryotes, post-translational modifications, Suppressor mutations, Regulation of gene expression - Lac and trp operons.

UNIT IV Recombinant DNA Technology

DNA cloning, vectors, restriction enzymes**,** Construction of cDNA and genomic libraries. Screening of libraries with probes – Northern, Southern and Western blotting. PCR- Principle, application and types. RAPD, Site Directed Mutagenesis. Restriction mapping

UNIT – V Applications of Recombinant DNA Technology

Cloning in plants, transgenic and knockout animals. Recombinant cytokines and antibodies, vaccines, gene-therapy, stem cell therapy. Invitro fertilization, embryo transfer technology.

Text Book

1..Primrose SB & Twyman , "Principles Of Gene Manipulation, An Introduction To Genetic Engineering ", Blackwell Science Publications, 2006.
2. David Friefelder, Molecular Biology, Narosa Publ. House. 1999

Reference books

1. Sandhya Mitra, “Genetic Engineering Principles and Practice”, Rajiv Beri for Macmillan India Ltd publications, 2008.
2. P.K.Gupta, “Elements of biotechnology”, Rastogi publications,2004.
3. Gardner / Simmons / Snustad, Principles of Genetics, Eighth Edition, John Wiley, 2000

09BI208 ANALYTICAL BIOCHEMISTRY LAB

Credit : 0:0:2

1. Qualitative Analysis Of Carbohydrates
2. Estimation Of Glucose By Glucose Oxidase Method
3. Qualitative Analysis Of Amino Acids
4. Estimation Of Protein By Lowry’s Method
5. Estimation Of Amino Acid By Ninhydrin Method
6. Assay Of Acid Phosphatase Enzyme In Potato Extract
7. Estimation Of Cholesterol By Zak’s Method
8. Identification of Amino acids by Paper Chromatography
9. Identification of Sugars by Paper Chromatography

10. Conductometric Titration
11. Determination of Turbidity by Nephelometry
12. Gas Chromatography Study
13. High Performance Liquid Chromatography Study

09BI209 BIOINFORMATICS NETWORKS AND APPLICATIONS

Credit : 4:0:0

Objective:

1. This course provides the necessary basic protocols in computers and various biological databases available on the internet.
2. It consists of the tools used for biological sequential data analysis and methods of analyzing genetic and protein information.
3. It explains the methods used for Phylogenetic analysis and DNA mapping & sequencing.

Outcome:

1. Know the core algorithms in bioinformatics and experience in implementing simple solutions
2. Be familiar with the available biological database resources and analysis.
3. Serves as input to other courses in the B.Tech Bioinformatics curriculum.

Unit I Introduction to Bioinformatics

Scope of Bioinformatics – Elementary commands and Protocols, ftp, telnet, http. Printer on information theory. Databanks – nucleotide databanks – Genbank, NCBI, EMBL, DDBJ – protein databanks – sequence databanks – PIR, SWISSPROT, TrEMBL _ structural databases – PDB, SCOP, CATH, SSEP, CADB, Pfam and GDB.

UNIT II : Sequence Alignment and Dynamic Programming

Introduction – Strings – Edit distance two strings – string similarity local alignment -gaps – Parametric sequence alignments – suboptimal alignments – multiple alignment – common multiple alignment methods.

Unit III : Sequence Databases and Their Uses

Introduction to databases – database search – Algorithms issues in database search – sequence database search – FASTA – BLAST – Amino acid substitution matrices PAM250 and BLOSUM62. GCG Sequence Analysis(Basic concepts only)

UNIT IV : Evolutionary Trees and Phylogeny

Ultrametric trees – parsimony – Ultrametric problem – Perfect phylogeny – Phylogenetic alignment – connection between multiple alignment and tree construction.

UNIT V : Special Topics in Bioinformatics

DNA Mapping and sequencing – Map alignment – Large scale sequencing and alignment – Shotgun – DNA sequencing – Sequence assembly – Gene predictions – Molecular predictions with DNA strings.

Text Book

1. T.K.Attwood & D.Parry-Smith, Introduction to Bioinformatics, Pearson Education, 2001.
2. R.Durbin, R.Eddy, K.Anders and M.Graeme, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, 1999

Reference Books

1. Dan Gusfield, Algorithms On Strings Trees And Sequences, Cambridge University Press, 1997.
2. Lesk, Introduction to Bioinformatics, Oxford University Press, 2002.

09BI210 BIOPHYSICS

Credit : 4:0:0

Objectives

This course aims to study the strategy and tactics of biophysical concepts of macromolecules, the conformational analysis and forces that determine the protein and nucleic acid structure. This course emphasis kinetics study of ligand interaction with macromolecules. To study and analyze the size and shape of the macro molecule using different techniques like X-ray crystallography, and NMR.

Outcomes

From this course the student would learn about the different levels of structures in biological macromolecules based on their size, shape and their conformations. They would understand the forces that are involved in stabilizing these macro molecules. They would learn how the different tools are used to analyze the various structures and properties of the macro molecules. The kinetic study of these macromolecules will be useful to understand ligand interaction with other macromolecules.

UNIT I Introduction

Levels of structures in Biological macromolecules. Central questions in biophysics, basic strategies in biophysics.

UNIT II Conformational Analysis

Forces that determine protein and nucleic acid structure, basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions and water structures ionic interactions, disulphide bonds.

UNIT III Structural Analysis of Macromolecules

Prediction of proteins structure, nucleic acids, general characteristics of nucleic acid structure, geometrics, glycosidic bond rotational isomers and those puckering backbone rotational isomers and ribose puckering forces stabilising ordered forms, base pairing, base stacking tertiary structure of nucleic acids.

UNIT IV Kinetics of Ligand Interaction

Biochemical Kinetics studies, unimolecular reactions, simple biomolecular multiple intermediates, steady state kinetics, catalytic efficiency, relaxation spectrometry, ribonuclease as an example.

UNIT V Techniques for the Study of Biological Structure & Function

Size and shape of macromolecules, methods of direct visualisation, macromolecules as hydrodynamic particles, macromolecular diffusion, ultracentrifugation, viscometry X-ray crystallography – X–ray diffraction, determination of molecular structures ,electron microscopy, neutron scattering, light scattering.

Text Book

1. Cantor R., Schimmel P.R., Biophysical Chemistry, Vol. I, II, W.H. Freeman & Co., 1985.

Reference Book

1. Daniel. M, Basic Biophysics for Biologists, 1998.

09BI211 OBJECT ORIENTED PROGRAMMING - C++ AND JAVA

Credit : 4:0:0

Objective

This course aims to describe Object Oriented Programming concepts with the help of methods and classes present in C++ and Java languages.

Outcome

The goal is to help students understand techniques and methods in C++ and Java so that they can learn how the program works in already available Bioinformatics application and also they can develop their own Bioinformatics applications.

UNIT I

Object oriented programming - Introduction, Basic concepts, Object oriented Languages, Applications. Object oriented programming system – C++ - Key concepts, classes, features , functions, operators, variables, C++ program, structures

UNIT II

Tokens, expressions, control structures – tokens, keywords, Identifiers and constants, Data types, Functions, classes and objects, Constructors and Destructors. String manipulation – creating string objects, manipulation, relational operation, accessing character in strings

UNIT III

Operator overloading – Defining unary and binary operators Inheritance – Defining derived class, single inheritance, Multiple inheritance, constructors in derived class Pointers – to objects, to derived classes, to virtual functions Working with files – File stream operation, file pointers and their manipulation, File updation

UNIT IV

Java features, Java program structures, constants, variables, & data types, classes &J Objects, Packages, Arrays, string and vectors.

UNIT V

Managing errors and exception handling, Java applets programming, Multi-threading, I / O streams, Sample Java program in Bioinformatics.

Text book

1. E.Balaguruswamy, Object oriented programming with C++, Second edition, Tata Mc Graw Hill publications,2001
2. E.Balaguruswamy, Programming with Java, second edition, Tata McGraw Hill publications,2000

Reference Book

Robert Lafore, OOPS in C++, Third edition, Galgotia publications, 2001

09BI212 GENOMICS

Credit : 4:0:0

Objectives

- To develop skills of the students in the area of genomics in both theory and practical.
- To provide knowledge on genome analysis through experimental and computational methods.

Outcomes

- Students may get interest in gene and genome analysis through experimental or computational methods.
- Students may know well about the genome features of prokaryote and eukaryote and it may help to develop sequence analysis tools.

UNIT I

Introduction - organization and structure of genomes - Genome size - sequence complexity - Introns and Exons - Genome structure in viruses and prokaryotes - Isolation of chromosomes - chromosome microdissection - Retrofitting

UNIT II

Sequencing methods and strategies - Automated DNA sequencing - DNA sequencing by capillary array electrophoresis - High throughput sequencing - restriction enzyme fingerprinting - marker sequences - Hybridization assays - physical mapping without cloning

UNIT III

Genome annotation - traditional routes of gene identification - detecting open-reading frames - software programs for finding genes - Identifying the function of a new gene - gene ontology - overview of comparative genomics - protein structural genomics - introduction - determining gene function by sequence comparison and through conserved protein structure

UNIT IV

Global expression profiling - Introduction - traditional approaches to expression profiling - analysis of RNA expression - applications of genome analysis and genomics

UNIT V

Genome Projects: Human - Mouse - Plasmodium falsiparum - Saccharomyces cerevisiae - Mycobacteriam tuberculosis

Text Books:

1. S.B. Primrose and R.M. Twyman, Principles of Genome analysis and Genomics, Blackwell publishing, 2003.

Reference books

2. T.A. Brown, Genomes, 2nd edition, BIOS Scientific Publishers Ltd, 2002.
3. Sándor Suhai, Genomics and Proteomics-Functional and computational Aspects, Springer, 2000.
4. A. Malcolm Campbell and Laurie J. Heyer, Discovering genomics, proteomics and bioinformatics, Pearson/Benjamin cummings, 2006.

09BI213 PROTEOMICS

Credit : 4:0:0

Objectives

- To develop skills of the students in the area of proteome analysis
- To know more about proteins and their differential expression during normal and disease states which poise main target for drug development
- To know about the various tools of proteomics
- To understand the various application of proteomics including Microarrays

Outcomes

- Knowledge in the technique, methodology and Application of Proteomics tools
- An overview of application of Microarrays in medicine

UNIT I Introduction to Proteomics

The Proteome, Genomics Vs Proteomics, Proteomics and the new biology. Tools of Proteomics: Two dimensional PAGE, Tandem Liquid chromatography, Types of Mass spectrometers.

UNIT II Analysis of proteomes

Two-dimensional polyacrylamide gel electrophoresis: Sample preparation- Solubilization, Reduction, Resolution and Reproducibility of 2-DE, Detecting proteins in polyacrylamide gels (the names of stains is only required), Image analysis of 2-DE gels

UNIT III Mass spectrometry based methods for protein identification

Correlative mass spectrometric based identification strategies, De novo sequencing using mass spectrometric data, Separation methods for phosphorylation site analysis, Peptide mass fingerprinting, Mining proteomes, Bridging Genomics and Proteomics

UNIT IV Introduction to Microarrays

Introduction to Microarrays, Types of micorarrays .Cancer and Genomic Microarrays: Improving diagnosis, understanding complexity, Discover genome dynamics in cancerous cells. Improving health care with DNA Microarrays

UNIT V Application of proteome analysis

Application of proteome analysis: Drug development and toxicology,, Phage antibodies as tools, Glycobiology and Proteomics, In plant genetics and breeding

Text book

1. Pennington SR and Dunn MJ, Proteomics: from protein sequence to function, First Indian edition, 2002.

Reference books

1. Daniel C.Liebler, Introduction to Proteomics: Tools for the New Biology, Humana Press, Totowa, New Jersey, 2002

2. A. Malcolm Campell and Laurie J. Heyer, Discovering Genomics, Proteomics & Bioinformatics, Pearson Education, New Delhi, 2004

09BI214 MOLECULAR EVOLUTION AND PHYLOGENY

Credit : 4:0:0

Objective

This course aims to combine the concepts of molecular biology, evolutionary biology and population genetics to understand recent discoveries on the structure and function of nucleic acids and proteins. An important area within the study of molecular evolution is the use of molecular data to determine the correct biological classification of sequences and organisms called phylogenetics.

Outcome

The students would be able analyze the techniques and methods used in molecular evolution and phylogeny in processing the molecular data in building phylogenetic trees. They will also be able to study epidemiology based on molecular data.

UNIT I

Introduction to molecular evolution- Archaeology of the genome- fundamentals of Population genetics-The nature of molecular evolution- Driving forces in evolution, evolutionary changes in nucleotide sequences.

UNIT II

Molecular phylogenetics- Terminology of phylogenetic trees- Trees and distances- Molecular phylogenetic archaeology - Molecular phylogenetic examples- The universal phylogeny.

UNIT III

Measuring genetic change- Sequence alignment and homology- Genetic distance-Measuring evolutionary change on a tree- kinds of data- Methods of reconstruction- Distance matrix methods, Maximum parsimony methods, Maximum likelihood methods- analysis of true tree-Problems associated with phylogenetic reconstruction

UNIT IV

Models of molecular evolution- Modes of evolutionary process- Functional constraints and the rate of substitution patterns of codon usage and base composition- Molecular clocks, evaluation of molecular clock hypothesis - Neutral theory- Genetic variation within species- Natural selection

UNIT V

Applications of molecular phylogenetics- Organismal phylogeny- Gene trees and species trees-Age and rates of diversification phylogeny in molecular epidemology- Host parasite co-speciation

Reference books:

1. Dan Graur and Wen-Hsiung Li.Fundamentals of Molecular evolution, II edition, Sinauer Associates, INC. 2000
2. Roderic D. M. Page, Edward C. Holmes Molecular evolution, A phylogenetic approach, Blackwell Science Inc; (October 1998)

09BI215 MOLECULAR MODELLING AND DRUG DESIGN

Credit : 4:0:0

Objective

- To understand the critical relationship among biomolecular structure, function and force field models.
- To be able to utilize basic modeling techniques to explore biological phenomena at the molecular level.
- To emphasize Modelling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

Outcome

- Students are introduced to the principles and practice of Molecular modeling and modern drug discovery.
- An awareness of rational drug design, based on understanding the three-dimensional structures and physicochemical properties of drugs and receptors will be created.

UNIT I: Introduction to Molecular Modelling

Introduction - Useful Concepts in Molecular Modelling : Coordinate Systems. Potential Energy Surfaces. Molecular Graphics. Surfaces. Computer Hardware and Software. The Molecular Modelling Literature.

UNIT II: Force Fields

Force Fields. Bond Stretching. Angle Bending. Introduction to Non-bonded Interactions. Electrostatic Interactions. Van der Waals Interactions. Hydrogen Bonding in Molecular Mechanics. Force Field Models for the Simulation of Liquid Water.

UNIT III : Energy Minimisation and Computer Simulation

Energy Minimisation and Related Methods for Exploring the Energy Surface. Non-Derivative method, 1st and 2nd order minimisation methods. Computer Simulation Methods. Simple Thermodynamic Properties and Phase Space. Boundaries. Analyzing the Results of a Simulation and Estimating Errors. GROMACS and CNS.

UNIT IV: Molecular Dynamics & Monte Carlo Simulation

Molecular Dynamics Simulation Methods. Molecular Dynamics Using Simple Models. Molecular Dynamics with Continuous Potentials. Molecular Dynamics at Constant Temperature and Pressure. Metropolis Method. Monte Carlo Simulation of Molecules. Models Used in Monte Carlo Simulations of Polymers. Molecular Modeling software: BIOSUITE

UNIT V: Structure Prediction and Drug Design

Protein Structure Prediction - Introduction to Comparative Modeling. Sequence Alignment. Constructing and Evaluating a Comparative Model. Predicting Protein Structures by 'Threading', Molecular Docking, AUTODOCK and HEX. Structure based De Novo Ligand design, Drug Discovery – Chemoinformatics – QSAR.

Reference Books:

1. A.R.Leach, Molecular Modelling Principles and Application, Longman, 2001.
2. J.M.Haile, Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons, 1997.
3. Satya Prakash Gupta, QSAR and Molecular Modeling, Springer - Anamaya Publishers, 2008.

09BI216 MACHINE LEARNING IN BIOINFORMATICS

Credit : 4:0:0 **B**

Objective

- This course aims to machine learning techniques and methods in integrating and interpreting the bioinformatics data sets and improving effectiveness and efficiency and quality for bioinformatics data analysis.
- The goal is to help students understand techniques and methods in bioinformatics to design HMM and Neural Net based applications development.
- To know the working principles of existing Neural net and HMM based protein structure prediction programs.

Outcome

- The students will be able to understand the logic of usage of probability techniques in machine learning.
- HMM and Neural net based data parameterization can be done.

UNIT I

Machine-Learning Foundations: The Probabilistic Framework -Introduction: Bayesian modeling The Cox Jaynes axioms - Bayesian inference & induction -Model structures: graphical models & other tricks - Probabilistic Modeling & Inference: Examples -The simplest sequence models - Statistical mechanics

UNIT II

Machine Learning Algorithms - Introduction -Dynamic programming -Gradient descent - EM/GEM algorithms –Markov chain Monte-Carlo methods - Simulated annealing – Evolutionary & genetic algorithms. Learning algorithms: miscellaneous aspects

UNIT III

Neural Networks: The Theory -Introduction - Universal approximation properties – Priors & likelihoods - Learning algorithms: backpropagation - Neural Networks: Applications - Sequence encoding & output interpretation- Sequence correlations & neural networks – Prediction of protein secondary structure - Prediction of signal peptides & their cleavage sites - Applications for DNA & RNA nucleotide sequences - Prediction performance evaluation - Different performance measures

UNIT IV

Hidden Markov Models: The Theory - Introduction -Prior information & initialization -Likelihood & basic algorithms - Learning algorithms -Applications of HMMs: general aspects -Protein applications - DNA & RNA applications - Advantages & limitations of HMMs

UNIT V

Probabilistic Graphical Models in Bioinformatics - Markov models & DNA symmetries - Markov models & gene finders - Hybrid models & neural network parameterization of graphical models -The single-model case - Bi-directional recurrent neural networks for protein secondary structure prediction

Reference books

1. Pierre Baldi and Søren Brunak, Bioinformatics: the Machine Learning Approach – Publisher: MIT Press,1998.
2. David W. Mount, Bioinformatics: Sequence and Genome Analysis ,Cold spring Harbour laboratory, 2004

09BI217 PERL PROGRAMMING

Credit : 4:0:0

Course Objective:

This course is intended for students who are new to the Perl programming language. Because Perl is such a versatile language, and is used for many different tasks, this course will appeal to a wide variety of professionals: System administrators, Web developers, and application programmers will all benefit from attending.

Course outcomes

- Understanding of basic Perl
- Ability to apply prerequisite basic programming concepts to Perl
- Write, compile, and run Perl programs, Analyze the effects of using Perl structures that implement decisions, loops, and store arrays and use these structures in a well-designed, OOP program.
- Create Perl programs that make use of various directories and use several files linked together. Create Web sites with Perl programs and compare and contrast the effectiveness of using Web programming modules from CPAN.

Unit I: Introduction to Perl

Perl interpreter and it's working. Variables and Data types: Perl variables, Scalar values, Calculations, Interpolation and Escapes. Arrays and Hashes: Arrays and Array manipulation, Push and Pop Shift and Unshift, Splice and other array function.

Unit II: Control Structures

Comparisons, Choices, loops, Intermediate Loops and Loop exits. Subroutines: Creating a subroutine, Arguments, Return and Scope. String Manipulations: Array based character manipulations, Regular expressions Match, Substitue and Translate. Patterns.

Unit III: Input and Output
Program parameters, File I/O, File handles, working with file handles, Built-in file handles,file safety. Inter process communications, Processes, Process pipes, Creating and monitoring pipes.Perl modules and packages: modules, packages, CGI, Getopt, Io.

Unit IV: Advanced Perl
Creating references, ref( ), Object-Oriented programming: Introduction to Objects, OOP Approach, Class design, inheritance. Perl objects: Rules, methods, constructors and Accessors,OOP versus Procedural, exercises.

Unit V: Bioperl
Sequences, Seqfeature, A class for Restriction enzymes, Perl in Bioinformatics, Perl and relational database, Perl and the web, Perl and the graphics. Installation of bioperl and its applications. Bioperl problems. bio-python.

Reference Books:

1. D. Curtis Jamison, Perl Programming for Bioinformatics and Biologists, Wiley-Dreamtech, 2004.
2. James D. Tisdall, Mastering Perl for Bioinformatics, O'Reilly & Associates, 2003.

09BI218 STRUCTURAL BIOINFORMATICS

Credit : 4:0:0

Objectives

This course aims to study the strategy and tactics of biophysical concepts of macromolecules and the conformational analysis and forces that determine the protein and nucleic acid structure and ligand interaction with macromolecules. Study of the size and shape of the macro molecule using different techniques using various tools like X-ray Crystallography and NMR is explained in the course

Outcomes

The student would learn the different structural levels of biological macromolecules, its size, shape, their conformations and the forces that are involved in stabilizing these molecules. The tools by which this analysis is done will be learned. The student would also learn about the ligand interaction with macromolecules.

Unit I : Introduction

Levels of structures in Biological macromolecules - basic strategies in biophysics- Principles and concepts used in biophysical analysis of life processes - Biomolecules and their interactions, size and shape of macromolecules.

Unit II : Conformational Analysis
Forces that determine protein and nucleic acid structure, basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions and ionic interactions, disulphide bonds.

Unit III : Structural Analysis of Macromolecules
Prediction of proteins structure, nucleic acids, general characteristics of nucleic acid structure, geometrics, glycosidic bond rotational isomers and those puckering backbone rotational isomers and ribose puckering forces stabilising ordered forms, base pairing, base stacking tertiary structure of nucleic acids.

Unit IV: Spectroscopy and methods of visualization:
Absorption spectroscopy, Linear and Circular Dichroism, Emission spectroscopy, Nuclear Magnetic Resonance spectroscopy. Methods of direct visualisation, macromolecules as hydrodynamic particles, macromolecular diffusion, ultracentrifugation, viscometry.

Unit V: X–ray diffraction
X-ray crystallography – X–ray diffraction, determination of molecular structures, electron microscopy, neutron scattering, light scattering.

Text Book
1. Cantor R., Schimmel P.R., Biophysical Chemistry, Vol. I, II, W.H. Freeman & Co., 1985.

Reference Book
1. Daniel. M, Basic Biophysics for Biologists, 1998.
2. Kensal E. van Holde, W. Curtis Johnson and P. Shing Ho, Principle of Physical Biochemistry, Prentice Hall, New York, 1998

09BI219: BIOCOMPUTING

Credits 4:0:0

Objectives

- To have an overview idea about parallel computing.
- To study the various techniques involved in RNA structure prediction, gene expression analysis, protein structure prediction and evolutionary tree and phylogeny

Outcomes

The course will give an overview idea about parallel computing. This course would also enable the student to under the various computing approaches used to analyze and predict various biological processes.

UNIT I Parallel Computing
Computational demands of modern science, Parallel processing technology, Processor organization- Mesh networks, Binary tree networks, Hyper tree networks, Pyramid networks, Hypercube networks, Flyn Taxanomy , Processor array, Multicomputers- Ncube2, Paragon XP/S, Overview of parallel programming languages – FORTRAN 90, Ncube C, SEQUENT C

UNIT II RNA structure prediction
Gene prediction: Introduction-Promoter prediction in E.Coli, Eukaryotes-Scoring matrix method used with aligned promoter sequences-Grail II-Gene parser, Features of RNA secondary structure, Limitations of predictions, RNA secondary structure prediction methods – Minimum free energy method, Suboptimal structure prediction by MFOLD and the use of energy plots.

UNIT III Gene expression analysis
Overview – Gene expression analysis tools, Microarray technologies, Measuring gene expression using microarray, Image processing and normalization, Analyzing microarray data- t-test, non-classic parametric test, one way anova.

UNIT IV Protein structure analysis
Overview – protein secondary structure from amino acid sequence, accuracy of secondary structure prediction, Methods for secondary structure prediction – Chou-Fasman/GOR method, Neural network method, Nearest- neighbor method, Prediction of three dimensional protein structure – structure profile method, contact potential method.

UNIT V Evolutionary Trees and Phylogeny
Concept of evolutionary trees, Maximum Parsimony method, Distance based method- Fitch and Margolish method, Neighbor joining method, Unweighted pair group method, Maximum Likelihood method.

Textbook:

1. Bioinformatics : Sequence and Genome analysis, 2nd edition, David W Mount , CBS Publishers,2004
2. Microarray Bioinformatics: Dov Stekel, Cambridge University Press, 2005.
3. Parallel Computing 2nd edition, Michael J.Quinn, Tata McGraw-Hill 2002.

09BI220: INTRODUCTION TO UNIX AND LINUX

Credit : 4:0:0

Objective

The Objective of this course is to understand the Operating System Concepts with the help of Unix Operating System and to have a good experience to work with the Open Source Linux Operating System.

Outcome

The goal is to help students to install and work with Open Source Software's.

UNIT I

UNIX Operating System – History – Understanding the Unix Command – General purpose utilities – Navigating the Filesystem – Handling ordinary files – The Shell – The Vi Editor – Advanced Vi - The Environment.

Unit II

Basic File Attributes – More File Attributes – System Administration II-The FileSystem revisited - Simple Filters – Regular Expressions and The grep family – Advanced filters – sed and awk.

Unit III

The Process - Communication and Electronic mail – Shell Programming – Advanced Shell Programming - System Administration – The Routine Duties.

UNIT IV

Linux Administration – GNOME and KDE – Managing users – The command line – Booting and Shutting down - File systems – Compiling the Linux Kernel

UNIT V

Linux Internet services – DNS – Setting up web server using Apache – the secure shell. Intranet services in Linux – NFS and NIS, Printing – Network configuration. Page 4

Text Books:

1. Sumitabha Das, Unix – Concepts and Applications, Tata McGraw Hill, 2ndEdition. (Chapters 2-17, 20, 23, 24, 25)
2. Steven Graham & Steve Shah, Linux Administration, Third Edition, Dreamtech, NewDelhi, 2003.

Reference Books:

1.Kenneth Rosen, Douglas Host, James Farber, Richard Rosinki, Unix-The Complete Reference, Mc-Graw Hill,1999.
2. Roderick W Smith, Linux in a Windows world, Oreilly, 2005.
3. Yaswanth Kanitkar, Unix Shell Programming, BPB Publications, 2003

09BI221 DATAMINING AND DATA WAREHOUSING

Credit : 4:0:0

Objective

This course helps the students to understand the overall architecture of a data warehouse and techniques and methods for data gathering and data pre-processing using OLAP tools. The different data mining models and techniques will be discussed in this course. Data mining and data warehousing applications in bioinformatics will also be explored.

Outcome

Students would learn data mining techniques and methods in integrating and interpreting the bioinformatics data sets and improving effectiveness, efficiency and quality for bioinformatics data analysis.

UNIT I :

Overall Architecture of Data warehouse, Access Tools, Data marts, Data warehouse administration & management. Mapping the data warehouse to a multiprocessor architecture-relational database technology, database architecture for parallel processing.

UNIT II :

Meta – definition, repository, management and trends. From data warehousing to data mining

UNIT III :

OLAP – need guidelines, categorization, OLAP tools and internet, Patterns and models, Statistics –Data counting and probability, hypothesis testing, contingency tables, Prediction.

UNIT IV :

Data mining models – Introduction – Decission trees –nearest neighbor and clustering, selecting and using right technique, Data visualization.

UNIT V :

Applications of data warehousing and data mining in Bioinformatics.

Text books

1. Alex Berson, Stephen J. Smith, Data warehousing, data mining & OLAP, Tata McGraw Hill Publication, 2004
2. Sushmita Mitra, Tinku Acharya, Data mining- Multimedia, Soft computing and Bioinformatics, John Wiley & Sons, 2003

09BI222 INTRODUCTION TO DATABASE MANAGEMENT SYSTEMS

Credit : 4:0:0

Objective

This subject introduces students to relational database design and SQL (Structured Query Language) used with relational databases. Students will be presented with a methodology for relational database design using Entity Relationship Diagrams and normalization of data. An overview of the functions of the Database Management System (DBMS) and of a Database Administrator (DBA) will also be presented.

Outcome

After completing this course students must be able to demonstrate the knowledge and ability to analyze and design a database in some implementation. It would provide them to implement the structural constraints of relationships and use different keys for data access. They would gain skill of performing normalization and draw ER diagram of any database application.

UNIT I : Introduction

Purpose of Database systems - overall system structure - Entity relationship model: entities and entity sets relationships - mappings constraints - primary keys - E.R diagram.

UNIT II : Relational Model

Structure - Formal Query languages - Relational Algebra - Commercial Query languages – SQL, QUEL.

UNIT III : Relational Database Design

Pitfalls - Normalisation using functional dependencies - Decomposition - Boyce-codd Normal form - third normal form - fourth normal form, normalisation using join dependencies - domain-key normal form.

UNIT IV : Query Processing and Query Optimisation

Query processing - Overview, selection, operation, sorting, join operation, other operation, evaluation of operations

Query optimisation - Estimating statistics of expression, Transformation, materialised views, Distributed data base.

UNIT V : Oracle

ORACLE - Database design and querying tool, SQL variation and extension, storage and indexing, concurrency control and recovery, system architecture, replication, distribution and external data

Text books

Abraham Silberschatz, Henry K Korth, Sudarshan S, Database concepts, Fourth edition, Mc Graw Hill International publications, 2002.

Reference book

Ramesh Elmasri, Shamkant B. Navathe, Fundamentals of Database systems, Fourth edition, Addison –Wesley Publications, 2004.

09BI223 BIOPHARMACEUTICAL TECHNOLOGY

Credit: 3:0:0

Objective

The course introduces students to disciplines of the pharmacy and health sciences fields. The course gives general view of topics related to pharmacy and the ethics and regulations of these areas. To examine closely the subjects of greater actuality in pharmaceutical technological field. The students learn the techniques and methods of formulation development especially with reference to advanced formulation techniques, novel drug delivery systems, introduction of pharmaceutical bio-technology and role of pharmacist and bioengineers in the development of different useful biotechnological products. The course is designed to meet the challenges of the present and future Pharmaceutical workforce needs. Core modules develop the base technical skills and are subsequently augmented by modules which allow for the development of specific areas of expertise.

Outcome

- Develop an ability to apply principles and generalizations already learned about science and technology to new problems and situations. Learn terms and facts of biotechnology. Learn concepts and theories of biotechnology.
- Develop an ability to synthesize and integrate information and ideas. Improve speaking skills. Develop an informed understanding of the role of science and technology in society.
- Describe biotechnology as an industry and business. Differentiate between pharmaceutical, biopharmaceutical and biotechnology products. Describe the drug development process.. Identify methods of recombinant DNA technology. Analyze and solve problems related to recombinant DNA technology. Describe genomics and the Human Genome Project.
- Demonstrate competency in using web-based tools to solve Bioinformatics problems. Describe specific examples of biotechnology used in human health, food technology and industrial applications.Examine ethical implications of biotechnology.

Unit I: Introduction of drug action

History & Definition of Drugs- Sources of Drugs - Plant, Animals, Microbes and Minerals-Different dosage forms- Routes of drug administration- Pharmacodynamics- Physico-Chemical Principles. Mechanism of drug action- drug receptors- and Physiological receptors- structural and functional families -Pharmacokinetics- Drug absorption- factors that affect the absorption of drugs-Distribution of drugs- Biotransformation of drugs- Bioavailability of drugs.

Unit II: Important Unit Processes and their Applications

Chemical conversion processes – Alkylation – Carboxylation – Condensation and Cyclization – Dehydration, Esterification (Alcoholysis) – Halogenation – Oxidation, Sulfonation – Complex Chemical Conversions – Fermentation

Unit III: Manufacturing Principles
Compressed tablets – wet granulation – Dry granulation or slugging – Direct compression – Tablet presses formulation – Coating – Pills – Capsules sustained action dosage forms – Parental solutions and injections – Oral liquids –ointments – standard of hygiene and good manufacturing practice.

Unit IV: Production & analysis of Biopharmaceuticals
Vitamins – Cold remedies – Laxatives – Analgesics – Non-steroidal contraceptives – External Antiseptics – Antacids and others. Antibiotics – Biological hormones – Vitamins – preservation-Analytical methods and tests for various drugs and pharmaceuticals- Packing – Packing Techniques – Quality Control - Recent advances in the manufacture of drugs using r-DNA technology.

Unit V: Drug delivery systems
Biomaterials and their applications-Controlled and sustained delivery of drugs- Biomaterial for the sustained drug delivery- Liposome mediated drug delivery- Drug delivery methods for therapeutic proteins- Drug development process- Drug discovery- Patenting- Delivery of pharmaceutical-Preclinical trials- Drug regulatory authorities.

Text Book

1. A C Guyton, Text Book of Medical Physiology, WB Saunders, Hong Kong,1986.
2. Remington's Pharmaceutical Sciences, Mack Publishing and Co, 2004

Reference Books

1. Tripathi, Essential of medical pharmacology,4th edition ,1999
2. R.S. Satoskar, S.D. Bhandarkar and Nirmala N. Rege text book of Pharmacology and Pharmacotherapeutics , popular prakasam 2006

09BI224: INTRODUCTION TO ALGORITHM

Credits: 4:0:0

Objective

- This course will provide a rigorous introduction to the design and analysis of algorithms.
- We will discuss classic problems (e.g., sorting), classic algorithm design strategies (e.g., divide-and-conquer, greedy approaches), and classic algorithms and data structures.

Outcome

- Knowledge about algorithm designing techniques.

- Build and analyze algorithm

UNIT I

Introduction and Divide and Conquer: Algorithm - Complexity analysis - Introduction to random algorithms - General Method - Finding maximum and minimum - Strassens's matrix multiplication - Quick sort - selection sort

UNIT II

Greedy method: General method - Tree vertex splitting - Job sequencing with dead lines - Shortest path - Knapsack

UNIT III

Dynamic Programming: General method - Multistage graphs - String matching algorithm - The Rabin - Karp algorithm - String matching with finite automation - The Knutter - Morris Pratt - algorithm, The Boyer- Moore algorithm

UNIT IV

Back Tracking : General Method - Sum of Subsets - Graph coloring - Depth First search - Breadth first search

UNIT V

Branch and Bound: General Method - 0/1 knapsack Problem - Travelling Salesperson.

Text Book

E.Horowitz, S.Sahni and S.Rajasekaran – Fundamentals of Computer Algorithms – Galgotia publications - 1999

Reference books

1. Pevzner PA, Computational Molecular Biology – An Algorithmic Approach, PHI 2004
2. G.Brassard and P.Bratley - Fundamentals of Algorthmics – Prentice Hall India -1997

09BI225 BIOLOGICAL DATABASE LAB

Credit : 0:0:2

1. GenBank
2. NCBI
3. EMBL
4. DDBJ
5. SWISS-PROT
6. PIR
7. TrEMBL
8. PDB
9. SCOP

10. CATH
11. Pfam
12. PROSITE and BLOCKS

09BI226 BIOLOGICAL SEQUENCE ANALYSIS LAB

Credit : 0:0:2

1. Overview of Linux commands and file systems
2. EMBOSS.
3. Fasta analysis
4. BLAST analysis
5. Protein sequence analysis using GCG software
6. Pairwise comparison using GCG software
7. Gene finding and pattern recognition using GCG software
8. Multiple comparison using GCG software
9. Sequence utilities, Translation and nucleic acid secondary structure using GCG software.
10. Database reference searching and database sequence searching using GCG software
11. Evolution analysis and sequence Hidden Markov Model Alignment using GCG software
12. Enzyme analysis using GCG software.

09BI227 MOLECULAR MODELLING LAB

Credit : 0:0:2

1. Model building of oligosaccharides using CHEM SHETCH
2. Model building of oligopeptides using CHEM SHETCH
3. Structural Analysis of Protein
4. Structural analysis of Nucleic Acids
5. Conformational parameters for oligosaccharides
6. Conformational parameters for polypetides
7. Connoly surface studies of macromolecules using VMD
8. Homology modeling using SWIIS-PDB
9. Energy minimization for protein using Schrodinger software
10. Energy Minimization for carbohydrates using Schrodinger software
11. Molecular Dynamics for Protein using Schrodinger software
12. Molecular Dynamics for carbohydrates using Schrodinger software

09BI228 QSAR & DRUG DESIGN LAB

Credit : 0:0:2

1. Disease identification through web search

2. Identification of target protein for selecte d disease
3. Comparitive protein structure modeling
4. Comparitive modelling by modeller tool
5. Model validations and refinement
6. Active site & pocket prediction
7. Lead identification
8. Molecular description calculation
9. Molecular docking
10. QSAR

09BI229 PERL LAB

Credit : 0:0:2

1. Perl Basics and Variables - I
2. Perl Basics and variables – II
3. Control and Loop statements
4. Functions and Subroutines
5. Command line argument
6. File handle
7. Regular expressions
8. Perl web server
9. Modules:LWP and Bio-Perl
10. Basic Linux commands & Linux text editors
11. File permissions & job management
12. User administration commands

09BI230 C++ AND JAVA LAB

Credit : 0:0:2

C++

1. Objects, classes, Inheritance, Polymorphism.
2. Operator overloading.
3. Data type conversion.
4. Constructors, Pointers.
5. Virtual functions, Friend Functions, Static Functions
6. This pointer, Streams.
7. Exception handling, Templates, File operations.

JAVA

8. Program to create a simple applet and application
9. Using Java Classes and Objects
10. Using inheritance and interface
11. Using arrays in Java
12. Using exceptions
13. Using threads (Synchronization, communication, critical section)

14. Program using AWT packages: Windows, controls and message layout managers
15. Using package.net
16. Using I/O package (files and streams)
17. Create a simple web page for college information system

Create a web page to implement of searching technique

09BI231 DATABASE MANAGEMENT SYSTEM LAB

Credit : 0:0:1

1. Usage of DDL commands
2. Usage of DML and DCL commands
3. Usage of TCL commands
4. Multiple sub-queries
5. Correlated sub-queries
6. Arrays manipulation
7. Usage of explicit cursors & implicit cursors
8. Usage of functions
9. Usage of procedures
10. Exception handling
11. Usage of database triggers

09BI232 UNIX & LINUX LAB

Credit : 0:0:1

A list of 10 experiments will be given by the HOD from time to time.

UNIX / LINUX
Directory structure
Command-line file-system browsing,
Bash shell basics
Rpms usage
Mounts,
File creation and editing using vi editor
User administration
File/dir compression using tar and gzip.

09BI233 MOLECULAR BIOLOGY & GENETIC ENGINEERING LAB

Credit : 0:0:1

1. Isolation of bacterial DNA
2. Isolation of plant cell and animal cell genomic DNA

3. Agarose gel electrophoresis
4. Restriction enzyme digestion
5. Competent cells preparation
6. Transformation and screening for recombinants
7. Preparation of plasmid DNA
8. Ligation of DNA into expression vectors
9. Optimisation of time of inducer for recombinant protein expression
10. SDS-PAGE
11. Western blotting
12. Hybridisation with anti-sera
13. PCR.

09BI234 BIOORGANIC CHEMISTRY

Credit : 4:0:0

Objective

This course provides a detailed view of the reactions and concepts used in modern Organic chemistry. Reactions will be introduced for all common organic functional groups. The relative reactivities of these groups will be analyzed and their formation andConversion thoroughly studied. The theories of these techniques as well as their applications to the characterization and identification of a variety of molecules will be covered.

Outcome

- Reason and think analytically in solving problems and making decisions in matters involving bioorganic chemistry. Attainment of this learning outcome will be reflected by the student's ability to: Understand the reactions and synthesis of natural products as well as the mechanism of action and synthesis of selected medicinal agents.
- Apply a basic understanding of the systematic methods of scientific inquiry, principles and procedures to investigate problems. Attainment of this learning outcome will be reflected by the student's ability to: Use chemical logic to describe the mechanisms of new organic reactions not covered in general organic chemistry.
- To communicate matters of organic synthesis with clarity. Attainment of this learning outcome will be reflected by the students ability to: Successfully complete written and oral assignments, and examinations.

Unit – I Concepts in organic chemistry

Stereochemistry- R, S notation, E, Z Isomerism- Mechanism of SN1 and SN2 reactions. Mechanisms of E1 and E2 reactions. Enantiomers, Optical isomers, optical activity and optical rotation-polarimeter.

Unit – II Chemistry of enzymes

Structure of atom, chemical bonding and its characteristics, Chemical bonding involved in Protein structure, Specificity of enzymes. Concept of Free energy and its importance in

Biology. Chemistry of active oxygen species, free radicals systems.

Unit – III Case studies of enzyme structure and mechanism
Acid base and covalent catalysis**,** Stereochemistry of amino acids, Structure and mechanism of pyruvate dehydrogenase, proteases, ribonucleases, Carboxy peptidase, lysozyme. NAD, Dependent oxidation and reduction reactions.

Unit IV: Hydrolysis in chemical synthesis
Ester hydrolysis, Amide hydrolysis, peptide synthesis, structure and mechanism of FAD THF Coenzymes, Application of enzymes in industry and medicine.

UNIT V : Protein folding kinetics and folding pathways
Structure of proteins- an overview, Basic methods of protein folding – two state ineticsmultistate kinetics-in protein folding**.** Protein folding, its dynamics, stability of proteins and molecular chaperones. NMR, Circular dichorism - Principles, types, components and Applications in Biology.

Text Book

1. Text-H.Dugas, Bioorganic chemistry, Springer verlag publishers, 1999.
2. Mathew, Van Holde, Athwen , Biochemistry by, Pearson publishers LTD, Newdelhi, 2000.

Reference Books

1. J.L.Jain & Sunjay Jain, Fundamental of biochemistry 6th Edition, 2004.
2. Paula yurkari Bruice, Organic chemistry, 3rd edition ,Pearson LTD, New Delhi;2002
3. Trevor Palmer, Enzymes, East West Press P LTD, New Delhi, 2005.

09BI235: INTRODUCTION TO SYSTEMS BIOLOGY

Credit : 4:0:0

Objective
This course focuses on the systematic study of complex interactions between the components of biological systems and how these interactions give rise to the function and behavior of that system. One of the major role of system biology is to discover new emergent properties that may arise from the systemic view used by this discipline in the order to understand better the entirety of processes that happen in a biological system.

Outcomes
This course helps the student to understand the complex interaction between different components that are responsible for various functions in a biological system.

UNIT I
Introduction - System-level Understanding of Biological Systems - Advanced Measurement Systems Modeling Genetic Networks

UNIT II

Modeling the Activity of Single Gene - A Probabilistic Model of a Prokaryotic Gene and its Regulation Modeling Biochemical Networks - Atomic-Level Simulation and Modeling of Biomacromolecules

UNIT III

Kinetic Models of Excitable Membranes and Synaptic Interactions - Stochastic Simulation of Cell Signaling Pathways -Analysis of Complex Dynamics in Cell Cycle Regulation

UNIT IV

Modeling Large Biological Systems from Functional Genomic Data: Parameter Estimation - Cellular Simulation - Towards a Virtual Biology Laboratory - Computational Cell Biology : The Stochastic Approach

UNIT V

Computer Simulation of the Whole Cell - Computer Simulation of the Cell: Human Erythrocyte Model and its Application - Software for Modeling and Simulation – E-CELL, V-CELL and GROMOS

Reference books:

1. Hiroaki Kitano (Editor),Foundations of Systems Biology, ,MIT Press, 2001
2. James M. Bower, Hamid Bolouri,Computational Modeling of Genetic and Biochemical Networks, MIT Press,2000.
3. Julio Collado-Vides (Editor), Ralf Hofestadt (Editor)Gene Regulation and Metabolism: Postgenomic Computational Approaches, ,MIT Press,2002

09BI236 PROTEIN ENGINEERING

Credit: 4:0:0

Objectives:

- To develop the skills of the students in the area of Protein Engineering.
- To verify the structure of naturally occurring peptides as determined by degradation techniques.
- To study the relationship between structure and activity of biologically active protein and peptides and establish their molecular mechanisms.

Outcome

- Students learnt about the amino acids and their characteristics, structure of proteins, bonds & interactions and methods to determine the protein structures, protein structure and function relationship and principles involved in production of engineered proteins.
- Students learned about peptide synthesis in the laboratory scale with using various chemicals and the method of peptide formation.

UNIT I Bonds And Energies In Protein Makeup

Covalent, Ionic, Hydrogen, Coordinate, hydrophobic and Vander walls interactions in protein structure. Interaction with electromagnetic radiation (radio, micro, infrared, ultraviolet, X-ray) and elucidation of protein structure.

UNIT II Amino Acids And Their Characteristics

Amino acids (the students should be thorough with three and single letter codes) and their molecular properties (size, solubility, charge, pKa), Chemical reactivity in relation to post-translational modification (involving amino, carboxyl, hydroxyl, thiol, imidazole groups) and peptide synthesis.

UNIT III Protein Architecture

Primary structure: peptide mapping, peptide sequencing - automated Edman method & mass-spec. High-throughput protein sequencing setup Secondary structure: Alpha, beta and loop structures and methods to determine Super-secondary structure: Alpha-turn-alpha, beta-turn-beta (hairpin), beta-sheets, alpha-beta-alpha, topology diagrams, up and down & TIM barrel structures nucleotide binding folds, prediction of substrate binding sites Tertiary structure: Domains, folding, denaturation and renaturation, overview of methods to determine 3D structures, Quaternary structure: Modular nature, formation of complexes.

UNIT IV Structure-Function Relationship

DNA-binding proteins: prokaryotic transcription factors, Helix-turn-Helix motif in DNA binding, Trp repressor, Eucaryotic transcription factors, Zn fingers, helix-turn helix motifs in homeodomain, Leucine zippers, Membrane proteins: General characteristics, Trans-membrane segments, prediction, bacteriorhodopsin and Photosynthetic reaction center, Immunoglobulins: IgG Light chain and heavy chain architecture, abzymes and Enzymes: Serine proteases, understanding catalytic design by engineering trypsin, chymotrypsin and elastase, substrate-assisted catalysis other commercial applications.

UNIT V Protein Engineering

Advantages and purpose, overview of methods, underlying principles with specific examples: thermal stability T4-lysozyme, recombinant insulin to reduce aggregation and inactivation, de novo protein design.

Text Books

1. Voet D. and Voet G., "Biochemistry", Third Edn. John Wiley and Sons, 2001
2. Branden C. and Tooze J., "Introduction to Protein Structured, Second Edition", GarlandPublishing, NY, USA, 1999

References

1. Creighton T.E. Proteins, Freeman WH, Second Edition, 1993
2. Moody P.C.E. and Wilkinson A.J. "Protein Engineering", IRL Press, Oxford, UK, 1990.

09BI237 NEUROBIOLOGY AND COGNITIVE SCIENCE

Credit : 4:0:0

Objective:

- To understand the nervous system and neuro-anatomy.
- To get an insight into Neurophysiology and Neuropharmacology.
- To understand the Neurological Disorders and behaviour science.

Outcome:

- To acquire knowledge about the basics of neurobiology and cognitive scinece.
- To apply the bioinformatics skills in the field of neural science.

Unit I: Introduction to Nervous System

Central and Peripheral nervous systems

Unit II: Neuro Anatomy

Structure and functions of neurons, synapse, their function, signals produced by neurons, Sensors function, Glial cells, molecular and cellular organisation of neuronal differentiation, characterization of neuronal cells.

Unit III: Neurophysiology and Neuropharmacology

Pharmaceutical mediator released by neurons, Hormones and their effect on neuronal function, Conduction of impulses by neurons, Correlation of sensory functions.

Unit IV: Neurological Disorders

Pathogenesis, Genetic basis of neurological disorders

Unit V: Behaviour Science

Neuronal mechanism of behaviour, Animal behaviour, Behaviour in various environments.

Text Books:

A.B. Schiebel, Neurobiology of higher cognetive function Guilford Press 1990.
Haynes, Neuron in Tissue Culture, 1998.
Beadle, Progress in Neuropharmacology and Neurotoxicology of pesticides and drugs, 1999.

09BI238 NANOBIOTECHNOLOGY

Credits: 4:0:0

Objective

- To understand the overview and concepts of nanotechnology.
- To know about nano-molecular manufacturing and the physics of the solid state.
- To understand the bulk nanostructured materials, organic compounds and polymers.

Outcome

- To acquire knowledge about the principles and applications of nanotechnology.

- To develop skills by applying the knowledge of bioinformatics in the field of nanotechnology.

UNIT – I

Overview and History of Nanotechnology – Generations of nanotechnology - Nanoparticles / Nanomaterials - Journals of Nanotechnology – Challenges of Nanotechnology – Applications of Nanotechnology – National and International Nanotechnology centers – Current and Future Research in Nanotechnology – Patent in Nanotechnology

UNIT - II

Molecular Manufacturing – Nano simulation; Is nanotechnology bad or good? - Implications of nanotechnology: Health and safety implications from nanoparticles: Health issues - Environmental issues - Need for regulation - Societal implications: Possible military applications - Potential benefits and risks for developing countries - Intellectual property issues - Criticism of Nanotechnology - Studies on the implications of Nanotechnology

UNIT - III

Introduction to physics of the solid state: Structure – energy bands – Localized particles; Methods of measuring properties: Atomic structure – Particle size determination – Surface structure; Properties of Individual Nanoparticles: Metal Nanoclusters – Semiconducting nanoparticles – Rare Gas and Molecular Clusters; Carbon Nanostructures; Carbon Molecules – Carbon Clusters – Carbon Nanotubes – Applications of Carbon Nanotubes

UNIT - IV

Bulk Nanostructured materials: Solid disordered Nanostructures – Nanostructured crystals - Nanostructured Ferromagnetism; Optical and vibrational spectroscopy: Infrared Frequency Range – Luminescence – Nanostructures in Zeolite Cages; Quantum wells, Wires and Dots: Preparation of Quantum Nanostructures – Size and Dimensionality Effects – Excitons – Single Electron Tunneling – Applications – Superconductivity; Self Assembly and Catalysis

UNIT - V

Organic Compounds and polymers: Forming and Characterizing polymers – Nanocrystals – Polymers – Supramolecular structures; Biological Materials: Biological building blocks – Nucleic Acids – Biological Nanostructures; Nanomachines and Nanodevices: Microelectrochemical systems – Nanaoelectromechanical systems – Molecular and Supramolecular switches

Reference Books

1. Charles P. Poole Jr. and Frank J. Owens, Introduction to Nanotechnology, A Wiley-Interscience puplication, India, 2003.
2. R.S. Greco, F.B.Prinz and R.L.Smith , Nanoscale Technology in Biological Systems, ,CRC press, 2005.

3. M. Wilson, G. Smith, K. Kannangara, M. Simmons and Burkhard Raguse,, Nanotechnology: Basic Science and Emerging Technologies, CRC press, 2002.
4. Rebecca L. Johnson, Nanotechnology, Springer, 1999

09BI239 NEURAL NETWORKS IN BIOINFORMATICS

Credits: 4:0:0

Objective:

- To acquire knowledge about the overview and basic concepts of neural networks
- To know about Genome Informatics using neural networks .
- To understand the applications of neural networks in Drug Design and metabolism.

Outcome:

- To develop skills in the field of neural networks in bioinformatics.
- To understand and apply the skills of neural networks in life science modeling application.

Unit I:

Neural Network Basics. - Introduction to Neural Network Elements - Neurons - Connections between Elements - Transfer Functions - Summation Operation - Thresholding Functions- Other Transfer Functions - Simple Feed-Forward Network

Unit II:

Perceptrons and Multilayer Perceptrons - Introduction to Radial Basis Functions. Training of Neural Networks.

Unit III:

Genome Informatics Applications – Design – Data Encoding and Neural Networks

Unit IV:

Applications of Neural Networks - Nucleic Acid Sequence Analysis- Protein Structure Prediction - Protein Sequence Analysis

Unit V:

Neural Networks in Drug Design - Modeling Metabolic Energy by Neural Networks

Reference books:

1. Cathy H. Wu and Jerry W. McLarty - Neural Networks and Genome Informatics - Elsevier Science., 2000
2. J. Zupan, J. Gasteiger - Neural Networks in Chemistry and Drug Design. Wiley-VCH, 2000.

09BI240 ADVANCED IMMUNOLOGY

Credits: 4 : 0 : 0

Objective

- This module is designed to acquaint students with fundamental cellular processes involved in the generation of an immune response.
- It will provide students with detailed knowledge of the cells and organs of the immune system, their organisation and diversity, and their specialised functions at different anatomical locations.
- To provide knowledge on advanced immunotechniques

Outcomes

By the end of the module students should have a knowledge of;

- The concepts of natural and acquired immunity and their roles and interaction in immune responses
- The functions and properties of different cell types and organs that comprise the immune system
- Advanced knowledge of the underlying principles of immunology and its application in solving problems in biological systems.
- An awareness of some current research activities in the field and possible applications of this knowledge.

Unit I: Immune System

Introduction, cells and organs of the immune system, antigens, their structure and classification, complement and their biological functions, Active and passive immunity

Unit II: Humoral Immunity and Cellular Immunology

B-lymphocytes and their activation, structure, and function of immunoglobulin, immunoglobulin classes and subclasses, Major histrocompatibility complex – MHC gene, structure of MHC I and II and their functions. Thymus derived lymphocytes (T cells) their classification, mechanism of phagocytosis

Unit III: Immunity of infection and autoimmunity

Hypersensitivity reactions (reactions and examples only), mechanisms of T cell activation, cytokines and their role in immune response, Auto antibodies in humans, pathogenic mechanism, Graft rejection, evidence and mechanisms of graft rejection, prevention of graft rejection, immunosuppressive drugs..

Unit IV: Antibodies & Immunodiagnosis

Monoclonal antibodies – their production and applications, Western blot analysis, immuno electrophoresis, SDS-PAGE, purification and synthesis of antigens, ELISA-principle and applications, radio immuno assay(RIA)-principles and applications, Immunoflorescecnce techniques

Unit V: Molecular Immunology

Preparation of vaccines, application of recombinant DNA technology for the study of the immune system, , catalytic antibodies, application of PCR technology to produce antibodies and other immunological reagents, immunotherapy with genetically engineered antibodies

Text Books:

1. Benjamin E and Leskowitz S, Immunology a Short Course, Wiley Liss, NY, 2000.
2. Richard A. Goldsby, Thomas J.Kindlt, barabara A. Osborns and Janes Kuby, Immunology, Fifth edition, Freeman, 2003.

Reference books

1. Roitt I, Brostoff, J and Male D. Immunology, 6th edition, Mosby, Edinburgh 2001.
2. Talwar GP and Gupta SK, A handbook of practical and Clinical immunology, Volume I & II, CBS Publications 2000

09BI241 BIOETHICS, IPR AND BIOSAFETY

Credits: 3:0:0

Course Objective

- To create an awareness on Engineering Ethics and Human Values.
- To study the moral issues and decisions confronting individuals and organizations engaged in engineering profession
- To study the related issues about the moral ideals, character, policies, and relationships of people and corporations involved in technological activity.

Course Outcome

- Students learnt the moral issues and moral problems in engineering and how to find the solution to those problems.
- Students learnt the need for professional ethics, codes of ethics and roles, concept of safety, risk assessment.
- Students got exposure in Environment Ethics. &computer ethics; know their responsibilities and rights.

Unit – I

Epidemiology, Etiology, Pathogenesis, Prevention and Control of Communicable Diseases, like Malaria, Cholera, Tuberculosis, Leprosy, Diarrhoea, ARI, Poliomyelitis, Viral Hepatitis, Measles, Dengue, Rabies, AIDS, etc.

Unit – II

Health planning in India including various committees and National Health Policy and Health Goals set from time to time. Organized sector with reference to centre, State, District and Block level structures and local bodies and Panchayat Raj. Organization and functions of community health centers and primary health centers

Unit – III
Problems of Population growth, Birthrates, death rates, fertility rates, age-specific mortality rates, MMR, CPR, etc.

Unit-IV
Environmental sanitation, Nutrition, Family Welfare and Planning, Reproductive and Child health

Unit – V
Objectives and organization of important agencies, like WHO, UNICEF, FAO, ILO, Indian Red cross Society, UNFPA, World Bank, Asia Development Bank, Ford Foundation, CARE, Rockefeller Foundation, etc. and their role in Health care activities in India.

Reference Books:

1. Sasson A, Biotechnologies and Development , UNESCO Publications, 1988.
2. Sasson A, Biotechnologies in developing countries present and future , UNESCO Publishers, 1993.
3 M.Govindarajan ,S.Natarajan, Engineering Ethics, Prentice Hall of India, 2004.

09BI242 COMMUNITY HEALTH AND SOCIAL AWARENESS

Credit: 3:0:0

Objective

- To identify, interpret and appropriately use basic techniques for describing health status and estimating the risk of disease development in a population.
- To identify the major environmental factors that affect community health and explain the processes through which they operate..
- To identify the major methods for health promotion, health protection, disease prevention and disease control.

Outcome
- Students learnt the role of biological, historical, cultural, social and behavioral factors in determining disease, disease prevention, and health promoting behavior, and medical service organization and delivery.

- Students learnt how individual, environmental, sociodemographic and organization factors interact to affect the occurrence of a specific health problem in a population

Unit – I

Epidemiology, Etiology, Pathogenesis, Prevention and Control of Communicable Diseases, like Malaria, Cholera, Tuberculosis, Leprosy, Diarrhoea, ARI, Poliomyelitis, Viral Hepatitis, Measles, Dengue, Rabies, AIDS, etc.

Unit – II
Health planning in India including various committees and National Health Policy and Health Goals set from time to time. Organized sector with reference to centre, State, District and Block level structures and local bodies and Panchayat Raj. Organization and functions of community health centers and primary health centers

Unit – III
Problems of Population growth, Birthrates, death rates, fertility rates, age-specific mortality rates, MMR, CPR, etc.

Unit-IV
Environmental sanitation, Nutrition, Family Welfare and Planning, Reproductive and Child health

Unit – V
Objectives and organization of important agencies, like WHO, UNICEF, FAO, ILO, Indian Red cross Society, UNFPA, World Bank, Asia Development Bank, Ford Foundation, CARE, Rockefeller Foundation, etc. and their role in Health care activities in India.

Reference Books:

1. Park J, Park K. Park's textbook of prevention and social medicine. Jabalpur, Banarsidas Bhanot, 1991
2. Vidhyapooshan Sachdava, An introduction to Sociology, 1999

09BI243: BIOINFORMATICS

Credit : 3:0:0

Objective
- This course provides the necessary basic protocols in computers and various biological databases available on the internet.
- It provides basic idea of bioinformatics databases and applications for the non-biology students

Outcome:
- Be inculcated in basic biology and their applications.
- Be familiar with the available biological database resources and analysis.
- Will be able to work with bioinformatics application and tools.

Unit I

Biology for Bioinformatics :- Basic concepts - cells- Archaebacteria, Biomembranes, Nucleus, Organelles, Mitochondria, Chloroplasts, Viruses, BacterioPhage,Genetic contents of a cell - Viral Proteins - Amino acid, DNA and RNA - Forms of DNA.

Unit II

Genetic Code :- Genome - Gene Expressions - Protein Synthesis - Transcription RNA - Processing- Capping- Splicing - Editing, Cell Signalling, DNA cloning Genomic library - cDNA library - Probes - Screening.

Unit III

Databases :- Characteristics of Bioinformatics, Database - Categorizing, Navigating, Information Retrieval systems, Sequence Databases, Structure Databases.

Unit IV

Other Databases :- Enzyme Databases, MEROPS, BRENDA, Pathway Databases: CAZy, Disease Databases, Literature Databases, Other specified Databases.

Unit V

Bioinformatics algorithms: Design – Dynamic programming, greedy algorithm, probabilistic algorithm. Data analysis algorithm: Dot plots –uses, drawbacks. Substitution matrices algorithm: PAM, BLOSUM (concepts only)

Text Books :-

1. Orpita Bosu, Simminder Kaur Thukral, BIOINFORMATICS Databases, Tools and Algorithms, Oxford University Press, 2007

References :-

1.T. K. Attwood, D J Parry-Smith, Introduction to Bioinformatics.,., Pearson Education, 2003
2.Jin Xiong, Essential Bioinformatics, Cambridge University Press, 2007
3.Dan E. Krane, Michael L. Raymer, Fundamental Concepts of Bioinformatics, Pearson Education 2006
4.Arthur M. Lesk, Introduction to Bioinformatics, Oxford University press, 2003

09BI244 BASICS OF CHEMICAL ENGINEERING

Credit: 3:0:0

OBJECTIVE:

This course is intended to provide a clear overview of the field of chemical engineering.

OUTCOME:

The students can gain basics of chemical engineering principles applied in Biotechnology and biochemical engineering.
Throughout the course, students will develop basic skills in problem solving, computation, process design, and communication that will help them in all future engineering courses

Unit I Process calculations
Basic units and dimensions. Basics gas calculations-mole, mole percentage, weight, weight percentage.molarity, molality, normality. Ideal gas laws. Material balance, energy balance.

Unit II Fluid mechanics
Concept of fluid, types of fluid, properties of fluid, fluid flow, fluid flow pattern, flow control, fluid flow measurements and transportation of fluid.

Unit III Unit operations
Concept of unit operations, heat transfer – modes of heat transfer, equipments – heat exchanger (double pipe, shell& tube, plate type), LMTD, heat transfer coefficients, concept of evaporator, filtration and mechanical separation.

Unit IV Mass transfer operations
Diffusion in fluids – molecular and eddy diffusion, concept of NTU and HTU. Distillation-concept, types, design calculation – Mc Cabe Thiele method, poncho savant method. Basic concept of absorption, adsorption, drying and leaching.

Unit V Chemical Reaction Engineering
Law of mass action, rate equation, order of reaction, elementary and non elementary reactions, performance equation for CSTR, PFR. Types of reactions and reactors, definition of space time, mean residence time

Text books:

1. Bhatt B.I. and Vora S.M. "Stoichiometry", Fourth Edition, Tata McGraw-Hill Pub. Co. Ltd., 2004.
2. Mccabe, W.L, Smith J.C., "Unit Operations in Chemical Engineering ", McGraw-Hill, seventh Edition, 2006
3. Octave levenspiel, Chemical reaction engineering, John Wiley, fifth edition,2006
4. Robert Treybal, Mass transfer operations, third edition, 2003

Reference books:

1. Himmelblau D.M., "Basic Principles and Calculations in Chemical Engineering", Sixth Edition, Prentice-Hall of India Pvt. Ltd., 2004.
2. Felder R.M. and Rousseau R.W., "Elementary Principles of Chemical Processes", Third Edition, John Wiley and Sons, Inc., 2000.

09BI245 BIOLOGICAL DATABASES

Credit: 3:0:0

Objectives:

This course aims to provide the basic knowledge about the field of Bioinformatics.

It highlights the need for the databases in the field of Bioinformatics.

It provides knowledge about various Biological databases available and their diverse utilities to benefit the researchers.

Outcome:

From this course the students would learn about the needs for biological databases and practical knowledge on retrieving various, yet useful information that would encourage them to take part in the research activities pertaining to the field of Bioinformatics and are motivated to use their knowledge and skills to solve biological problems.

Unit I Introduction to Bioinformatics

Basic concepts:-Cell - Gene- Genome- Genetic code – Central dogma – Nucleic acids and proteins – Biological sequence data – Need for Biological Databases.

Unit II Sequence Databases

Databanks – nucleotide databanks – Genbank, NCBI, EMBL, DDBJ – protein sequence databanks – PIR, SWISSPROT, TrEMBL.

Unit III Structural Databases

Protein secondary structure- Ramachandran plot- Tertiary and quaternary structure of proteins Databases: - PDB, SCOP, CATH, SSEP, CADB, THGS, SMS, Pfam and GDB.

Unit IV Other Databases

Role of enzymes in Biochemical pathways- Enzyme Databases:- MEROPS, BRENDA. Pathway Databases: - CAZy. Disease Databases and Literature Databases.

Unit V Special Topics in Bioinformatics

New directions of Bioinformatics research – Essential prerequisites – Scope of Bioinformatics – Useful sites – Bioinformatics in pharmaceutical industry – Bioinformatics orientation in IT industry.

Text Book:

1. Orpita Bosu, Simminder Kaur Thukral, BIOINFORMATICS Databases, Tools and Algorithms, Oxford University Press, 2007

References:

1. T.K.Attwood & D.Parry-Smith, Introduction to Bioinformatics, Pearson Education, 2001.

2. R.Durbin, R.Eddy, K.Anders and M.Graeme, Biological Sequence Analysis:Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, 1997.

09BI322 MOLECULAR BIOLOGY AND GENETIC ENGINEERING

Credit : 4:0:0

Objectives:

This course will enable students to

- Know the basics of molecular biology and genetics.
- Life information transfer through information molecules ie genes and proteins.
- Molecular interactions which can be used in drug design

Outcomes:

- Students can understand and apply fundamental biological principles from the major areas of biology.
- Students can acquire in-depth knowledge from the major areas of biology.
- Students develop enhanced critical thinking skills.

Unit I:

Classical Genetics: Mendelian genetics, linkage, crossing over, Mutations – chemical and physical mutagens – DNA damage and repair mechanisms, recombinations, classical experiments – Hershey and chase; Avery McLeod & McCarty. Bacterial conjugation, transduction and transformation. Lytic and lysogeny cycle

Unit II:

DNA Replication : Replication in prokaryotes and eukaryotes, D-loop and rolling circle mode of replication, replication of linear viral DNA. Organization of eukaryotic chromosome – cot value, replication of telomeres in eukaryotes, DNA mutation and repair.

Unit III:

Transcription:Prokaryotic and eukaryotic transcription, features of promoters and enhancers, transcription factors, inhibitors, post-transcriptional modification - RNA splicing, ribozyme. RNA editing. RNA interference in medical applications

Unit IV:

Translation and Regulation of Gene Expression: Elucidation of genetic code, process of translation in prokaryotes and eukaryotes, suppressor mutation, post-translational modifications, inhibitors of protein synthesis. Regulation at various stages of gene expression in eukaryotes and prokaryotes - Lac and trp operons.

Unit V:

Genetic engineering : Cloning – vectors – plasmids – cosmids – restriction enzymes – steps in cloning – genomic and cDNA library – gene amplification using PCR, Agarose gel electrophoresis in DNA separation, Advances in genetic engineering methods and applications.

Text books:

1. David Friefelder, Molecular Biology, Narosa Publ. House. 2000
2. Gardner / Simmons / Snustad, Principles of Genetics, Eighth Edition, John Wiley, 2000

Reference books:

1. Benjamin Lewin, Gene VII, Oxford University Press. 2000
2. Watson JD, Hopkins WH, Roberts JW, Steitz JA, Weiner AM,. Molecular Biology of the Gene. 1987

09BI323 MICROARRAYS AND DATA ANALYSIS

Credit : 4:0:0

Objectives:

At the end of this course, students will be able to:

- Explain how microarray technology works, including the various types, and analyze data sets that are produced by microarrays, including the following steps: image processing, normalization, differential expression analysis and gene clustering.

Outcomes:

- Students can understand the primary literature on gene expression networks (genetic networks) and will be able to analyze data sets and design simple gene regulatory networks for a few genes and assess its performance.

Unit I

Introduction to Microarrays-making microarrays-Spotted microarray - insitu microarray-Microarray technologies - Affymetrix technology – maskless photodeprotection technology, Using microarray – Steps needed to measure gene expression in a sample.

Unit II

Oligonucleotide probes – filtering of low complexity sequence – prediction of cross-hybridization to related genes – thermodynamics of nucleic acid duplexes – Prediction of melting temperatures.

Unit III

Image feature extraction – Identifying the positions of the features - Identifying the background pixel Normalization – Data cleaning and transformation – Within array normalization – Linear and non linear regression of log ratio against average density.

Unit IV

Calibration experiments – Classical parametric statistics – T tests – Non-classic parametric test - One way annova

Unit V

Microarray standard and databases: LIMS – Local data warehousing - MGED - MAGE – Minimal information about a microarray experiment - Microarray sequence databases - primary and secondary databases

Text Book:

Dov Stekel "Microarray Bioinformatics" Cambridge university press, 2005

09BI324 BIOSTATISTICS

Credit : 3:1:0

Objectives:

- To develop skills of the students in the area of probability and statistics
- To know more about descriptive and inferential statistics
- To know about the various reliability methods.
- To understand the various application design experiments

Outcomes:

- Knowledge in the technique, methodology and Application of statistics.
- A basic understanding in collection, presentation and drawing conclusion about biological data

Unit I

Introduction to biostatistics; basic concepts; measurement & measurement scales; the simple random sample; computers & biostatistical analysis.

Descriptive statistics: the ordered array; grouped data, the frequency distribution; measures of central tendency; measures of dispersion.

Basic probability concepts: the objective & subjective views of probability; elementary properties of probability; calculating the probability of an event; Bayers's theorem, screening tests, sensitivity, specificity, predictive value.

Unit II

Probability distributions: probability distributions of discrete variables; the binomial distribution; the Poisson distribution; continuous probability distributions; the normal distribution; normal distribution applications.
Sampling distributions: constructions & characteristics; distribution of the sample mean; distribution of the difference between two sample means; distribution of the sample proportion; distribution of the difference between two sample proportions.

Unit III

Estimation: confidence interval for a population mean; the t distribution; confidence interval for the difference between two population means; confidence interval for a population proportion; confidence interval for the difference between two population proportions; determination of sample size for estimating means; determination of sample size for estimating proportions;

confidence interval for the variance of a normally distributed population; confidence interval for the ratio of the variances of two normally distributed populations.
Hypothesis testing: a single population mean; the difference between two population means; paired comparisons; a single population proportion; the difference between two population proportions; a single population variance; the ratio of two population variances; the type II error and the power of a test; determining sample size to control type II errors.

Unit IV
Analysis of variance: the completely randomized design; the randomized complete block design; the repeated measures design; the factorial experiment.

Unit V
Simple linear regression & correlation: the regression model; the sample regression equation; evaluating the regression equation; using the regression equation; the correlation model; the correlation coefficient; precautions.

Textbook

1. W. W. Daniel, “Biostatistics: A Foundation for Analysis in the Health Sciences,” 7/e, John Wiley & Sons, 2000.

09BI325 BIOCOMPUTING I

Credit: 4:0:0

Objectives:

- To provide opportunities for students in computer science, biology and the life sciences to interact with each other to understand the real issues arising in the computational analysis of sequence data.
- To understand the basic information passing in worldwide web.

Outcome:
Students will be better able to:

- Recognize biological processes important in generating biodiversity,
- Describe the scientific method, Know the importance of biology to human society.
- Develop technology based on the natural world.

Unit I
Introduction to Bioinformatics :Elementary commands and Protocols, ftp, telnet, http. Printer on information theory. Databanks – nucleotide, protein sequence and structural databases, World wide web – search engines – finding scientific articles -Pubmed – public biological databases.

Unit II
Sequencing Alignment and Dynamic Programming :Introduction – Strings – Edit distance two strings - gaps - Sequence alignment. Global & local alignment using the - Smith-Waterman

algorithm & Needleman -Wunsch algorithm. Matrices - PAM, BLOSUM. Sequence alignment using BLAST , FASTA.

Unit III

DNA Mapping and sequencing: DNA Mapping and sequencing – Physical and Genetic mappingh-Map alignment – Large scale sequencing and alignment – Shotgun – DNA sequencing – Sequence assembly

Unit IV:

Phylogeny :Introduction-Concept of evolutionary trees-methods of construction-Maximum parsimony-Distance methods-FM,NJ,UPGMA-Maximum likelihood method.

Unit V:

Gene prediction : Introduction-Promoter prediction in E.Coli,Eukaryotes-Scoring matrix method used with aligned promoter sequences-Grail II-Gene parser

Textbook

1. Dan Gusfield, Algorithms On Strings Trees And Sequences, Cambridge University Press, 2000
2. David W Mount , Bioinformatics : Sequence and Genome analysis, 2nd edition, CBS Publishers,2004

Reference Books

1. Arthur M. Lesk, Introduction to Bioinformatics, Oxford University press, 2003
2. SR Pennington, MJ Dunn, Proteomics from Protein Sequence to Function, Viva Books Ltd, 2002

09BI326 BIOPROGRAMMING

Credit: 4:0:0

Objectives

At the completion of this course, the student will be able to:

- Understand the structure of a C/C++ language program including the use of variable.
- Definitions, data types, functions, scope and operators.
- Be able to develop, code, and test well structured programs using:
  Various forms of Input/Output--including files .
- Assignments , if-then logic , while, do, and for loops , functions
  Arrays strings and string functions
- Be prepared for programming in C++ and Java, by looking at some of the differences between structured and object oriented programs, and some of the features of C++..

Outcomes:

- Write, compile, and run C/C++ programs, Analyze the effects of using structures that implement decisions, loops, and store arrays and use these structures in a well-designed, OOP program.
- Create programs that make use of various directories and use several files linked together.

Unit I

UNIX. History and Principles, GNU Project and the GPL, Linux Origins & Benefits.
Linux File Hierarchy Concepts, Current Working Directory, Changing directories, Listing Directory Contents, the Home Directory, Absolute Path-names, Relative Path-names, File Names, Copying Files & Directories, Moving & Renaming Files & Directories, Removing & Creating Files, Creating & Removing Directories, Viewing an Entire Text File, Viewing Files One Screen-full at a Time, Getting Help: man pages.

Unit II
Algorithm / pseudo code, flowchart, program development steps, structure of C program, A Simple C program, identifiers, basic data types and sizes, Constants, variables, arithmetic, relational and logical operators, increment and decrement operators, conditional operator, bit-wise operators, assignment operators, expressions, type conversions, conditional expressions, precedence and order of evaluation.
Input-output statements, statements and blocks, if and switch statements, loops- while, do-while and for statements, break, continue, goto and labels, programming examples.

Unit III
Designing structured programs, Functions, basics, parameter passing, storage classes- extern, auto, register, static, scope rules, block structure, user defined functions, standard library functions, recursive functions, header files, C preprocessor, example c programs. Arrays-concepts, declaration, definition, accessing elements, storing elements, arrays and functions, two-dimensional and multi-dimensional arrays.

Unit IV
Classes and Objects: OOPS Introduction- Specifying and using a class-Defining member functions-Private member functions-Memory allocation for Objects-Friendly functions- Array of Objects-Objects as Functions arguments-Returning Objects
Constructors and Destructors: Introduction-parameterized constructor-Default constructor-copy constructor-Constructor overloading-Destructors

Unit V
Inheritance: Introduction- Defining derived class-Single inheritance- multiple and multilevel inheritance- Hierarchical and hybrid inheritance.
Polymorphism-Introduction-Function overloading with different number of arguments and different types of arguments

References

1. Maruice J. Bach, The design of the UNIX operating system, Prentice Hall of India, 1986.
2. B.W. Kernighan, Dennis M.Ritchie The C Programming Language, PHI/Pearson Education,2001
4. Kenneth Rosen, Douglas Host, James Farber, Richard Rosinki, Unix-The Complete Reference, Mc-Graw Hill, 1999.

5. E.Balaguruswamy, Object oriented programming with C++, Second edition, Tata Mc Graw Hill publications,2001
6. Robert Lafore "Object oriented programming in C++" 4 th edition pearson education SAMS Publications 2002.

09BI327 RELATIONAL DATABASE MANAGEMENT SYSTEMS

Credit : 4:0:0

Objectives:

- This subject introduces students to relational database design and SQL (Structured Query Language) used with relational databases.
- Students will be presented with a methodology for relational database design using Entity Relationship Diagrams and normalization of data.
- An overview of the functions of the Database Management System (DBMS) and of a Database Administrator (DBA) will also be presented.

Outcomes:

- After completing this course students must be able to demonstrate the knowledge and ability to analyze and design a database in some implementation.
- It would provide them to implement the structural constraints of relationships and use different keys for data access.
- They would gain skill of performing normalization and draw ER diagram of any database application.

Unit I

Introduction: DBMS architecture; models; networked; hierarchical; relational; data independence; integrity constraints; advantages of DBMS.

File system and Organization. Secondary storage devices; buffer management; file organization; sequential; indexed sequential; B-tree indexing; secondary indexes.

Unit II

Entity relationship model; fundamental ER constructs; degree of a relationship; connectivity of a relationship; attributes of a relationship; existence of an entity in a relationship; alternative ER notations; transformation of the ER model to relational database.

Unit III

Relational Data Model (with reference to MySQL). Basic definition & terminology; relational algebra; SQL 92; query writing in SQL 92; use of aggregate operators

Unit IV

Decomposition of schema; functional dependency; multi-valued dependency; join dependency; normal forms; 1NF; 2NF; 3NF; applications of data bases like distributed databases; temporal databases; logic-based databases.

Unit V
Database Security & Data Recovery. Security & integrity threats for data storage & transmission – legal & ethical issues; policy issues; system-related issues. Control measures – concurrency control techniques; locking techniques; recovery techniques. Multilevel security – data back-up & recovery from catastrophic failures.

References

1. C. J. Date, ”An Introduction to Database,” 7/e, Addison-Wesley Publishers, 2000.
2. R. Elmasri & S. B. Navathe, ”Fundamentals of Database Systems,” Addison-Wesley Publishers, 2000.

09BI328 STRUCTURAL BIOINFORMATICS

Credit : 4:0:0

Objectives:

This course aims to study the strategy and tactics of biophysical concepts of macromolecules and the conformational analysis and forces that determine the protein and nucleic acid structure and ligand interaction with macromolecules. Study of the size and shape of the macro molecule using different techniques using various tools like X-ray Crystallography and NMR is explained in the course

Outcomes:

The student would learn the different structural levels of biological macromolecules, its size, shape, their conformations and the forces that are involved in stabilizing these molecules. The tools by which this analysis is done will be learned. The student would also learn about the ligand interaction with macromolecules.

Unit I
Introduction: Levels of structures in Biological macromolecules,basic strategies in biophysics,Principles and concepts used in biophysical analysis of life processes ,Biomolecules and their interactions, size and shape of macromolecules.

Unit II
Amino acids and Proteins **:**Structure of amino acids; dipolar ions; isoelectric point of amino acids; configuration of natural amino acids; amino acids by hydrolysis of proteins; geometry of the peptide linkage; classification & functions of proteins; denaturation; side chain, isoelectric point & electrophoresis; conjugated proteins; prosthetic groups & coenzymes; secondary structure of silk & wool. Amino acid sequencing in proteins: Peptide structure by partial hydrolysis & Edman method. Case study: determination of the amino acid sequence in insulin by Sanger

Unit III

Conformational Analysis : Forces that determine protein structure, basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions and ionic interactions, disulphide bonds.

Unit IV

Structural Analysis of Macromolecules : Prediction of proteins structure, nucleic acids, general characteristics of nucleic acid structure, geometrics, glycosidic bond, rotational isomers and those puckering backbone rotational isomers and ribose puckering forces stabilising ordered forms, base pairing, base stacking tertiary structure of nucleic acids.

Unit V

X–ray diffraction : X-ray crystallography – X–ray diffraction, determination of molecular structures, electron microscopy, neutron scattering, light scattering.

Text Book

1. Cantor R., and Schimmel P.R., Biophysical Chemistry, Vol. I,& II, W.H. Freeman & Co., 1997.

Reference Book

1. Daniel. M, Basic Biophysics for Biologists, 1998.
2. Kensal E. van Holde, W. Curtis Johnson and P. Shing Ho, Principle of Physical Biochemistry, 1998, Prentice Hall, New York.

09BI329 GENOMICS AND PROTEOMICS

Credit : 4:0:0

Objectives:

- To develop skills of the students in the area of genomics and proteomics in both theory and research.
- To provide knowledge on genome, transcriptome and proteome analysis through computational methods.

Outcomes:

- Students may get interest in gene, genome, transcriptome and proteome analysis through computational methods.
- Students may come to know well about the genome features of prokaryote and eukaryote and also they may develop sequence analysis tools based on any genome and proteome feature.
- Students may join with Genome Projects and they may get interest in personalized medicine research.

Unit I

Overview –Research areas and related journals in genomics and proteomics - Concepts of central dogma – Structure and organization of prokaryotic & eukaryotic genome – Changes and regulation of genome activity in prokaryote and eukaryote - Brief outlook of various genome projects and their outcomes - Human genome project

Unit II

Genome mapping and sequencing: Mapping techniques – Genetic markers – RFLP, SSLP, STRs, VNTRs – Physical markers – EST, STS, FISH, SNP - Radiation hybrids – Mapping resources - Sequencing methods: chemical and enzymatic method - High throughput method – Automated sequencing methods – Whole genome shotgun sequencing method

Unit III

Sequence assembly and annotation: Assembly of contiguous DNA sequence - shotgun, directed shotgun and clone contig approach - Genomic DNA library – cDNA library – Primer walking, Chromosome walking, Chromosome jumping – Tools for sequence assembly - Structural and functional genomics - Transcriptome and Microarray approach — Comparative genomics - Population genomics – Pharmacogenomics

Unit IV

Proteomics: Introduction to proteome – Proteome and technology – Information and the proteome – Importance of 2D Electrophoresis in proteomics - Protein identification in proteome projects - Primary and secondary attributes for protein identification –Cross species protein identification – Detection and analysis of co- and post-translational modification

Unit V

Proteome databases: protein sequence databases - SWISS-PROT and TrEMBL – Pattern and profile databases – PROSITE and BLOCKS - 2D PAGE databases – Structure databases - PDB - Metabolic databases – post translational modification databases – Application of proteomics to medicine, proteomics, toxicology and pharmaceuticals

Text Books:

1. T.A. Brown, Genomes, 2nd edition, BIOS Scientific Publishers Ltd, 2002.
2. Marc R. Wilkins, Keith L. Williams, Ron D. Appel and Denis F. Hochstrasser Proteome Research: New Frontiers in Functional Genomics, Springer, 1997.

Reference books:

1. Greg Gibson, Spencer V. Muse, A primer of genome science, Sinauer associates Inc. Publishers, 2002.
2. David W. Mount, Bioinformatics: sequence and genome analysis, 2nd edition, CBS publishers, 2004.
3. Pennington, Proteomics from protein sequence to function, 2nd edition, Viva Books Ltd, 2002.

09BI330 MOLECULAR MODELING AND DRUG DESIGN

Credit : 4:0:0

Objectives:

- To understand the critical relationship among biomolecular structure, function and force field models.
- To be able to utilize basic modeling techniques to explore biological phenomena at the molecular level.
- To emphasize Modelling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

Outcomes:

- Students are introduced to the principles and practice of Molecular modeling and modern drug discovery.
- An awareness of rational drug design, based on understanding the three-dimensional structures and physicochemical properties of drugs and receptors will be created.

Unit I

Quantum mechanics and concepts in molecular modeling: Introduction – coordinate systems – potential energy surfaces – introduction to computer hardware and software – introduction to quantum mechanics – postulates – Schrodinger wave equation – hydrogen molecule – Born-Oppenheimer approximation.

Unit II

Molecular mechanics and energy minimization: Empirical force field models – Bond stretching – angle bending – torsional term – nonbonding interactions – thermodynamics properties using a forcefield – derived and non derived energy minimization method – simplex – sequential univariate method – steepest descent method – conjugate gradient method- Newton-Raphson method.

Unit III

Molecular Dynamics and Monte Carlo - Introduction – Using single Model – time steps – Multiple steps – Setting up MD – energy conservation in MD Simulation Examples – Monte Carlo – Random number generation – Difference in MD & MC.

Unit IV

Homology modeling: comparative modeling of proteins – comparison of 3D structure – Homology – steps in homology modeling – tools – databases – side chain modeling – loop modeling.

Unit V

Drug design: General approach to discovery of new drugs - lead discovery – lead modification – physiochemical principles of drug action – drug stereo chemistry –drug action - 3D database search – computer aided drug design – docking - molecular modeling in drug design – structure based drug design – pharmacophores - QSAR.

Text Book:

1. A.R.Leach, Molecular Modeling Principles and Application, Longman, 1996
2. R.K.Prasad, Quantum chemistry , Halsted Press, 2002 .

09BI331 BIOCOMPUTING – II

Credit : 3:1:0

Objectives:

- To introduce the student to the biology of bioinformatics to understand how computer science algorithms solve problems
- Discover new knowledge in genomics, proteomics, metabolomics, transcriptomics, and other omics.

Outcomes:

- Thoroughly describe and apply different algorithms for sequence analysis, analysis of gene expression data and molecular biological networks.
- Independently implement commonly used algorithms for sequence comparisons, analysis of gene expression data and graph theoretical problems relating to bioinformatics

Unit I

Algorithms and Complexity: What is an algorithm-Biological algorithm versus computer algorithms -The change problem-Correct versus Incorrect algorithms-Big O notation- Algorithm design techniques.

Unit II

Exhaustive Search: Restriction Mapping-Impractical restriction mapping Algorithm- A practical restriction mapping Algorithm-Profiles-The motif finding problem

Unit III

Graph Algorithms: Introduction to Graphs- Directed Graphs-Undirected graphs-weighted and unweighted graphs -Eulerian cycle-Hamiltonean cycle-Graphs and genetics-Sequencing by Hybridization-SBH as a Hamiltonean path problem

Unit IV

Combinatorial Pattern matching: Repeat finding-Hash tables- Exact pattern matching-Suffix trees-Heuristic similarity search Algorithms-Approximate Pattern matching-BLAST

Unit V

Evolutionary trees-Distance based tree Reconstruction-Reconstructing trees from additive matrices-Evolutionary trees and Hierarchical clustering-CG islands-Gibbs sampling

Textbook:

1. Neil Jones & Pavel Pevzner An Introduction to Bioinformatics Algorithms, , MIT Press, 2004.

Reference Book

1. M. Waterman, “Introduction to Computational Biology: Maps, Sequences & Genomes,” CRC Press, 1995.

09BI332 BIOPROGRAMMING LAB

Credit : 0:0:2

LINUX:
Directory structure-Command-line file-system browsing,
Bash shell basics Rpms usage mounts, vi editor, file permissions,
User administration File/dir compression using tar and gzip.

C and C++
Basic syntax
Input and Outputs in C
Control structures;
Arrays and strings
Functions.

09BI333 BIOCOMPUTING LAB

Credit : 0:0:2

Nucleotide database search and analysis
Protein database search and analysis\
Structural database
EMBOSS
GCG
PHYLIP

09BI334 MOLECULAR MODELING AND DRUG DESIGN LAB

Credit : 0:0:2

MOLECULAR MODELING

1. Model building of Biomolecules using CHEM SHETCH
2. Structural Analysis of Protein/Nucleic Acids
3. Conformational parameters for oligosaccharides/ polypetides
4. Homology modeling using SWISS-PDB
5. Energy minimization for protein/ carbohydrates – Schrodinger software
6. Molecular Dynamics for Protein/carbohydrates - Schrodinger software

QSAR/STRUCTURE BASED DRUG DESIGN

7. Docking and binding site analysis - Schrodinger software
8. Combinatorial Screening of small molecules database – GOLD, ZINC
9. CORINA and SMILES for target molecule
10. Quantitative structure activity relationship and QSAR equation - Schrodinger software
11. Hydrogen bond interaction for Proten-Lead complex - Schrodinger software
12. Structure based inhibitor design - Molecular mechanics and Molecular dynamics calculation for Protein ligand (inhibitor) complex - Schrodinger software

09BI335 DBMS LAB

Credit : 0:0:2

MySQL basics : Installation and Configuration
Creating Databases in MySQL
Creating Tables
Inserting, deleting and modifying records
Creating queries using basic SQL commands
Creating a relational database
Creating queries for a multi table environment
Performing Calculations
Schema design

09BI336 COMPUTER HARDWARE & NETWORKING

Credit: 4:0:0

Objectives:
This course will enable students to
- Know the basics of computer hardware and networking
- Components of computer and data transfer among them.
- Different types of operating systems and protocols in network data transfer.

Outcomes:
- Students can understand and apply fundamental computer network principles.
- Students can acquire in-depth knowledge Data communication concepts.

Unit I
DATA: Analog data, digital data, bits, binary number system, ASCII tables. PC: History, Construction, POST, SETUP, BIOS, BOOT. Boot process, data flow on the mother-board, BUS, I/O, CHIP SETS, RAM.

Unit II
CPU: Introduction, history, working principle, Floating point Unit , Clock frequency, 5th generation CPU's, 6th generation CPU's.
Drivers and other storage: Drivers, Hard disks, Optic Storage media, other drives – ZIP, MO, TAPES. EXPANSION CARDS & INTERFACES: PCI, USB, AGP, ISA, EIDE, SCSI.

Unit III

OS components: Kernel, Shell, File system. OS types: LINUX, MAC, SOLARIS, IRIX, WINDOWS. FILE SYSTEMS: fat, ntfs, netware, udf, unix. BIOS-OS-HARDWARE.

Unit IV

Data communication concepts, network topologies, network protocols & standards, network configuration & management, security, client-server.

Unit V

Internet, Naming and addressing, TCP/IP, DNS, HTTP, FTP, URL, SOCKET, Subnet Masking, Switching and Routing. APACHE basics.

References

1. Bill McCarty "Learning Red Hat Enterprise Linux & Fedora," 4/e, O'Reilly Publishers, 2004 (ISBN: 0-596-00589-X).

2. J. Habraken & M. Hayden, "Sams Teach Yourself Networking in 24 Hours," 3/e, Sams Publishers, 2004 (ISBN: 0672326086).

09BI337 PYTHON LANGUAGE

Credit : 4:0:0

Objectives:

- Express fundamental programming constructs such as variables, arrays, loops, subroutines and input/output in Python.
- Understand several concepts relatively idiosyncratic to Python, such as associative arrays, regular expressions, and system interfaces.
- Programs for data manipulation, file maintenance and "Common Gateway Interface" Web applications.

Outcomes:

- Write, compile, and run Python programs, Analyze the effects of using Python structures that implement decisions, loops, and store arrays and use these structures in a well-designed, OOP program.
- Create Python programs that make use of various directories and use several files linked together. Create Web sites with Python programs.

Unit I

History of Python. Features of Python. Obtaining Python. Obtaining Python. Installing Python. Running Python Program Output, Program Input and the raw_input Built-in Function. Comments. Operators. Variables and Assignment. Numbers. Strings. Lists and Tuples. Dictionaries. Code Blocks Use Indentation. Conditionals and Loops. if statement. else Statement. elif Statement. while Statement. for Statement. break Statement. Continue Statement.

Pass Statement. Else Statement - the range Built-in Function. Files and the open Built-in Function.

Unit II

Statements and Syntax. Variable Assignment. Identifiers. Basic Style Guidelines. Memory Management. First Python Application. Python Objects. Standard Types. Other Built-in Types. Internal Types. Standard Type Operators. Standard Type Built-in Functions. Categorizing the Standard Types. Unsupported Types.
Variables: Introduction to Numbers. Integers. Floating Point Real Numbers. Complex Numbers. Operators. Built-in Functions. Sequences. Strings. Strings and Operators. String-only Operators. Built-in Functions. String Built-in Methods. Special Features of Strings. Related Modules.

Unit III

Functions: Introduction to Functions - Calling Functions. Creating Functions. Passing Functions. Formal Arguments. Variable-length Arguments. Functional Programming. Variable Scope. Introduction to Modules- Modules and Files. Namespaces. Importing Modules. Importing Module Attributes. Module Built-in Functions. Packages. Other Features of Modules
Regular Expressions: Introduction/Motivation. Special Symbols and Characters for REs. REs and Python. Regular Expression Adventures.

Unit IV

Network programming:Introduction. Sockets: Communication Endpoints. Network Programming in Python. Related Modules.

Unit V

Web Programming: Introduction. Web Surfing with Python: Creating Simple Web Clients. Advanced Web Clients. CGI: Helping Web Servers Process Client Data. Building CGI Application. Advanced CGI. Web (HTTP) Servers. Related Modules.

Textbooks

1. David Ascher, Mark Lutz "Learning Python," 2/e, O'Reilly Media Publishers,2003
2. Alex Martelli "Python in a Nutshell," O'Reilly Media Publishers, 2007.

09BI338 BIOPHYSICAL CHEMISTRY

Credit : 4:0:0

Objectives:

- To introduce students the techniques of modern chemistry in order to enhancing their understanding of molecular structure and reactivity especially with reference to small molecules and proteins -
- Structural elucidation of carbohydrates and lipids.

Outcomes:

- Students will be able to understand conformation of molecules and relationship of energy to molecular conformations.
- Discover applications of molecular modeling as well as learn its limitations

Unit I

Structure of Organic Molecules: Concept of bonding; valence of carbon; bond lengths & bond angles; hybridizations of carbon; hybridizations of nitrogen & oxygen; polar & nonpolar molecules; inductive effect; resonance. Secondary bonding: hydrogen bonding; dipole-dipole & dipole-induced dipole interactions; London dispersion forces. Exothermic & endothermic reactions. Organic acids & bases. Structural isomerism; geometrical isomerism; optical isomerism & optical activity. Conformational analysis of butane.

Unit II

Carbohydrates: Structure of D-glucose & D-fructose (proof not required); formation of glucosides & the cyclic structure of D-glucose; D-ribose & D-deoxyribose. Structure of amylose, amylopectin & glycogen; cellulose.

Lipids: Fats & oils; phospholipids. Nucleic Acids: Purines & pyrimidines; nucleotides & nucleosides; nucleic acids.

Unit III

Spectroscopy and methods of visualization: Absorption spectroscopy, Linear and Circular Dichroism, Emission spectroscopy, Nuclear Magnetic Resonance spectroscopy. Methods of direct visualisation, macromolecules as hydrodynamic particles, macromolecular diffusion, ultracentrifugation, viscometry.

Unit IV

Spectroscopy and structures of chemicals: IR spectrum. NMR spectrum: equivalent & non-equivalent protons; chemical shift; peak area & proton counting; spin-spin coupling & coupling constants. ESR spectrum.

Unit V

Crystal Geometry: crystal symmetry; crystal systems & classes; unit cell & space lattices; crystal structures; atomic coordination; Miller indices & crystal planes; crystal directions; atomic & ionic radii. Methods of Determining Structures: x-ray diffraction; the powder method; electron diffraction; neutron diffraction.

References

1. Arun Bahl & B. S. Bahl "A Textbook of Organic Chemistry,", S. Chand & Company, New Delhi, 2000.
2. R. T. Morrison & R. N. Boyd, "Organic Chemistry," 6/e., Prentice-Hall of India, New Delhi, 1995.
3. V. Raghavan "Materials Science & Engineering,", Prentice-Hall of India,2004.

09BI339 DATA MINING & WAREHOUSING

Credit : 4:0:0

Objectives:

- This course helps the students to understand the overall architecture of a data warehouse and techniques and methods for data gathering and data pre-processing using OLAP tools.
- The different data mining models and techniques will be discussed in this course. Data mining and data warehousing applications in bioinformatics will also be explored.

Outcomes:

- Students would learn data mining techniques and methods in integrating and interpreting the bioinformatics data sets and improving effectiveness, efficiency and quality for bioinformatics data analysis.

Unit I
Data Mining. Relational databases; transactional data bases. Concepts/class description; characterization & discrimination; association analysis; cluster analysis; outlier analysis; evolution analysis; data preparation; data cleaning; data integration & transformation; data reduction; discretization & concept hierarchy generation.

Unit II
Data Mining Primitives, Languages & system architecture. Data mining primitives; data mining query language; designing graphical user interfaces based on a data mining query language; architecture of data mining systems; introduction to Mining Association Rules in large databases.

Unit III
Basics of classification & prediction; cluster analysis; types of data in cluster analysis; partitioning methods. Neural networks & decision trees. Nearest neighbour induction rule.

Unit IV
Data Warehousing. Introduction; data marts (loading, metadata, data model, maintenance, nature & software components); on-line analytical processing; OLTP, OLAP tools.

Unit V
Developing a Data Warehouse. Design considerations; data content; metadata; distribution of data; performance considerations; applications; national data warehouses.

Textbooks
1. C. S. R. Prabhu "Data Warehousing – Concepts, Techniques, Products & Applications," , Prentice-Hall of India.2000.

2. Jiawei Han & Micheline, "Data Mining – Concepts & Techniques,"
Morgan Kauffman Publications, 2000.

Reference
Sid Adelman & Larissa T. Moss, "Data Warehouse Project Management," Addison-Wesley press, 2004.

09BI340 JAVA PROGRAMMING

Credit: 3:0:0

Objectives:

- Express fundamental programming constructs such as variables, arrays, loops, subroutines and input/output in Java.
- Programs for data manipulation file maintenance and sequence manipulation.

Outcomes:

- Write, compile, and run Java programs, Analyze the effects of using Java structures that implement decisions, loops, and store arrays and use these structures in a well-designed, OOP program.
- Create Java programs that make use of various directories and use several files linked together.
- Apply the object-oriented programming features available with Java to programs designed for professional business environments

Unit I

Introduction to internet and www. Introduction to Java applications. Introduction to Java applets: objects; sample applets; Java virtual machine.

Unit II

Control structures Part I: if, if/else, while, assignment operators, increment & decrement operators, primitive data types.

Control structures Part II: for, switch, do/while, break & continue, logical operators.

Unit III

Methods: program modules, methods definitions, Java API packages, recursion, method overloading , method of class J applet.

Arrays: Declaring & allocating arrays, passing arrays to methods, sorting arrays, searching arrays, multiple-scripted arrays.

Unit IV

Object-oriented programming: superclass & subclass, protected members, constructors, finalizers, composition vs. inheritance, polymorphism, type fields, switch statements, dynamic-method binding, final methods & classes, inner class, type wrapper classes for primitive types.

Unit V

BioJava: symbols & Symbol Lists, sequences & features, sequence I/O basics, Change Event overview, Change Event example using distribution objects, implementing Changeable, Blast-like parsing (NCBI Blast, WU-Blast, HMMER), Dynamic programming examples.

Textbook

1. H. M. Deitel & P. J. Deitel “Java: How to Program,” 3/e, , Pearson Education Asia, 2001.

References

1. Patrick Naughton & Herbert Schildt, "Java 2, The Complete Reference," 3/e, Osborne/McGraw-Hill. 2006
2. http://www.biojava.org/tutorials/index.html
3. Keyar Shah, "Java 2 Programming," Tata McGraw-Hill, 2002.

09BI341 SERVER-SIDE PROGRAMMING

Credit: 3:0:0

Objectives:

- Understanding fundamental components of Web.
- Getting guidelines in making websites.
- Understanding client server communication in internet technology.

Outcomes:

- Making a website using java scripts, and basic html coding.
- Knowing how to use xml for data storage.
- Understanding the server side issues.

Unit I

Web architecture and HTTP: Components of the Web, HTTP Analysis, Web Yesterday, Today & Tomorrow, Other than HTTP.

Unit II

Web Usability: Guidelines for Web Site Design, Psychology of the users and Usability Tools & Metrics

Hyper Text Markup Language: The concept of markup, an overview of HTML 4.01 specification.

Unit III

Client-side scripting: Core JavaScript, Client side JavaScript.

XML: Generalized Markup Languages, SGML, Document Type Definitions an overview of XML, the XML Document Object Model, and XSL.

Unit IV

Server-side programming: Concept, issues, JSP and Servlets, Remote Method Invocation, JNDI, Java Beans, Enterprise Java Beans, Session Beans, Entity Beans, CMP, BMP, Message Driven Beans, Transactions and Security.

Unit V

Web Services: Concept, Components, Operations and Standards.

Design Patterns: Concept, Benefits, and Categories.

Textbook

1. Brian Pfaffenberger et al. “HTML, XHTML & CSS Bible,” (Also covering JavaScript), 3/e,2004
2. Marty Hall & Larry Brown “Core Servlets and Java Server Pages, Volume 1: Core Technologies,” 2/e, 2003
3. Richard Monson-Haefel “Enterprise Java Beans,” 4/e, (Covers EJB 2.1 & EJB 2.0, includes workbook for Jboss 4.0), 2001

09BI342 PERL AND XML

Credit: 4:0:0

Objectives:

- Express fundamental programming constructs such as variables, arrays, loops,subroutines and input/output in Perl.
- Understand several concepts relatively idiosyncratic to Perl, such as associative arrays,Perl regular expressions, and system interfaces.
- Programs for data manipulation, file maintenance and "Common Gateway Interface" Web applications.
- Giving basic knowledge in XML

Outcomes:

- Write, compile, and run Perl programs, Analyze the effects of using Perl structures that implement decisions, loops, and store arrays and use these structures in a well-designed, OOP program.
- Create Perl programs that make use of various directories and use several files linked together. Create Web sites with Perl programs and compare and contrast the effectiveness of using Web programming modules from CPAN.
- Create and implement Web applications using Perl libraries available on the World Wide Web, Analyze Web scripts written by experts (NMS) and evaluate whether or not they improve the functionality of various Perl programs. Apply the object-oriented programming features available with Perl to programs designed for professional business environments.

Unit I

History of Perl -Perl Advantages & Disadvantages -The Perl Interpreter-Perl File Conventions Using Perl on UNIX-Creating a script-running a script-Context -Data types-variables-Operators-Commands-Predefined functions-Subroutines-formats

Unit II

PERL. Control Structures, Arrays, Hashes, Loops and File handles-Regular Expressions.

Unit III

PERL: Subroutines-Modules- Object-Oriented concepts in Perl - modules- References & Objects

Unit IV

Perl and relational database: Database applications, Perl and the web - CGI program in Perl, Perl and the graphics . Bioperl: Installation of bioperl and its applications, Sequences, Seqfeature, ,. Bioperl problems.

Unit V

XML syntax and semantics- mark up: structure implicit- XML records structure: formatting- XML schemas: the semantics- XML and relational databases-- XML and dynamic Web publishing- benefits of XML schemas to applications-- syntax of XSL - XML Stylesheet- XSLT -XML to HTML

References

1. Sriram Srinivasan ,"Advanced Perl Programming,", O'Reilly Publishers, 1997 .
2. Maruice J. Bach, The design of the UNIX operating system, Prentice Hall of India, 1986.
3. Kenneth Rosen, Douglas Host, James Farber, Richard Rosinki, Unix-The Complete Reference, Mc-Graw Hill, 1999.
4. James Tisdall ,Beginning Perl for Bioinformatics ., O'Reilly Publishers, 2001
   Eric.T.Ray "Learning XML," 2/e O'Reilly Publications,2003

09BI343 PYTHON LAB

Credit : 0:0:2

1. Basic syntax
2. Input and Output programs
3. Variables Declaration and usage
4. Control structures;
5. File operations,
6. Subroutines,
7. Modules, Functions.
8. BIOPYTHON: objects in Biopython; using Biopython
9. Webserver application development using Python.

09BI344 CHEMINFORMATICS LAB

Credit : 0:0:2

Creating models of molecules and energy minimization.
Measuring bond lengths, bond angles, and dihedral angles.
Calculation and visualization of steric effects in substituted cyclohexanes.
MO calculations of molecular geometry, bond orders, atomic charges, and hybridization.
Molecular Recognition in Cyclodextrins.
Study of Binding. Predict Binding Constants of Activity.
3-D Database Searching for Tight Binding Guests.
3-D Sub-structure Spatial Relationships.

09BI345 RELATIONAL DATABASE MANAGEMENT SYSTEMS

Credit: 4:0:0

Objective:

- This subject introduces students to relational database design and SQL (Structured Query Language) used with relational databases.
- Students will be presented with a methodology for relational database design using Entity Relationship Diagrams and normalization of data.
- An overview of the functions of the Database Management System (DBMS) and of a Database Administrator (DBA) will also be presented.

Outcomes:

- After completing this course students must be able to demonstrate the knowledge and ability to analyze and design a database in some implementation.
- It would provide them to implement the structural constraints of relationships and use different keys for data access.
- They would gain skill of performing normalization and draw ER diagram of any database application.

Unit I

Introduction: DBMS architecture; models; networked; hierarchical; relational; data independence; integrity constraints; advantages of DBMS.

File system and organization. Secondary storage devices; file organization; sequential; B-tree indexing.

Unit II

Entity relationship model: entity types, entity sets, attributes, keys; relationships- relation types, degree of relationship, constraints on relationship types; E R diagram- Notations of ER diagram, alternate notation for ER diagram, ER to Relational mapping

Unit III

Relational Model: Structure of relational database, keys, query languages; fundamental relational algebra operations; SQL- basic structure of SQL queries, basic SQL operations, aggregate functions, views.

Unit IV

Decomposition of schema: functional dependency; multi-valued dependency; join dependency; normalization; 1NF; 2NF; 3NF,BCNF.

Unit V

Database Security & Data Recovery: Transaction processing, concurrency control techniques- locking techniques; Recovery techniques- deferred update, immediate update; Data back-up & recovery from catastrophic failures, Database security and DBA, discretionary access controls.

Text Books:

1. Ramesh Elmasri, Shamkant B. Navathe, Fundamentals of Database systems, Fourth edition, Addison –Wesley Publications, 2004.
2. Abraham Silberschatz, Henry K Korth, Sudarshan S, Database concepts, Fifth edition, Mc Graw Hill International publications.

Reference:

1. C. J. Date, "An Introduction to Database," 7/e, Addison-Wesley Publishers, 2000.
2. Martin James, Principles of Database Management, Prentice – hall of India Pvt. Ltd.,2001
3. Naveen Prakash, Introduction to Data Base Management, Tata McGraw Hill Publications, 2002.

Ramakrishnan, Gehrke, Database Management System, McGraw Hill Publications, 2003.

BIOINFORMATICS

ADDITIONAL SUBJECTS

Code	Name of the Subject	Credits
10BI201	Algorithms for Bioinformatics	3:0:0
10BI202	Pharmacogenomics	3:0:0
10BI203	Chemoinformatics	3:0:0
10BI204	Basics of Molecular Modeling	3:0:0
10BI205	Molecular Simulation and Engineering	3:0:0
10BI206	Medical Informatics	3:0:0
10BI207	Structural Bioinformatics and Sequence Analysis Lab	0:0:2
10BI208	Computational Chemistry and MATLAB	0:0:2

10BI201 ALGORITHMS FOR BIOINFORMATICS

Credits: 3:0:0
Objectives

- To provide the student with an overview and in-depth understanding of Bioinformatics algorithms.
- Enable the student to first evaluate which algorithm(s) are best suited for answering a given biological question

Outcomes

- Understand the details of the algorithms commonly used in bioinformatics.
- Develop computer programs implementing these algorithms.
- Identify which type of algorithm is best suited to describe a given biological problem.
- Understand the concepts of data redundancy and homology reduction.
- Develop bioinformatics prediction algorithms describing a given biological problem.

Unit I
Introduction: Analyzing algorithm, Algorithms and Complexity, Algorithm Design Techniques, Tractable versus Intractable Problems. Restriction Mapping, Graphs, Measuring Fragment Size, Restriction Mapping Algorithms.

Unit II
Dynamic Programming: Sequence alignment, Local alignment – Smith waterman algorithm , global alignment- Needleman wunsch algorithm. Scoring matrices – PAM and BLOSUM matrices. Multiple sequence alignment (MSA), tools and applications of MSA.

Unit III
Hidden Markov Models - Markov Chains, Baum – Welch algorithm , CG Islands, Forward & Backward Algorithm, HMM Parameter estimation, Profile HMM, Building viterbi Algorithm, Multiple Sequence Alignment by profile HMM's.

Unit IV
DNA Sequencing, Shortest Superstring Problem. Sequence comparison, Sequence similarity search- FASTA and BLAST algorithms. Computational methods for protein classification and prediction Chou-Fasman and GOR method. Motif based assignment method ,Motif program, Motif alignment and search tool.

Unit V

Gene Prediction – Grail, Genparser. Phylogenetic Reconstruction, Parsimony Method, Evolutionary Methods, Maximum Likelihood Method. Protein Folding: Levels of Proteins Structures, Prediction by Profile HMMs, Molecular Modeling.

Text book

Neil C Jones & Pavel A. Pevzner, An Introduction to Bioinformatics Algorithms, Ane Books, 2005.

Reference Books

1. Hans-Joachim Böckenhauer and Dirk Bongartz, Algorithmic aspects of bioinformatics, Natural computing series 2007.
2. David W. Mount , Bioinformatics Sequence and Genome Analysis, Second Edition , CBS publishers 2005
3. Durbin R, Eddy S, Krogg A and Mitchison, G, Biological Sequence Analysis: Probabilistic Models of proteins and Nucleic acids, Cambridge Edition, 2003
4. Pavel A.Pevzner, Bioinformatics and Functional Genomics, Second Edition, Wiley Publications, 2003

10BI202 PHARMACOGENOMICS

Credits: 3:0:0

Objectives

- To analyze the genome, transcriptome, proteome, metabolome, and further derivatives of –omics
- To create an integrative attempt to put all the pieces back together in treating diseases using genomics approach.

Outcome

- Provide students with an understanding of the principles and applications of human genetics and genomics in drug therapy optimization, patient care, and counseling.

Unit I

Introduction to Pharmacogenomics: Promises, Opportunities & Limitations. The Human Genome. Turning SNPs into Useful Makers of Drug Response. Association Studies in Pharmacogenomics.Genomics Application that Facilitate the Understanding of Drug Action & Toxicity.

Unit II

The Role of Pharmacogenetics in Drug Discovery & Therapeutics. Pharmacogenomics and Drug Design. The Pharmacogenomics of Human P-Glycoprotein. Pharmacogenomics of Drug Transporters. Pharmacogenomics of Asthma Treatment.

Unit III

Endothelial Cells as Targets for Hydroxy Urea: Relevance to the Current Therapeutic Strategy in Sickle Cell Disease. Pharmacogenomics and Complex Cardiovascular Disease – Clinical Studies in Candidate Genes. Pharmacogenomics of Lipid-Lowering Agents.Pharmacogenomics of Chemotherapeutic Agents in Cancer Treatment. Pharmacogenomics of the Blood-Brain Barrier.

Unit IV

Pharmacogenomics and the Treatment of Neurological Disease. Pharmacogenomics of Neurodegenerative Diseases: Examples & Perspectives. Psychiatric Pharmacogenetics: Prediction of Treatment Outcomes in Schizophrenia. Pharmacogenomics of Major Depression and Antidepressant Treatment. Pharmacogenomics of Bipolar Disorder.

Unit V

Pharmacogenomics of Alcoholism. Pharmacogenomics of Tobacco Addiction. Pharmacogenomics of Opioid Systems. Ethnicity and Pharmacogenomics.
Pharmacogenomics: Ensuring Equity Regarding Drugs Based on Genetic Difference.
Translation of Vascular Proteomics into Individualized Therapeutics.

Text Books

1. Julio Licinio & Ma-Li Wong (Eds.), Pharmacogenomics: The Search for Individualized Therapies, First Edition, Wiley – VCH Publishers, 2002.
2. Mark A. Rothstein, Pharmacogenomics: social, ethical, and clinical dimensions, Wiley –LISS Publishers, 2003

10BI203 CHEMOINFORMATICS

Credits: 3:0:0

Objective

The course objectives are to introduce different methods of chemoinformatics with particular emphasis on applications including modern drug discovery.

Outcomes

- The course will introduce the students preparing for professional work in chemistry must learn how to retrieve specific information from the enormous and rapidly expanding chemical literature.
- The course will provide a broad overview of the computer technology to chemistry in all of its manifestations
- The course will expose the student to current and relevant applications in QSAR and Drug Design.

Unit I Introduction

Introduction to chemoinformatics, History and Evolution of chemoinformatics, Use of chemoinformatics, Prospects of chemoinformatics, Molecular Modeling and Structure Elucidation

Unit II Representation of Molecules and Chemical Reactions

Nomenclature; Different types of Notations; SMILES Coding; Matrix Representations; Structure of Molfiles and Sdfiles; Libraries and toolkits; Different electronic effects; Reaction classification

Unit III Searching Chemical Structure

Full structure search; sub structure search; basic ideas; similarity search; Three dimensional search methods; Basics of Computation of Physical and Chemical Data and structure descriptors; Data visualization and Non-linear Mapping

Unit IV Computer Assisted Virtual screening design

Structure Based Virtual Screening- Protein Ligand Docking, Scoring Functions for Protein Ligand docking, Practical aspects of structure based Virtual Screening; Prediction of ADMET Properties, 2 D and 3D data searching, Chemical databases, Role of computers in Chemical Research.

Unit V Application of Chemoinformatics in Drug Design

Quantitative Structure-Property Relations; Descriptor Analysis; Computer Assisted Structure elucidations; Target Identification and Validation; Lead Finding and Optimization; Analysis of HTS data; Design of Combinatorial Libraries; Ligand-Based and Structure Based Drug design

Text Book

1. Andrew R. Leach, Valerie J. Gillet, Introduction to Chemoinformatics, Kluwer Academic Publishers, Netherlands, 2003.

Reference Books

1. Lisa B. English, Combinatorial Library Methods and Protocols, Humana Press Inc, Volume 2, 2002.
2. Frank Jensen, Introduction to Computational Chemistry, Wiley Publisher, Second Edition, 2006.

10BI204 BASICS OF MOLECULAR MODELING

Credits: 3:0:0

Objective

- The aim of this course is to provide the student with the basic molecular modeling principles and also be able to utilize basic modeling techniques to explore biological phenomena at the molecular level.
- To emphasize Modeling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

Outcomes

- The course will provide a broad overview of molecular mechanics force fields, parameterization, and their limitations.
- They should further be able to carry out energy minimization and molecular dynamics simulations of simple systems.
- The course will expose the student to describe advanced molecular modeling methods such as free energy calculation and solvation energies for small molecules, docking, and modern drug design applications.

Unit I Introduction to Molecular Modeling
Concepts of Molecular Modeling, Coordinate System: Cartesian and Internal, Surfaces, Potential Energy Surfaces, Molecular Graphics and Structure visualization, Applications of Molecular Graphics in Molecular Modeling.

Unit II Force Field
Force Fields: Molecular mechanics and Quantum mechanics, Features of Molecular mechanics force fields. Bond stretching, Angle bending, Torsion terms, and Non- bonded interactions: Electrostatic interaction, Vander walls interactions, and Local and Global energy minima.

Unit III Energy Minimization
Energy minimization methods: Derivatives and Non derivatives methods, Applications of energy minimization, Energy minimization by Systematic search.

Unit IV Molecular Simulation
Methods and simulations, Monte Carlo method, Difference between Molecular dynamics and Monte Carlo method, Conformational Search

Unit V Modeling Drug – Receptor Interaction
Molecular Recognition by Receptor and Ligand Design, Ligand – Receptor Interaction, Binding site properties, Ligand Binding Prediction, The pahramacophore concept, Biding Energy, Aqueous and Nonaqueous Solvent models.

Text Books

1. Allan Hinchkliffe, Molecular Modeling for Beginners, Wiley Publisher, 2003
2. N. Claude Cohen, Guidebook on Molecular Modeling in Drug Design, Academic Press, 2006

10BI205 MOLECULAR SIMULATION AND ENGINEERING

Credits: 3:0:0

Objective

The aim of this course is to provide the student with the basic statistical mechanics principles behind current methods in molecular simulation and also introduce these simulation techniques. It is expected that the student will have a deeper understanding of the molecular basis of physical behavior.

Outcome

- The course will introduce the student to the chemistry and physics behind the methods, accomplished through self-contained lectures on classical and quantum mechanics, and fundamentals of statistical mechanics.
- The course will provide a broad overview of the many different (both established and recent) simulation techniques.
- The course will expose the student to current and relevant applications in molecular simulation and modeling.

Unit I Introduction

Introduction - Useful Concepts in Molecular simulation: Coordinate Systems. Computer Hardware and Software. Potential Energy Functions, Energy Minimization, and Molecular Dynamics. Introduction to LINUX

Unit II Computer Simulation methods
Force Fields. Hydrogen Bonding in Molecular Mechanics. Calculation of thermodynamic properties – Phase space – Practical aspects pf computer simulation – Boundaries monitoring Equilibrium – Long range Process – Analyzing result of simulation and estimating errors

UNIT III Molecular dynamics simulation method
Molecular Dynamics using simple modules – Molecular Dynamics with continuous potentials – Running Molecular Dynamics simulation – Constant dynamics – Time dependent properties – Molecular Dynamics at constant temperature and pressure

UNIT IV Monte Carlo Simulation method
Metropolis methods – Monte Carlo simulation of molecules – Monte Carlo simulation of polymers – Calculating chemical potentials – Monte Carlo or Molecular Dynamics-Models Used in Monte Carlo Simulations of Polymers. Molecular Modeling software

UNIT V Bimolecular Interaction and Drug design
Molecular modeling in drug discovery – deriving and using 3D Pharmacores – Molecular docking – Structure Based methods to identify lead components- Denovo ligand design

Text Books

1. A.R.Leach, Molecular Modelling Principles and Application, Longman, 2001.
2. J.M.Haile, Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons, 1997.

Reference Book

1. Satya Prakash Gupta, QSAR and Molecular Modeling, Springer - Anamaya Publishers, 2008.

10BI206 MEDICAL INFORMATICS

Credits: 3:0:0

Objective
To introduce students to the concepts and practices of health informatics.

Outcome:
Know the issues in health practices. Students are expected to gain insight in planning and building healthcare information systems; software design and human-computer interaction issues.

Unit I Introduction to medical informatics
Basic concepts in health informatics and its history, definitions, sub disciplines and professional organizations and activities.

Unit II Major applications and commercial vendors
Major health informatics applications including electronic medical records (EHR) and computerized physician order entry (CPOE). Data interoperability of records; Medical

controlled vocabularies and electronic data interchange standards. Commercial and open source applications.

Unit III Good clinical practices (GCP)
GCP history and guidelines; India and the world in GCP; Standard operating procedure and guidelines; Current issues in India and abroad. Institutional review boards and protection of human health.

Unit IV Information systems design and engineering
Planning and implementing issues of healthcare information systems. Software engineering principles, human factors and human-computer interaction issues, and evaluation methods of end user acceptance and outcomes.

Unit V New opportunities and emerging trends
Information technologies in healthcare; wireless and handheld devices, social computing paradigms, and eHealth applications, web-based tools.

Text Book
Taylor Paul, From Patient Data to Medical Knowledge: The Principles and Practice of Health Informatics, Blackwell Scientific Publishing, 2006.

10BI207 STRUCTURAL BIOINFORMATICS AND SEQUENCE ANALYSIS LAB

Credits: 0:0:2
Objective

- This course aims to study and analysis the sequence of protein and DNA using the online databases.

Outcome

- The students learned the different online biological database and analyzed the sequence of protein and DNA molecules.

I. Sequence analysis
1. Reference retrival from NCBI &EBI Database.
2. DNA sequence retrival from NCBI, EBI and DDBJ.
3. Protein sequence retrival from SWISS PROT,PIR, UNIPROT.
4. Pairwise alignment of protein and DNA sequences.
5. Multiple alignment of protein and DNA sequences.
6. To run BLAST and FASTA.

II. Structure analysis

1. Molecular weight , Molecular composition of protein structures.
2. Determine/Analysis of secondary structure of proteins.
3. Determine/Analysis of Tertiary structure of proteins.
4. Determine/Analysis of secondary structure of DNA.
5. Analysis of protein from protein Databank.
6. Analysis of protein from protein Databank.

10BI208 COMPUTATIONAL CHEMISTRY AND MATLAB

Credits: 0:0:2

Objective

To give the students practical experiences of physico-chemical principles as reflected by modern computational techniques. The emphasis will be on the connection between quantum chemistry principles and observed spectra. Taught in the context of biological research, this course helps biologists learn how to use the technical computing language MATLAB to automate certain tasks

Outcome

- Understanding of small molecular properties.
- It can be used in biochemical research.
- Identifying Differential Gene Expression
- Annotating Up-Regulated Genes Using Gene Ontology
- Finding the Differentially Expressed Genes in Pathways

Experiments

1. Molecular Mechanics of Hydroxyl group, H_2O_2, Methanol,
2. Amino Acids using Insight/Charm.
3. Molecular Orbital Theory Application for Oxygen Molecule.
4. Organic Radicals: Cations, Neutral Radicals, Anions.
5. Electron Distribution in Allyl Ions
6. Stability of Butyl Cation
7. MATLAB Basics
8. Biological File Formats and Database Access
9. Biological Sequence Analysis and Alignment
10. Biological Sequence Utilities and Statistics
11. Phylogenetic Tree Analysis
12. Protein Feature Analysis
13. Microarray Data Analysis and Visualization
14. Microarray Normalization, Data Analysis and Visualization

DEPARTMENT OF BIOINFORMATICS

REVISED AND NEW SUBJECTS

CODE	SUBJECT NAME	CREDIT
10BI301	Structural Bioinformatics	3:0:0
10BI302	Bioinformatics Algorithms	3:0:0
10BI303	Programming with Perl	4:0:0
10BI304	Biomedical Informatics	3:0:0

10BI301 STRUCTURAL BIOINFORMATICS

Credit: 3:0:0

Objectives:
This course aims to study the strategy and tactics of biophysical concepts of macromolecules and the conformational analysis and forces that determine the protein and nucleic acid structure and ligand interaction with macromolecules. Study of the size and shape of the macro molecule using different techniques using various tools like X-ray Crystallography and other techniques is explained in the course

Outcomes:
The student would learn the different structural levels of biological macromolecules, its size, shape, their conformations and the forces that are involved in stabilizing these molecules. The tools by which this analysis is done will be learned. The student would also learn about the ligand interaction with macromolecules.

Unit I: Introduction
Levels of structures in Biological macromolecules, basic strategies in biophysics, Principles and concepts used in biophysical analysis of life processes, Biomolecules and their interactions, size and shape of macromolecules.

Unit II: Amino acids and Proteins
Structure of proteins: Properties of amino acids, Ionization of amino and carboxyl groups in amino acids and peptides, Ionization of side chains, configuration of natural amino acids, polarity of amino acid side chains, Composition of proteins, amino acid composition, Predicting properties from amino acid compositions,

Unit III: Conformation Analysis
Forces that determine protein structure, basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions and ionic interactions, disulphide bonds.

Unit IV: Structural Analysis of Macromolecules
Prediction of proteins structure, nucleic acids, general characteristics of nucleic acid structure, geometrics, glycosidic bond, rotational isomers and those puckering backbone rotational isomers

and ribose puckering forces stabilizing ordered forms, base pairing, base stacking tertiary structure of nucleic acids.

Unit V: X–Ray Diffraction

X-ray crystallography – X–ray diffraction, determination of molecular structures, electron microscopy, neutron scattering and light scattering.

Text Book

1. Cantor R. & Schimmel P.R., Biophysical Chemistry, Vol. I, II, W.H. Freeman & Co., 1985.

10BI302 BIOINFORMATICS ALGORITHMS

Credit: 3:0:0

Objectives:

- To introduce the student to the biology of bioinformatics to understand how computer science algorithms solve problems
- Discover new knowledge in genomics, proteomics, metabolomics, transcriptomics, and other omics.

Outcomes:

- Thoroughly describe and apply different algorithms for sequence analysis, analysis of gene expression data and molecular biological networks.
- Independently implement commonly used algorithms for sequence comparisons, analysis of gene expression data and graph theoretical problems relating to bioinformatics

Unit I

Algorithms and Complexity: What is an algorithm-Biological algorithm versus computer algorithms-The change problem-Correct versus Incorrect algorithms-Recursive algorithm-Towers of Hanoi problem- Big O notation- Algorithm design techniques.

Unit II

Exhaustive Search: Molecular Biology Primer- Branch and Bound Algorithm- Greedy Algorithm- Restriction Mapping-Impractical restriction mapping Algorithm- A practical restriction mapping Algorithm-Profiles-The motif finding problem-Search Trees.

Unit III

Graph Algorithms: Introduction to Graphs- Directed Graphs-Undirected graphs-weighted and unweighted graphs– NP- Complete problem-Eulerian cycle-Hamiltonean cycle-Graphs and genetics- Shortest Superstring Problem- DNA array sequencing technique- Sequencing by Hybridization-SBH as a Hamiltonean path problem

Unit IV

Combinatorial Pattern matching: Repeat finding-Hash tables- Exact pattern matching-Suffix trees-Heuristic similarity search Algorithms-Approximate Pattern matching-BLAST

Unit V

Evolutionary trees-Distance based tree Reconstruction- Character based Tree Reconstruction. Reconstructing trees from additive matrices-Evolutionary trees and Hierarchical clustering

Textbook:

1. Neil Jones & Pavel Pevzner An Introduction to Bioinformatics Algorithms, MIT Press, 2004.

Reference

1. M. Waterman, “Introduction to Computational Biology: Maps, Sequences & Genomes”, CRC Press, 1995.

10BI303 PROGRAMMING WITH PERL

Credit: 4:0:0

Objectives:

- Express fundamental programming constructs such as variables, arrays, loops, subroutines and input/output in Perl.
- Understand several concepts relatively idiosyncratic to Perl, such as associative arrays, Perl regular expressions, and system interfaces.
- Programming basics and working with DNA sequences and strings
- Regular expressions and finding motifs in data
- Using Perl to parse PDB records, annotations in GenBank, and BLAST output

Outcomes:

- Write, compile, and run Perl programs, Analyze the effects of using Perl structures that implement decisions, loops, and store arrays and use these structures in a well-designed, OOP program.
- Create Perl programs that make use of various directories and use several files linked together. Create Web sites with Perl programs and compare and contrast the effectiveness of using Web programming modules from CPAN.
- Design and analyze to get you quickly over the Perl language barrier by approaching programming as an important new laboratory skill, revealing Perl programs and techniques that are immediately useful in the lab.

Unit I

Intoduction-History of Perl –Perl Benefits –Installing Perl-Running Perl Programs-
Using Perl on Windows and UNIX - Data types – Operators – variables -Variable Interpolation

Unit II

Perl Control Structures - Deciding If, If-else if- else, For loops ,While loops , Until -Lists-simple list , Accessing list values- Arrays - Array functions – Push and Pop , Shift and unshift – Hashes.

Unit III

Subroutines – subroutines for calculation, Reference to subroutine, Passing arrays and hashes to subroutines. Regular Expression – Working with regular expression. File Handling – Writing to Files

Unit IV
Modules – Types , Perl standard modules. Object oriented Perl – Working with objects. Perl and Databases – Perl and DBM

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

Text Books

1. Simon Cozens and Peter Wainwright, Beginning Perl, Shroff publishers, Apress reprint 2005
2. James Tisdall, Beginning Perl for Bioinformatics, O'Reilly Publications, Fourth Indian reprint 2004.

10BI304 BIOMEDICAL INFORMATICS

Credit: 3:0:0

Objectives:
Develop computer based clinical data analysis skill to recognise the existence of patterns for medical care.

Outcomes:
This paper will give an overview on terms in biomedical side. This will also provide various types of data and its management for meaningful application in health care.

Unit I: Introduction
Medical language and terminology; Human anatomy and physiology; Relationships among medical terms and concepts; role of informatics approaches in preventing disease

Unit II: Data
Data type, collection, organization, representation and analysis. Data form that support computer based analysis.

Unit III: Data Management
Organisation of multidimensional clinical data into database for management and mining. Data management methods and tools. Statistical approaches. Database searches using logical operators; refinement of retrieved information for completeness.

Unit IV: Pattern recognition
Recognise the patterns, uses, errors and limitations on the data analysis. Uncertainty in decision making; Systematic and predictable errors.

Unit V: Application
Suggestions and improvement over inferred patterns; Case study.

Text Book

1. Shortliffe E.H. and Cimino J.J, Biomedical Informatics: Computer Applications in Health Care and Biomedicine,. Springer, 3rd Edition, 2006.

ADDITIONAL SUBJECTS

Sub. Code	Name of the Subject	Credits
11BI201	Biocomputing	4:0:0
11BI202	Immunotechnology and Informatics	3:0:0
11BI203	Introduction to Genetic Algorithms	3:0:0
11BI 301	Numerical Methods and Biostatistics	3:0:0
11BI302	Molecular Biology and Genetics	3:0:0
11BI 303	Computational Genomics	3:0:0
11BI304	Bioinformatics Algorithms	3:0:0
11BI305	Perl Programming	3:0:0
11BI306	Molecular Biology and Genetics Lab	0:0:2
11BI307	Computational Genomics Lab	0:0:2
11BI308	Bioinformatics Algorithm Lab	0:0:2
11BI309	Perl Programming Lab	0:0:2
11BI310	Structural Bioinformatics and Instrumental Techniques	3:0:0
11BI311	Molecular Modeling and Simulation	3:0:0
11BI312	Pattern Recognition and Machine Learning	3:0:0
11BI313	Python for Bioinformatics	3:0:0
11BI314	Graph Theory and System Biology	3:0:0
11BI315	Structural Bioinformatics and Instrumentation Lab	0:0:2
11BI316	Molecular Modeling and Simulation Lab	0:0:2
11BI317	Machine Learning Lab	0:0:2
11BI318	Python for Bioinformatics Lab	0:0:2
11BI319	System Biology and Simulation Lab	0:0:2
11BI320	Cheminformatics	4:0:0
11BI321	Medical Informatics	3:0:0
11BI322	Enzyme Engineering	3:0:0
11BI323	Microarray and Image Processing	3:0:0
11BI324	Support Vector Machine	3:0:0
11BI325	Web Programming for Bioinformatics	3:0:0
11BI326	Cheminformatics Lab	0:0:2
11BI327	Medical Informatics Lab	: 0:0:2
11BI328	Enzyme Engineering Lab	0:0:2
11BI329	Microarray and Image Processing Lab	0:0:2
11BI330	Vector Machine Lab	0:0:2
11BI331	Web Programming Lab	0:0:2

11BI201 BIOCOMPUTING

Credits 4:0:0

Course Objective

To have an overview idea about modern biology and computation.

To study the various techniques involved in RNA structure prediction, microarray, protein structure prediction and phylogenetic analysis

Course Outcomes

- The course will give an overview idea about biocomputing.
- This course would also enable the student to under the various computing approaches used to analyze and predict various biological molecules.

UNIT I: Introduction

An elementary introduction to modern molecular biology: reductionist programme, the cell, information pathways, genetic information storage and transfer, genome organization, sequencing projects, A brief overview of information technology and science: history, hardware and software, data base management system and Internet. An introduction to bioinformatics and sequence analysis: definition and elemental tasks

UNIT II: Nucleic Acid Structure Prediction

RNA structure prediction: Dynamic programming: Nussinov and Zuker algorithm, prediction by analysis of sequence covariance, RNA tertiary structure prediction and RNA folding, DNA structural polymorphism: regular DNA helices, sequence specific DNA structures, DNA bending, DNA supercoiling, unusual DNA structure.

UNIT III: Microarrays

Data quality, gene expression matrices, grouping expression data, clustering methods, feature reduction, Microarray data tools and resources: microarray data format, tools for microarray data analysis, Proteomic data analysis: raw data from 2D-PAGE, gel matching, protein expression matrices, 2D-PAGE databases, Arrays: DNA arrays, chip hybridization, application of DNA microarray, Protein arrays, application of protein array, RNA array.

UNIT IV: Protein Structure Analysis

Protein secondary structure prediction: measures of prediction accuracy, statistical technique (CF and GOR algorithm), neural network (PHD) nearest neighbor method (PREDATOR and NNSSP), consensus methods (JPRED and NPS), Protein tertiary structure prediction: homology modeling, threading and Abs Initio structure prediction, Other issues: CASP, Levinthol paradox and protein folding.

UNIT V: Phylogenetic Analysis

Graphs and trees: phylogenetics trees and cladogram, Building phylogenetic trees: similarity and distance table, distance matrix methods, maximum parsimony methods, limitations of phylogenetic algorithms, phylogenetic software, reliability of phylogenetic trees, Evolution of macromolecular sequences: molecular phylogeny, choice of macromolecular sequence, rapidly evolving macromolecular sequences.

Text Books

1. N. Gautham, Bioinformatics: Databases and algorithms, Narosa publishing house, Chennai 2006.
2. P. Shanmughavel Principles of Bioinformatics, , Pointer publishers, Jaipur 2005.

Reference Books

1. David Mount,Bioinformatics: Sequence and Genome Analysis, Second Edition, CBS Publishers 2005.
2. J. Pevzner Bioinformatics and functional genomics, 2nd edition, John wiley & sons, 2009.

11BI202 IMMUNOTECHNOLOGY AND INFORMATICS

Credits 3:0:0

Course Objective

The course objectives are to introduce Immunological foundations and apply Informational technology to study immune systems

Course Outcomes

- This course gives a complete understanding of the concepts of Immunology & Immunotechniques.
- The course will help the students to understand Immunoinformatics and its application

UNIT I: Overview of Immune System

Types of Immunity - Innate and Adaptive. Cells and organs of the immune system. Antigens – epitopes, antigenicity, factors influencing antigenicity

UNIT II: Immunoglobulins

Structure and types of Immunoglobulins, Biological activities. Monoclonal antibodies-productions and applications. Cytokines – types and immune response. complement system

UNIT III: Antigen Antibody Interactions

Antibody affinity and activity – precipitation, agglutination, Radio Immuno Assay, ELISA, Western blotting, Immunoprecipitation, Immunofluorescence, Flow cytometry for separation of immune cells. Major Histocompatiblity Complex (MHC). Antigen processing and presentation

UNIT IV: T Cell & B Cell Activation

T cell & B cell maturation, activation and differentiation. Leukocyte migration and inflammation. Hypersensitive reactions.

UNIT V: Immunoinformatics

Immunoinformatics - Introduction & Methods. Applications – prediction of epitopes, vaccine design, Web based tools for vaccine design

Text Books

1. Richard A. Golds, Thomas J Kindt, Kuby Immunology, Edited by Barbara Osborne. W.H.Freeman & Company, 4th edition, 2000.
2. Ole Lund, Immunological Bioinformatics, MIT Press, 2005

Reference Books

1. A. K. Chakravarthy, Immunology & Immunotechnology, Oxford University Press, 2006
2. Darren R.Flower, Immunoinformatics: Predictive Immunogenicity insilico, Humana Press, 2007.

11BI203 INTRODUCTION TO GENETIC ALGORITHMS

Credits: 3:0:0

Course Objective

The course objectives are to introduce mathematical foundations for Genetic algorithm, operators and to study genetic based machine learning and its applications.

Course Outcomes

- This course gives a complete understanding of the concepts of Genetic algorithm.
- The course will acquired an understanding of the basic algorithm and its theory of operation
- The course will expose the student to current and relevant applications of genetic algorithm in problem solving.

UNIT I: Genetic Algorithm: an Overview

A Brief History of Evolutionary Computation-The Appeal of Evolution-Biological Terminology-Search Spaces and Fitness Landscapes-Elements of Genetics Algorithms-Genetic Algorithms and Traditional Search Methods-Some Application of Genetics Algorithms and Example-How Do Genetic Algorithm Work.

UNIT II: Genetic Algorithms in Problem Solving

Evolving Computer Programs-Data Analysis and Prediction-Evolving Neural Network-Application of Genetic Algorithm in problem solving

UNIT III: Genetic Algorithm in Scientific Models

Modeling Interaction between Learning and Evolution-Modeling Sexual Selection-Modeling Ecosystem-Measuring Evolutionary Activity-Application of Genetic Algorithm in Scientific Models

UNIT IV: Theoretical Foundations of Genetic Algorithms

Schema and the Two-Armed Bandit Problem-Royal Roads-Exact Mathematical Models of Simple Genetic Algorithms-Statistical-Mechanics Approaches-Application of Genetic Algorithms in Mathematical Modeling

UNIT V: Implementing a Genetic Algorithm

Applications of Genetic Algorithm - Encoding a Problem for a Genetic Algorithm-Adapting the Encoding-Selection Methods-Genetic Operators-Parameters of Genetic Algorithms.

Text Book

1. Melanie Mitchell, An Introduction to Genetic Algorithms, The MIT Press, 2004**.**

Reference Book

1. David E. Gold Berg, Genetic Algorithms in Search, Optimization & Machine Learning, Pearson Education, 2001.

11BI 301 NUMERICAL METHODS AND BIOSTATISTICS

Credits: 3:0:0

Course Objectives

- At the end of the course, the students would be acquainted with the basic concepts in numerical methods and their uses.
- Upon completion of this course, students will understand and be able to apply basic techniques in descriptive and inferential statistics.

Course Outcomes

- With the present development of the computer technology students will be developing efficient algorithms for solving problems in science, engineering and technology.
- Students will be able solve different kinds of problems occur in engineering numerically.

Unit I: Iterative Methods and Solution of Simultaneous Equations
Introduction, Newton's relations, Evaluation of polynomials, Solution of quadratic equation, Bisection method, Newton-Raphson method, Existence of solutions, Gauss-Seidel iteration method, Gauss-Jordan method, Gauss-Jordan Matrix inverse, Eigenvalues and Eigenvectors.

Unit II: Interpolation and Numerical Integration
Introduction, linear interpolation, polynomial interpolation, Difference tables, Gregory-Newton interpolation, Trapezoidal rule, Simpson's rule, Newton's Three-eights rule, Gausian Quadrature

Unit III: Solution of Differential Equations
Introduction, Euler's Method, Taylor's Method, Runge-Kutta Methods, Predictor Corrector Methods, Automatic Error Monitoring and Stability of solution

Unit IV: Distributions
Frequency Distribution: Sampling, frequency distribution, measure of central tendency: mean, median and mode, measure of dispersion, moments: arithmetic mean, variance, skewness and kurtosis, Probability Distribution: probability, binomial distribution, Poisson distribution

Unit V: Curve Fitting and Correlation
Linear least square fit, nonlinear fit, polynomial fit, coefficient of correlation, multiple correlation, partial correlation, rank correlation

Text Books

1. E.Balagurusamy, "Computer Oriented Statistical and Numerical Methods", MacMillan series, Madurai (1988).
2. V.Rajaraman, Computer oriented numerical methods, Prentice-Hall publications, 2007.

Reference book

1. M.K.Jain, S.R.K.Iyengar and R.K.Jain, Numerical methods for scientific and engineering computation, Third Edition, New Age International (1993)

11BI302 MOLECULAR BIOLOGY AND GENETICS

Credits: 3:0:0
Course Objectives
This course will enable students to

- Know the concepts and applications of molecular biology and genetics.
- Provide an insight to molecular biology and techniques before stepping into the computational biology

Course Outcomes

- Students can understand and apply fundamental biological principles from theory to lab

- Students develop enhanced critical thinking and problem solving skills.

Unit I: Concepts of Genetics
Science of genetics – objectives, terminologies, methods, Mendelian genetics, Linkage, crossing over and Mapping , Genetics of Bacteria and Bacteriophages,

Unit II: Application of genetics
DNA mutation- types, repair and transposition, Genetics of populations, Genetics and evolution, Genetics and diseases: Cancer, HIV-AIDS

Unit III: Chromosome organization and replication
DNA structure and chromosome organization,. DNA Replication Mechanism of DNA synthesis, Enzymes, origin and termination of replication, other replicative structures, Eukaryotic DNA replication. Different tools and techniques in molecular biology: Cloning, construction of DNA libraries, PCR

Unit III: Transcription
Transcription: Central dogma, Prokaryotic and eukaryotic transcription, post-transcriptional modification - RNA splicing, ribozyme. RNA editing.

Unit IV: Translation
Translation: Process of translation in prokaryotes and eukaryotes, post-translational modifications, inhibitors of protein synthesis.

Unit V: Regulation of gene expression
Regulation of Gene Expression: Control in Bacteria and phages – Inducible and catabolite repression (Lac operon), Repressible and Attenuation (Trp operon), Lytic and Lysogenic cycles in Phage λ. Control in Eukaryotes: Cis and trans regulatory elements, Chromatin in gene regulation, transcriptional control, translational control, RNA interference in medical applications

Text books

1. David R Hyde, Genetic and Molecular Biology, Tata McGraw Hill Publications, New Delhi, 2010
2. David Friefelder, Molecular Biology, Narosa Publ. House. 2000

Reference Book

1. Gardner / Simmons / Snustad, Principles of Genetics, Eighth Edition, John Wiley, 2000

11BI 303 COMPUTATIONAL GENOMICS

Credits: 3:0:0

Course Objectives

- To provide opportunities for students in computer science and biology to interact with each other.
- To understand the real issues arising in the computational genomics analysis of data.

Course Outcome

Students will be better able to:

- Recognize biological central dogma important in generating biodiversity
- Describe the computational methods and algorithms applied in biology to human society.
- Develop technology based on the natural world.

Unit I: Introduction to Computational Genomics
Central dogma in molecular biology: DNA, RNA, splicing, gene structure, proteins – Introduction to Bioinformatics: Elementary commands and Protocols, ftp, telnet, http. Databanks – nucleotide, protein sequence and structural databases, World wide web – search engines – finding scientific articles - Pubmed.

Unit II: Sequence Alignment and Dynamic Programming
Strings – Edit distance between two strings - gaps - Sequence alignment. Global & local alignment - Smith-Waterman algorithm & Needleman-Wunsch algorithm. Matrices - PAM, BLOSUM. Sequence alignment using: BLAST, FASTA.

Unit III: Genomic sequencing and DNA Mapping
DNA Mapping – Physical and Genetic Mapping - Sequencing methods: Sanger sequencing, cloning – Large scale sequencing, Shotgun sequencing – Sequence assembly.

Unit IV: Comparative Genomics and Gene recognition
Introduction - Comparative Genomics based Gene Recognition, Suffix Trees – Gene finding methods - Grail II - Gene parser – GENSCAN – Procrustes - Evaluation of gene prediction methods.

Unit V: Phylogeny
Introduction - Concept of evolutionary trees - methods of construction - Maximum Parsimony - Distance methods - FM, NJ, UPGMA - Maximum likelihood method.

Textbooks

1. David W Mount, Bioinformatics: Sequence and Genome analysis, 2nd edition, CBS, Publishers, 2004
2. A. D. Baxevanis and B. F. F. Ouellette, Bioinformatics - A Practical Guide to the Analysis of Genes and Proteins, 2nd Edition, John Wiley & Sons Publication, 2001.

Reference Books

1. Arthur M. Lesk, Introduction to Bioinformatics, Oxford University press, 2003
2. SR Pennington, MJ Dunn, Proteomics from Protein Sequence to Function, Viva Books Ltd, 2002
3. Dan Gusfield, Algorithms On Strings Trees And Sequences, Cambridge University, Press, 2000

11BI304 BIOINFORMATICS ALGORITHMS

Credits: 3:0:0

Course Objectives

- To introduce the student to the biology of bioinformatics to understand how computer science algorithms solve problems
- Discover new knowledge in genomics, proteomics, metabolomics, transcriptomics, and other omics.

Course Outcomes

- Thoroughly describe and apply different algorithms for sequence analysis, analysis of gene expression data and molecular biological networks.
- Independently implement commonly used algorithms for sequence comparisons, analysis of gene expression data and graph theoretical problems relating to bioinformatics"

Unit I: Algorithms and Complexity

What is an algorithm-Biological algorithm versus computer algorithms-The change problem-Correct versus Incorrect algorithms-Recursive algorithm- Towers of Hanoi problem- Big O notation- Algorithm design techniques.

Unit II: Exhaustive Search

Molecular Biology Primer- Branch and Bound Algorithm- Greedy Algorithm- Restriction Mapping-Impractical restriction mapping Algorithm- A practical restriction mapping Algorithm-Profiles-The motif finding problem-Search Trees.

Unit III: Graph Algorithms

Introduction to Graphs- Directed Graphs-Undirected graphs-weighted and unweighted graphs–NP- Complete problem-Eulerian cycle-Hamiltonian cycle-Graphs and genetics- Shortest Superstring Problem- DNA array sequencing technique- Sequencing by Hybridization-SBH as a Hamiltonian path problem

Unit IV: Combinatorial Pattern matching

Repeat finding-Hash tables- Exact pattern matching-Suffix trees-Heuristic similarity search Algorithms-Approximate Pattern matching-BLAST

Unit V: Phylogeny

Evolutionary trees-Distance based tree Reconstruction- Character based Tree Reconstruction. Reconstructing trees from additive matrices-Evolutionary trees and Hierarchical clustering

Textbook

Neil Jones & Pavel Pevzner, An Introduction to Bioinformatics Algorithms, MIT Press, 2004.

Reference Book

M. Waterman, "Introduction to Computational Biology: Maps, Sequences & Genomes", CRC Press, 1995.

11BI305 PERL PROGRAMMING

Credits: 3:0:0

Course Objectives

- To express fundamental programming constructs such as variables, arrays, loops, subroutines and input/output in Perl.
- To understand several concepts relatively idiosyncratic to Perl, such as associative arrays,

Perl regular expressions, and system interfaces.
- To develop Perl code to work with DNA sequences and strings to finding motifs.
- Use Perl to parse PDB records, annotations in GenBank and BLAST output

Course Outcomes
- Students will be able write Perl code for local biological problems.
- Understand the first step in working with Internet through programming

Unit I: Introduction
History of Perl –Perl Benefits –Installing Perl-Running Perl Programs-Using Perl on Windows and UNIX – Data types – Operators – variables –Variable Interpolation

Unit II: Perl Control Structures
Deciding If, If-else if- else, For loops ,While loops , Until –Lists-simple list , Accessing list values- Arrays – Array functions – Push and Pop , Shift and unshift – Hashes.

Unit III: Subroutines
subroutines for calculation, Reference to subroutine, Passing arrays and hashes to subroutines. Regular Expression – Working with regular expression. File Handling – Writing to Files

Unit IV: Modules
Types, Perl standard modules. Object oriented Perl – Working with objects. Perl and Databases – Perl and DBM

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

Text Books
1. Simon Cozens and Peter Wainwright, Beginning Perl, Shroff publishers, 2005.
2. James Tisdall, Beginning Perl for Bioinformatics, Fourth Indian reprint O'Reilly Publications, 2005

11BI306 MOLECULAR BIOLOGY AND GENETICS LAB

Credits: 0:0:2

List of practical
1. Exercises and problems in Mendelian Genetics
2. Exercises and problems in Linkage and mapping
3. Isolation of plasmid DNA
4. Isolation of genomic DNA – from bacteria, chloroplast and human samples
5. Spectrophotmetric determination of Nucleic acid purity and concentration
6. Restriction enzyme digestion of DNA
7. Cloning: Preparation and transformation of competent E.coli cells
8. Agarose gel electrophoresis
9. Invitro amplification of DNA using PCR

11BI307 COMPUTATIONAL GENOMICS LAB

Credits: 0:0:2

List of Practical

1. Nucleotide Sequence databases
2. NCBI – Viral and Bacterial Genome analysis
3. Genome Browser Application
4. Proteins Sequence databases
5. Heuristic Methods of biological sequence analysis – FASTA and BLAST
6. Pairwise and Multiple alignment - GCG
7. Gene finding and Pattern recognition – GCG
8. Sequence Utilities, Translation and Nucleic Acid Secondary Structure – GCG
9. Evolution Analysis and Hidden Markov Model (HMM) Alignment – GCG
10. Gene prediction methods
11. PHYLIP, EMBOSS
12. Insilico molecular biology techniques using software

11BI308 BIOINFORMATICS ALGORITHM LAB

Credits: 0:0:2

List of Practical

1. Recursive problem
2. The change problem
3. Restriction mapping problem
4. Motif finding problem from a given sequence
5. Shortest superstring problem and DNA array sequencing techniques
6. Sequence by Hybridization as a Hamiltonian path and Eulerian path problem
7. Exact pattern matching
8. Approximate pattern matching
9. Distance based tree reconstruction
10. Character based tree reconstruction

11BI309 PERL PROGRAMMING LAB

Credits: 0:0:2

List of Practical

1. Getting familiar with Perl (Accessing and installing Perl and BioPerl, Editors, Getting help)
2. Running Perl (Running Perl , programming with BioPerl modules)
3. Using numbers and strings in Perl (Variables)
4. Finding motifs (dealing with sequences, flow control, file operation)
5. Using Hashes for translating RNA into protein
6. Using Regular Expressions
7. Using Perl modules for display of proteins
8. Working with DDBJ online
9. Using sequence and feature modules

10. Using the GFF processing module
11. Manipulation of nucleic acid and protein data
12. Pairwise alignment using bioperl module.

11BI310 STRUCTURAL BIOINFORMATICS AND INSTRUMENTAL TECHNIQUES

Credits: 3:0:0

Course Objectives

- To study the strategy and tactics of biophysical concepts of macromolecules and the conformational analysis and forces those determine the protein and nucleic acid structure and ligand interaction with macromolecules.
- To study the size and shape of the macro molecule using different techniques using various tools like X-ray crystallography and other techniques is explained.

Course Outcomes

- The student would learn the different structural levels of biological macromolecules, its size and shape, their conformations and the forces that are involved in stabilizing these molecules.
- The tools by which this analysis is done will be learned.
- The student would also learn about the ligand interaction with macromolecules.

UNIT I: Introduction

Levels of structures in biological macromolecules, basic strategies in biophysics, Principles and concepts used in biophysical analysis of life processes, biomolecules and their interactions, size and shape of macromolecules.

UNIT II: Amino acids and Proteins

Structure of proteins, Properties of amino acids, Ionization of amino and carboxyl groups in amino acids and peptides, Ionization of side chains, configuration of natural amino acids, polarity of amino acid side chains, composition of proteins, amino acid composition, predicting properties from amino acid compositions.

UNIT III: Conformational Analysis of Proteins

Basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions, ionic interactions, disulphide bonds, prediction of proteins structure.

UNIT IV: Structural Analysis of Nucleic Acids

General characteristics of nucleic acid structure, geometrics, glycosidic bond, rotational isomers and those puckering, backbone rotational isomers and ribose puckering, forces stabilizing ordered forms, base pairing, base stacking tertiary structure of nucleic acids.

UNIT V: Instrumental Techniques

X–ray diffraction-X-ray crystallography, determination of molecular structures, electron microscopy, neutron scattering and light scattering.

Text Book

1. Cantor,R., Schimmel,P.R., Biophysical Chemistry, Vol. I, II, W.H. Freeman & Co., 2004.

Reference Book

1. Gu,J., Bourne,P.E., Structural Bioinformatics, 2nd Edition, Wiley, 2009.

11BI311 MOLECULAR MODELING AND SIMULATION

Credits: 3:0:0

Course Objectives

- To understand the relationship among biomolecular structure, function and force field models.
- To be able to utilize basic modeling techniques to explore biological phenomena at the molecular level.
- To emphasize Modelling of protein/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

Course Outcomes

- Students are introduced to the principles of quantum mechanics and molecular mechanics applicable in Molecular modeling.
- An awareness of Computer simulation methods, based on understanding the three-dimensional structures and physicochemical properties will be created.

Unit I: Quantum mechanics and concepts in molecular modeling

Introduction – coordinate systems – potential energy surfaces – molecular graphics – surfaces - computer hardware and software – introduction to quantum mechanics – postulates – Schrodinger wave equation – Born-Oppenheimer approximation.

Unit II: Advanced ab initio methods and Molecular mechanics Force field

Practical considerations when performing ab initio calculations – Density functional theory - Empirical force field models – Bond stretching – angle bending – torsional term – nonbonding interactions – thermodynamics properties using a forcefield.

Unit III: Energy minimization

Energy minimization statement of the problem - Derivative and non derivative energy minimization methods –simplex – sequential univariate method – first order minimization methods: steepest descent method – conjugate gradient method - second order minimization method: Newton-Raphson method.

Unit IV: Molecular Dynamics and Monte Carlo Simulation

Introduction – Using simple Model – time steps –Multiple steps – Setting up MD – continuous potential in MD Simulation Examples – Monte Carlo simulation – Random number generation – Difference in MD & MC – Estimating errors in computer simulation.

Unit V: Applications of Molecular Modeling and Simulation

Comparative modeling of proteins – comparison of 3D structure – Homology – steps in homology modeling – tools – databases – side chain modeling – loop modeling – threading – molecular docking - Structure based drug design – molecular descriptors – QSAR.

Text Books

1. A.R.Leach, Molecular Modeling Principles and Application, 2nd Ed., Pearson, 2001.
2. R.K.Prasad, Quantum chemistry, Halsted Press, 2002.

11BI312 PATTERN RECOGNITION AND MACHINE LEARNING

Credits: 3:0:0

Course Objectives

This course will enable students to

- Know the concepts and applications of Machine Learning.
- Provide an insight to Machine Learning Technique before stepping into Artificial Intelligence and Mathematical Modeling.

Course Outcomes

- Students can understand and apply fundamental Machine Learning Techniques from theory to practical.
- Students develop enhanced critical and conceptual thinking and problem solving skills.

Unit I: Introduction

What is machine learning?, Example of Machine Learning Application, Polynomial Curve fitting, Probability Theory, Model Selection, The Curse of Dimensionality, Decision Theory, Information Theory.

Unit II: Bayesian Decision Theory

Introduction, Classification, Losses and Risk, Discriminant Functions, Utility Theory, Value of Information, Bayesian Networks, Influence Diagrams, Association Rules. Parametric Methods: Introduction, Maximum Likelihood Estimation, Evaluating an Estimator, The Bayes' Estimator, Parametric Classification, Regression, Tuning Model Complexity, Model Selection Procedures.

Unit III: Multivariate Methods and Clustering

Multivariate Data, Parameter Estimation, Estimation of Missing Values, Multivariate Normal Distribution, Multivariate Classification, Tuning Complexity, Discrete Features, Multivariate Regression. Clustering: Introduction, Mixture Densities, k-Means Clustering, Expectation-Maximization Algorithm, Mixtures of Latent Variable Models, Supervised Learning after Clustering, Hierarchical Clustering, Choosing the Number of Clusters.

Unit IV: Neural Network and Hidden Markov Model

Feed-forward Network Functions, Network Training, Error Back propagation, The Hessian Matrix, Regularization in Neural Networks, Mixture Density Networks, Bayesian Neural Networks. Hidden Markov Models: Introduction, Discrete Markov Processes, Hidden Markov Models, Three Basic Problems of HMMs, Evaluation Problem, Finding the State Sequence, Learning Model Parameters, Continuous Observations, The HMM with Input, Model Selection in HMM.

Unit V: Graphical Models

Bayesian Networks, Conditional Independence, Markov Random Fields, Inference in Graphical Models. Approximate Inference: Variational Inference, Illustration: Variational Mixture of Gaussians, Variational Linear Regression, Exponential Family Distributions, Local Variational Methods, Variational Logistic Regression, Expectation Propagation.

Text Books

1. Ethem Alpaydin, Introduction to Machine Learning, First Edition, MIT Press, 2004.
2. Christopher M. Bishop, Pattern Recognition and Machine Learning, First Edition, Springer, 2006.

11BI313 PYTHON FOR BIOINFORMATICS

Credits: 3:0:0

Course Objective

- This course teaches biologists how to use Python as a programming language to automate routine data management tasks in biological research and to solve difficult data-related computational problems.
- Data could be DNA or amino acid sequences, microarray data, images, mass spectrometry data, PDB data, or any other kind of biological information.

Course Outcomes

- It covers core data types, syntax, and functional programming, focusing on construction of programs from small, testable parts. Students will learn productive use of the Unix environment, focusing on Unix utilities (e.g., sort, uniq, grep) that are particularly useful in bioinformatics.
- The course will cover object-oriented programming, introduce analysis of algorithms and sequencing alignment methods, and introduce tools that are particularly useful in bioinformatics analysis, including R, BioPython, and Web services in bioinformatics.
- By the end of the class, students will have gained the ability to analyze data within the python interpreter and write well-documented, well-organized programs.

Unit I: Introduction

Strings- Lists- Dictionaries-Tuples- Files- Numeric type basic- Numbers in Action- Number extensions- Dynamic typing interlude- Shared References.

Unit II: Python in Statistics and Probability

Simple Statistics – average - standard deviation – distributions – normalization - multivariate statistics - Probabilities- Decisions from Distributions – correlations

Unit III: Sequence Alignment using Python

Alphabets – matching sequences- perfect matches- insertions and deletions- rearrangements- Global Vs. Local alignments- sequence length- simple alignment- direct alignment-statistical alignment, Brute Force alignment

Unit IV: Dynamic Programming using Python

Dynamic programming algorithm-the scoring matrix, the arrow matrix-extracting the Aligned sequences-Efficient programming- Global Versus Local alignments in Dynamic Programming- How Dynamic Programming can provide a good alignment.

Unit V: Microarray analysis using Python

gene expression array files-Raw data-GEL files- TIFF headers-the image file directory-reading the data- Spot finding – Intensity variations – block location-the coarse grid- fine-tuning the spot locations- spot measurement.

Text Books

1. Jason Kinser "Python for bioinformatics" First edition, Jones and Bartlett Publishers, 2009
2. Mark Lutz "Learning Python", Fourth Edition, O'REILLY Publication,2009

Reference book

Alex Martelli, David Ascher, Python cookbook, O'Reilly, 2002.

11BI314 GRAPH THEORY AND SYSTEM BIOLOGY

Credits: 3:0:0

Course Objectives

- This course helps them to understand the basic concept of graph theory to understand the network.
- The different algorithm related to Systems Biology and software used will be discussed in the course.

Course Outcome

- Students will understand the network properties and will be able to design their own network through systems biology software.

UNIT I: Graph Theory

Graphs-Graphs as models-connected graphs-k-connected graphs-2 connected graphs-connectivity of digraphs-k-connected and k-edge-connected graphs.

UNIT II: Basics of systems Biology

Introduction - Basic concepts in system Biology - Metabolic Networks- Transcriptional Regulatory Networks- Signaling Networks.

UNIT III: Modeling algorithms

Kinetic Modeling - Cellular Network reconstruction and Static Modeling - Construction and verification and verification of kinetic models- introduction to DBsolve - Enzyme Kinetics modeling.

UNIT IV: Modeling and simulation algorithms

Kinetic Models of Biochemical Pathways -Modeling Biochemical network - Kinetic Models of Excitable Membranes and Synaptic Interactions, Stochastic Simulation of Cell Signaling Pathways

UNIT V: Software's application in systems Biology

Statistical tools for gene expression analysis and system Biology- Software for modeling and simulation-The ERATO system biology work Bench, Cytoscape, Gepasi, and Cell Designer.

Text Books

1. Bernhard Q. Palsson, Systems Biology Properties of reconstructed networks, Publisher-Cambridge University Press, 2009
2. Oleg Demin and Igor Goryanin, Kinetic Modelling in Systems Biology, Publisher- CRC Press, 2009.

Reference Books

1. Hiroaki Kitano, Foundations of Systems Biology, MIT Press, 2001

2. Douglas B.West, Introduction to Graph Theory, Prentice-Hall India, 1996

11BI315 STRUCTURAL BIOINFORMATICS AND INSTRUMENTATION LAB

Credits 0:0:2

LIST OF PRACTICALS

1. The levels of protein structure.
2. The properties and composition of amino acids for different proteins.
3. The geometrical parameters for different proteins.
4. The Ramachandran diagram (Phi-Psi map) for different proteins.
5. Study and view the non-bonded interactions of proteins with/without ligands.
6. Study the protein data bank text files of one or two protein molecules.
7. The structural characteristics of different RNA molecules with/without protein.
8. The structural characteristics of different DNA molecules with/without protein.
9. The principle and working condition of X-Ray Diffractometer (demo).
10. Crystallization process for small and macro molecules (demo).
11. The principle and working condition of Electron Microscope (demo).

11BI316 MOLECULAR MODELING AND SIMULATION LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Molecular modeling – Small Molecule Databases
2. Molecular simulation of tripeptides and carbohydrate
3. ab initio structure prediction
4. Homology modeling/Comparative modeling
5. Energy minimization of biomolecules (1^{st} order and 2^{nd} order)
6. Molecular Dynamics simulation
7. Monte Carlo simulation
8. Visualization of Molecular Dynamics
9. Molecular Docking studies
10. Protein structure function relationship activity.

11BI317 MACHINE LEARNING LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Exercise for making Hypothesis and Model based on Probability theory.
2. Application of Bayesian Theory on the designed Model.
3. Application of Graph Theory for refining the Model.
4. Exercise on the Best Model Selection Procedures.
5. Designing of Model Based on Single Die.
6. Exercise for writing algorithms for solving basic Bioinformatics Problem.
7. Introduction to MATLAB.
8. Application of Fuzzy Logic concept.
9. Artificial Neural Network for Bioinformatics.
10. Practical Application of Bioinformatics Tools of MATLAB.

11. Application of Genetic Algorithm in Bioinformatics.
12. Problem Solving Based on Hidden Markov Model.

11BI318 PYTHON FOR BIOINFORMATICS LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Write a program to open the SWISSPROT sequence and find the length of the sequence.
2. Write a program to retrieve the PDB file from RCSB.
3. Write a program to open a file and read the X,Y and Z coordinates using PDB.
4. Write a program to calculate the bond length between two atoms using PDB.
5. Write a program to converting DNA sequences to Protein sequences.
6. Write a program to draw the plot using GnuPlot to find the average and deviations of ten samples.
7. Write a program to align two sequences using Direct Alignment method.
8. Write a program to align two sequences using Brute Force method.
9. Write a program to find scoring matrix
10. Write a program to find arrow matrix.
11. Write a program to open the file for reading in a binary format using the function ReadRawFile.
12. Write a program to read the data using the function ReadGEL.

11BI319 SYSTEM BIOLOGY AND SIMULATION LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Genomic tools for analyzing transcriptional regulatory networks
2. Essential gene identification
3. Diseased gene identification through GeneCards and Entrez Gene
4. Database analysis for protein-protein interaction
5. Microarray dataset analysis
6. Designing protein interaction through cell designer
7. Pathway analysis
8. Network creation and analysis
9. K-core analysis of the protein
10. Protein network simulation
11. Whole cell simulation through E-cell/V-cell
12. Statistical tool for gene expression analysis

11BI320 CHEMINFORMATICS

Credits: 4:0:0

Course Objective

- The course objectives are to introduce different methods of cheminformatics with particular emphasis on applications including modern drug discovery.

Course Outcomes

- The course will introduce the students preparing for professional work in chemistry must learn how to retrieve specific information from the enormous and rapidly expanding chemical literature.
- The course will provide a broad overview of the computer technology to chemistry in all of its manifestations
- The course will expose the student to current and relevant applications in QSAR and Drug Design.

UNIT I: Introduction to Cheminformatics
Introduction to cheminformatics, History and Evolution of cheminformatics, Use of cheminformatics, Prospects of cheminformatics, Molecular Modeling and Structure Elucidation

UNIT II: Representation of Molecules and Chemical Reactions
Nomenclature; Different types of Notations; SMILES coding; Matrix Representations; Structure of Molfiles and Sdfiles; Libraries and toolkits; Different electronic effects; Reaction classification

UNIT III: Searching Chemical Structure
Full structure search; sub structure search; basic ideas; similarity search; Three dimensional search methods; Basics of Computation of Physical and Chemical Data and structure descriptors; Data visualization.

UNIT IV: Computer Assisted Virtual screening design
Structure Based Virtual Screening- Protein Ligand Docking, Scoring Functions for Protein Ligand docking, Practical aspects of structure based Virtual Screening; Prediction of ADMET Properties, 2 D and 3D data searching, Chemical databases, Role of computers in Chemical Research.

UNIT V: Application of Cheminformatics in Drug Design
Quantitative Structure-Property Relations; Descriptor Analysis; Computer Assisted Structure elucidations; Target Identification and Validation; Lead Finding and Optimization; Analysis of HTS data; Design of Combinatorial Libraries; Ligand-Based and Structure Based Drug design

Text Book

1. Andrew R. Leach, Valerie J. Gillet, Cluwer , Introduction to Cheminformatics, Academic Publisher, Netherlands, 2003

Reference Books

1. Lisa B. English (Editor), Combinatorial Library Methods and Protocols, Humana Press Inc, Volume:201, 2002
2. Frank Jensen, Introduction to Computational Chemistry, Wiley Publisher, Second Edition, 2006

11BI321 MEDICAL INFORMATICS

Credits: 3:0:0

Course Objectives

- This subject gives the students an idea on the applications of information technology and math's in medical field.

Course Outcomes

- Overview of medical informatics as a discipline.
- Skills and concepts fundamental to more advanced topics in health informatics, including (but not limited to): a. Computer science, b. Decision analysis and c. Evaluation and technology assessment

INIT I: Introduction

Introduction- Hospital management and information system: functional area- pre-requisites- integrated hospital information systems- health information system- and disaster management plan

UNITII: Knowledge based and Expert systems

Artificial intelligence- expert systems- materials and methods- computer based patient Records- computer assisted medical education, modern medical equipments (Digital X-ray etc.).

UNITIII: Modules

Hospital Management and Information systems- structure and functions- computer assisted patient education, computer assisted patient surgery

UNIT IV: Computer assisted surgical techniques

Three-dimensional imaging: limitations of endoscopy and imaging- benefits of virtual endoscopy- materials and methods- limitations- applications- merits and demerits- surgical simulation- virtual environment

UNIT V: Telecommunication based systems

Tele-medicine- needs- materials and methods- Internet tele-medicine- controversial issues- reliability- cost analysis- applications- tele-surgery- the Internet, Database of medical informatics

Text Books

1. Mohan Bansal, Medical Informatics- a primer, Tata McGraw-Hill, 2003.
2. Charles P. Friedman, Jeremy C. (EDT) Wyatt, Evaluation Methods in Medical Informatics- Springer-Verlag, 1997.

Reference Books

1. Hsinnchun Chen, Medical Informatics: Knowledge Management and Data Mining in Biomedicine, Springer, 2005.
2. F. T. De Dombal, Medical Informatics: The Essentials, Butterworth-Heinemann, 1996.

11BI322 ENZYME ENGINEERING

Credits: 3:0:0

Course Objective

This course will enable students to

- Understand the concepts in enzymology and enzyme techniques

Course Outcomes

- Students will have clear understanding in isolation, purification and characterization of enzymes

- Understand the enzyme engineering technologies

Unit I: Applications of Enzymes
Classification of Enzymes; Purification and characterization of enzymes from natural sources Comparison of chemical and enzyme catalysis.

Unit II: Isolation of Enzymes:
Extraction and Purification of Crude Enzyme extracts from plant, animal and microbial sources-some case studies; methods of characterization of enzymes; development of enzymatic assays.

Unit III: Mechanisms and Kinetics of Enzyme Action
Mechanisms of Enzyme Action; Concept of active site and energetics of enzyme substrate complex formation; Specificity of enzyme action; Kinetics of single substrate reactions; turnover number; estimation of Michaelis-Menton parameters. Multi-substrate reaction mechanisms and kinetics.

UNIT IV: Enzyme Inhibition
Types of Inhibition- kinetic models; Substrate and Product Inhibition; Allosteric regulation of enzymes; Deactivation kinetics.

Unit V: Enzyme Immobilization
Physical and Chemical techniques for enzyme Immobilization - adsorption. matrix entrapment, encapsulation. cross-linking. covalent binding - examples; Advantages and disadvantages of different Immobilization techniques. overview of applications of immobilized enzyme systems.

Text book
1. Trevor palmer, Understanding Enzymes, East West Press, 2004

Reference
1. Colin Ratledge and Bjorm Kristiansen , Basic Biotechnology, Third edition, Cambridge University Press, 2002

11BI323 MICROARRAY AND IMAGE PROCESSING

Credits: 3:0:0

Course Objectives
This course will enable students to

- Understand the micro array concepts and apply the technical field of genomics and applied biological research.
- Provide a high throughput novel prediction to molecular and genomic science and techniques to identify the problems through the computational technology.

Course Outcomes
- Students can understand and apply fundamental micro array principles from theory to lab
- Students can enhance critical technical thinking and grow with problem solving skills.

Unit I: DNA Microarray

DNA array formats, DNA array readout methods, Gene expression profiling experiments: Problems, pitfalls, and solutions, Statistical analysis of array data: Inferring changes, Statistical analysis of array data: Dimensionality reduction, clustering, and regulatory regions

Unit II: Microarray Measurements to Analyses

Generic Features of Microarray Technologies, Replicate Experiments, Reproducibility, and Noise, Prototypical Objectives and Questions in Microarray Analyses, Preprocessing: Filters and Normalization

Unit III: Genomic Data−Mining Techniques

Hierarchy of Bioinformatics Algorithms Available in Functional Genomics, Data Reduction and Filtering, Self−Organizing Maps, Finding Genes That Split Sets, Phylogenetic−Type Trees, Relevance Networks, Determining the Significance of Findings, Genetic Networks

Unit IV: Image Analysis.

Gridding, Segmentation, Intensity Extraction, Background Correction, Software, Foreground Intensity Extraction, Background Correction, Image Output File, Image Analysis for Affymetrix GeneChipTM

Unit V: Quality Control

Probe-Level Quality Control for Two-Color Arrays, Gene Level Quality Control for Two-Color Arrays, Array-Level Quality Control for Two-Color Arrays, Quality Control for GeneChipTM Arrays, Data Imputation.

Text books

1. Pierre Baldiand g. Wesley Hatfield, DNA microarrays and gene expression From experiments to data analysis and modeling, Cambridge University press, New York,2002
2. Richard M. Simon Edward L. Korn, Design and Analysis of DNA Microarray Investigations, Springer Berlin Heidelberg New York. 2003
3. Isaac S. Kohane, Alvin Kho, Atul J. Butte, Microarrays for an Integrative Genomics, MIT Press, 2005.

Reference Book

1. Mark Schena, Steen Knudsen, Guide to Analysis of DNA Microarray Data, 2nd Edition John Wiley & Sons, 2004

11BI324 SUPPORT VECTOR MACHINE

Credits: 3:0:0

Course Objectives

This course will enable students to

- Know the concepts and applications of Support Vector Machine.
- Provide an insight to Support Vector Machine Technique before stepping into Artificial Intelligence and Mathematical Modeling.

Course Outcomes

- Students can understand and apply fundamental Support Vector Machines Techniques from theory to practical.

- Students develop enhanced critical and conceptual thinking and problem solving skills.

Unit I: Introduction and Loss Function
Statistical Learning, Support Vector Machines: An Overview, History of SVMs and Geometrical Interpretation, Alternatives to SVMs. Loss Functions: Definition and Examples, Basic Properties of Loss Functions and Their Risks, Margin-Based Losses for Classification Problems, Distance-Based Losses for Regression Problems.

Unit II: Surrogate Loss Functions
Inner Risks and the calibration Function, Asymptotic Theory of Surrogate Losses, Inequalities between Excess Risks, Surrogates for unweighted Binary Classification, Surrogates for Weighted Binary Classification, Template Loss Functions, Surrogate Losses for Regression Problems, Surrogate Losses for the Density Level Problem, Self-Calibrated Loss Functions.

Unit III: Kernels and Reproducing Kernel Hilbert Spaces
Basic properties and Example of Kernels, The Reproducing Kernel Hibert Space of a Kernel, Properties of RKHSs, Gaussian Kernels and Their RKHSs, Mercer's Theorem, Large Reproducing Kernel Hilbert Spaces. Existence and Uniqueness of SVM Solutions, A General Representer Theorem, Stability of Infinite-Sample SVMs, Behavior for Small Regularization Parameters, Approximation Error of RKHSs.

Unit IV: Basic Statistical Analysis of SVMs
Notions of Statistical Learning, Basic Concentration Inequalities, Statistical Analysis of Empirical Risk Minimization, Basic Oracle Inequalities for SVMs, Data-Dependent Parameter Selection for SVMs, Why Do We Need a Refined Analysis, A Refined Oracle Inequality for ERM, Some Advanced Machinery, Refined Oracle Inequalities for SVMs, Some Bounds on Average Entropy Numbers.

Unit V: Support Vector Machines for Classification
Basic Oracle Inequalities for Classifying with SVMs, Classifying with SVMs Using Gaussian Kernels, Advanced Concentration Results for SVMs, Sparseness of SVMs Using Hinge Loss, Classifying with other Margin-Based Losses. Support Vector Machine for Regression: Introduction, Consistency, SVMs for Quantile Regression, Median Regression with the eps-Insensitive Loss.

Text Book

1. Ingo Steinwart, Andreas Christmann, Support Vector Machines, Second Edition, Springer, 2008.

11BI325 WEB PROGRAMMING FOR BIOINFORMATICS

Credits: 3:0:0

Course Objective

- Enabling the student to build and manage web applications.
- Learning advanced html to optimize the web browsers.
- To build XML applications with DTD's.
- Learning common gateway interface and Perl scripting languages for web development.

Course Outcome

- The students would learn to design, develop and manage web applications in bioinformatics**.**

UNIT I: HTML
Introduction – Web pages and html – overview of html – Working with text – formatting with html tags – physical and logical styles – setting fonts – headings – presenting and arranging text – working with images – graphic formats –using clip art - creating images – link and lists – creating hyperlinks - creating lists – creating a table.

UNIT II: Advanced HTML
Working with frames – creating vertical and horizontal frames – working with style sheets – external and embedded style sheets –html document life cycle - advanced html – optimizing web page for internet explorer – embedding java script in html.

UNIT III: XML-I
Introduction – xml – xml applications – xml document - life of an xml document – structuring data - examining the data - xmlizing the data – the advantages of xml format – attributes – empty tags - XSL

UNIT IV: XML -II
Document type definition – document type declaration – validating against DTD – element declarations – entity declaration –internal general entities – external general entities – attribute declaration- declaring attributes in DTD's –declaring multiple attributes – attribute types – embedding non-xml data.

UNIT V: PERL AND CGI
Introduction – Perl and CGI – setting up GCI on Unix – apache – starting apache server-stopping apache server – writing CGI scripts – basic CGI – writing interactive CGI scripts.

Text Books
1. Steven Holzner , HTML, Dreamtech press, Reprint Edition 2008.
2. Elliotte Rusty Harold, "XML Bible", Second Edition, IDG Books India (P) Ltd, 2003,

Reference Books
1. Simon Cozens and Peter Wainwright, Beginning Perl, Shroff publishers, 2005
2. Reference book on HTML Complete, BPB publications, Second edition 2000.

11BI326 CHEMINFORMATICS LAB

Credits: 0:0:2

LIST OF PRACTICALS
1. Sketching the chemical reaction and calculate the properties
2. Sketching the small molecules
3. Small molecule search database
4. Optimization and minimization of small molecules
5. Calculation of physiochemical property
6. Overview of macromolecules and their interaction with micro molecules
7. Protein ligand Docking
8. Prediction of ADME properties
9. 2D QSAR based upon physiochemical properties
10. 3D QSAR based upon atomic orientation

11. Validation of QSAR model

11BI327 MEDICAL INFORMATICS LAB

Credits: 0:0:2

LIST OF PRACTICAL

1. Collect the patient data through internet.
2. Analysis the data
3. Collect the new forms of clinical information
4. Electronic Health Record analysis
5. Find the doctor using of information sources
6. How to apply Probability in health informatics data.
7. Use truth tables in medical informatics data
8. Apply predicate calculus in medical bioinformatics
9. Hospital Management and Information systems
10. Statistical hypothesis testing in Medical informatics

11BI328 ENZYME ENGINEERING LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Estimation of Acid Phosphatase from potato
2. Kinetic studies - Effect of pH on the activity of acid phosphatase
3. Kinetic studies - Effect of Temperature on the activity of acid phosphatase
4. Kinetic studies - Effect of substrate concentration on the activity of acid phosphatase
5. Kinetic studies - Effect of enzyme concentration on the activity of acid phosphatase
6. Estimation of Alkaline phosphatase from cucumber
7. Estimation of Urease from horse gram
8. Estimation of amylase from saliva
9. Estimation of serum SGPT (Kit method)
10. Estimation of serum SGOT (Kit method)
11. Isoenzyme analysis of Lactate Dehydrogenase
12. Enzyme immobilization- Entrapment in polyacrylamide gel

11BI329 MICROARRAY AND IMAGE PROCESSING LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Exercises protein sequence analysis using MATLAB
2. Exercises on Spatial Images of Microarray Data
3. Exercises on scatter plots of microarray data Analysis
4. Exercises on an example of gene expression profile analysis
5. Exercises on Quality assessment
6. Exercises on Normalization
7. Exercises on filtering, clustering gens
8. Micro array class prediction using ANN

9. Micro array Decision tree analysis and prediction
10. Genomic signal processing: from matrix algebra to genetic networks

11BI330 VECTOR MACHINE LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Introduction to SVM light.
2. Solving the classification and regression problems.
3. Solving ranking problems.
4. Computing XiAlpha-estimates of the error rate, the precision, and the recall.
5. Computing Leave-One-Out estimates of the error rate, the precision, and the recall.
6. Training large transductive SVMs (TSVMs).
7. Training SVMs with cost models and example dependent costs
8. assessing the generalization performance
9. SVM learning for multivariate and structured outputs like trees, sequences, and sets
10. Using the MATLAB Interface of SVM light

11BI331WEB PROGRAMMING LAB

Credits: 0:0:2

LIST OF PRACTICALS

1. Working with HTML – A simple web page
2. Web page - Presenting and Arranging text.
3. Working with images.
4. Working with hyper link and lists.
5. Web page with tables.
6. Working with frames.
7. Creating simple web page using XML.
8. Usage of database in XML.
9. Working with XML and XSL
10. Web page with animations effects.
11. Web page with applet.
12. CGI scripting with Perl

DEPARTMENT OF BIOINFORMATICS

LIST OF SUBJECTS AND SYLLABI

Sub. Code	Name of the Subject	Credits
12BI201	Intermediary Metabolism and Bioenergetics	4:0:0
12BI202	Basics of Bioinformatics	4:0:0
12BI203	Cell Biology and Microbiology	3:0:0
12BI204	Introduction to Bioinformatics Algorithms	3:0:0
12BI205	Instrumental Methods of Analysis	3:0:0
12BI206	Analytical Biochemistry Lab	0:0:2
12BI207	Cell Biology and Microbiology Lab	0:0:2
12BI208	Biological Sequence Analysis Lab	0:0:2
12BI209	Basics of Chemical Engineering	3:0:0
12BI210	Molecular Biology and Genetic Engineering	4:0:0
12BI211	Bioorganic Chemistry	3:0:0
12BI212	Data Structure and C++ Programming	3:0:0
12BI213	Molecular Biology and Genetic Engineering Lab	0:0:2
12BI214	Datamining Lab	0:0:1
12BI215	Computational Chemistry Lab	0:0:1
12BI216	C++ Programming lab	0:0:2
12BI217	Biophysics and Structural Biology	4:0:0
12BI218	Genomics and Proteomics	3:0:0
12BI219	PERL Programming	3:0:0
12BI220	Immunology and Immunoinformatics	3:0:0
12BI221	Database Management System	3:0:0
12BI222	Introduction to Unix and Linux	3:0:0
12BI223	Database Management System Lab	0:0:1
12BI224	Unix and Linux Lab	0:0:1
12BI225	PERL Lab	0:0:2
12BI226	Immunology and Immunoinformatics Lab	0:0:2
12BI227	Java Programming	3:0:0
12BI228	Molecular Modeling and Drug Design	4:0:0
12BI229	Molecular Evolution and Phylogeny	3:0:0
12BI230	Bioethics, IPR and Biosafety	3:0:0
12BI231	Systems Biology	3:0:0
12BI232	Machine Learning in Bioinformatics	3:0:0
12BI233	Java Programming Lab	0:0:1
12BI234	Systems Biology Lab	0:0:1
12BI235	Molecular Modeling Lab	0:0:2
12BI236	Computational Biology Lab	0:0:2
12BI237	Cheminformatics	3:0:0
12BI238	Pharmacogenomics	3:0:0
12BI239	Biopharmaceutical Technology	3:0:0
12BI240	Clinical Data Management	3:0:0

12BI241	Computer Aided Drug Design Lab	0:0:2
12BI242	Clinical Data Management Lab	0:0:2
12BI243	R Programming	3:0:0
12BI244	Web Programming	3:0:0
12BI245	Kernel Based Data Fusion Methods	3:0:0
12BI246	Python Programming	3:0:0
12BI247	Web Programming Lab	0:0:2
12BI248	Python Programming Lab	0:0:2
12BI249	Protein Engineering	3:0:0
12BI250	Plant Tissue Culture	3:0:0
12BI251	Bioprocess Technology	3:0:0
12BI252	Medical Informatics	3:0:0
12BI253	Plant Tissue Culture Lab	0:0:2
12BI254	Medical Lab Technology	0:0:2
12BI255	Biological Databases	3:0:0
12BI256	Molecular Simulation and Engineering	3:0:0
12BI257	Computer Aided Drug Design	3:0:0
12BI301	Molecular Cell Biology	4:0:0
12BI302	Computational Genome and Proteome Analysis	3:0:0
12BI303	Bioinformatics Algorithms	3:0:0
12BI304	Advanced PERL and BioPERL	3:0:0
12BI305	Molecular Cell Biology Lab	0:0:2
12BI306	Computational Genome and Proteome Analysis Lab	0:0:2
12BI307	Bioinformatics Algorithms Lab	0:0:2
12BI308	Advanced PERL Lab	0:0:2
12BI309	Structural Bioinformatics and Instrumental Techniques	3:0:0
12BI310	Molecular Modeling and Simulation	4:0:0
12BI311	Pattern Recognition and Machine Learning	4:0:0
12BI312	Microarray and Image Processing	4:0:0
12BI313	Graph Theory and Systems Biology	3:0:0
12BI314	Structural Bioinformatics and Instrumentation Lab	0:0:2
12BI315	Molecular Modeling and Simulation Lab	0:0:2
12BI316	Machine Learning in Bioinformatics Lab	0:0:2
12BI317	Microarray Data Analysis lab	0:0:2
12BI318	Systems Biology and Simulation Lab	0:0:2
12BI319	Cheminformatics and QSAR	3:0:0
12BI320	Medical Informatics	3:0:0
12BI321	Enzyme engineering	3:0:0
12BI322	Cheminformatics lab	0:0:2
12BI323	Medical Informatics lab	0:0:2
12BI324	Enzyme engineering lab	0:0:2
12BI325	Python for Bioinformatics	3:0:0
12BI326	Support Vector Machine	3:0:0
12BI327	Web Technologies for Bioinformatics	3:0:0
12BI328	Python for Bioinformatics lab	0:0:2
12BI329	Support Vector Machine lab	0:0:2

12BI330	Web Technologies for Bioinformatics lab	0:0:2

12BI201 INTERMEDIARY METABOLISM AND BIOENERGETICS

Credits: 4:0:0

Course Objective:

- To get knowledge in intermediary metabolism and its regulation.

Course Outcome:

- Students will get an overview of metabolism, bioenergetics and hormonal regulation.

Unit I

METABOLISM OF CARBOHYDRATES AND LIPIDS: Glycolysis, Oxidation of pyruvate, Pentose phosphate pathway, TCA cycle, Gluconeogenesis, Glycogen metabolism, Glycogen storage diseases. Lipid metabolism – Oxidation of fatty acids (beta oxidation and Ketone bodies formation), Biosynthesis of fatty acid, triacyl glycerol, cholesterol and steroids - Lipids transport and storage.

Unit II

METABOLISM OF PROTEINS AND NUCLEIC ACIDS: Protein degradation, Nitrogen metabolism, Biosynthesis and degradation of important aminoacids (Leu, Tyr,Phe, Trp, Cys), Urea cycle. Molecules derived from aminoacids – porphyrins , biological amines, bile pigments. Biosynthesis and degradation of nucleic acids – denova and salvage pathway. Inborn errors of metabolism.

Unit III

BIOENERGETICS: Concept of free energy, Role of ATP and other high energy phosphates in energy capture and transfer. Biological oxidation - Redox potential, Enzymes in oxidation reduction process. Respiratory chain and Oxidative phosphorylation – Chemi-osmotic theory (an outline).

Unit IV

HORMONAL REGULATION AND SIGNAL TRANSDUCTION: Types of signalling – autocrine, paracrine and endocrine. Signal transduction - Mechanism of action of steroid hormones, Signaling by catecholamines – G proteins, cAMP, cGMP and Protein kinases. Hormones acting through calcium or phosphatidyl inositols.

Unit-V

ENZYMES: Enzyme – Introduction, substrate specificity, Coenzymes, Rate of enzymatic reactions- chemical kinetics, inhibition, effect of pH, bisubstrate reactions, Michaelis menton equation.

Text book

1. Lehninger A. L, Nelson D. L. and Cox M. M, “Principles of Biochemistry”, Freeman Publishers, New York. 3rd Edition, 2000.

Reference books

1. Murray R. K, Granner B.K, Mayes P.A, Rodwell V.W, “Harper’s Biochemistry”, Prentice Hall International, New Delhi, 2000
2. Lubert Stryer, “Biochemistry”, WH Freeman and Co, New York, 4th Edition, 2000.

12BI202 BASICS OF BIOINFORMATICS

Credits: 4:0:0

Course Objective:

- This course provides the necessary basic protocols in computers and various biological databases.
- It consists of the tools used for biological sequential data analysis and methods of analyzing genetic and protein information.

Course Outcome:

- Know the basic essential tools in bioinformatics and implementation.
- Familiar with the available biological database resources and analysis.
- Serves as input to other courses in the B.Tech Bioinformatics curriculum.

Unit I

INTRODUCTION TO BIOINFORMATICS: Scope of Bioinformatics – Elementary commands and Protocols, ftp, telnet, http. Databanks – nucleotide databanks – Genbank, NCBI, EMBL, DDBJ – protein databanks – sequence databanks – PIR, SWISSPROT, TrEMBL - structural databases – PDB, SCOP, CATH.

Unit II

SEQUENCE ALIGNMENT AND DYNAMIC PROGRAMMING: Introduction – Strings – Edit distance two strings – string similarity - local alignment - gaps – Parametric sequence alignments – suboptimal alignments – multiple alignment – common multiple alignment methods.

Unit III

SEQUENCE DATABASES AND THEIR USES: Database search – Algorithms issues in database search – sequence database search – FASTA – BLAST – Amino acid substitution matrices PAM250 and BLOSUM62. GCG Sequence Analysis(Basic concepts only).

Unit IV

MOLECULAR PREDICTION: Gene prediction methods and evaluation – Gene prediction in microbial genome and eukaryotes - Molecular predictions with DNA strings – Protein secondary structure prediction methods.

Unit V

RNA SECONDARY STRUCTURE PREDICTION: Feature of RNA secondary structure – development of RNA prediction methods – Self complementary regions – Minimum free energy method – MFOLD – Sequence covariation – Applications of RNA structure prediction.

Text Books

1. Dan Gusfield, "Algorithms on Strings Trees and Sequences", Cambridge University Press, Cambridge, 2005.
2. David Mount W., "Bioinformatics sequence and genome analysis", CBS Publishers, New Delhi, 2nd Edition, 2005.

Reference Books

1. Attwood T. K. and Parry-Smith D., "Introduction to Bioinformatics", Pearson Education, Delhi, 2001.
2. Arthur Lesk M, "Introduction to Bioinformatics", Oxford University Press, New Delhi, 2003.

12BI203 CELL BIOLOGY AND MICROBIOLOGY

Credits: 3:0:0

Course Objective:

- To understand the structure and organization of cells.
- To get an overview of microbial systems.

Course Outcome:

- Will understand cell and its function, regulation of cell division.
- Will get fundamental knowledge in microbiology.

Unit I

BIOLOGY OF CELLS: Structure of prokaryotic and eukaryotic cells - Overview of organelles (Mitochondria, Chloroplasts, ER, Golgi, nucleus). Protein folding and processing in ER - Protein glycosylation and sorting in Golgi - Cytoskeletal proteins - contractile proteins – Actin and Myosin.

Unit II

TRANSPORT ACROSS CELL MEMBRANES: Organization of plasma membrane - Passive and active transport, Sodium potassium pump - Ca^{2+} ATPase pump - Lysosomal and vacuolar membrane, ATP dependent proton pumps - co transport, symport, antiport, ion-gated and ligand gated channels - Endocytosis and exocytosis.

Unit III

REGULATION OF CELL CYCLE AND CANCER: Cell division- mitosis and meiosis - Cell cycle and regulation - Cancer- types, development and causes – Mutagenesis - Tumor suppressor genes and Oncogenes.

Unit IV

MICROBIAL SYSTEMS: Classification and nomenclature of micro organisms - light and electron microscopy - principle of different staining techniques - gram staining - acid fast and capsular staining, Physical and chemical control of microorganisms - Microbial biosensors.

Unit V

MICROBIAL NUTRITION, GROWTH AND METABOLISM: Nutritional requirements of bacteria and different media used for bacterial culture - growth curve and different methods to quantitate bacterial growth - aerobic and anaerobic bioenergetics - utilization of energy for biosynthesis of important molecules.

Text Book

1. Verma P. S. and Agarwal V. K., “Cell Biology, Genetics and molecular Biology”, S. Chand and company, New Delhi, 2000.

Reference Books

1. Pelzer M. J., Chan E.C.S. and Krein N.R., “Microbiology”, Tata Mc Graw Hill Publishers, New Delhi, 2000.
2. Lodish H., Bert A., Matsudaria Kaiser C.A., Kriegar M., Scott M.P., Zipursky S.L. and Darnell J., “Molecular cell Biology”, WH Freeman and company, New York, 5th edition, 2004.

12BI204 INTRODUCTION TO BIOINFORMATICS ALGORITHMS

Credits: 3:0:0

Course Objectives:

- This course helps the students to understand the basic concept of various algorithm used in Bioinformatics.
- The different algorithm related to Protein structure, Sequence analysis will be discussed in this course.

Course Outcome:

- Students will understand the application of algorithms in different areas of Bioinformatics.

Unit I

ARTIFICIAL INTELLIGENCE AND COMPUTER SCIENCE: Introduction - Search algorithms, Heuristic search methods, Optimal search strategies, Problems with search techniques, Complexity of search, Use of graphs in bioinformatics.

Unit II

NEAREST NEIGHBOR AND CLUSTERING APPROACHES: Introduction – Nearest neighbor method, Nearest neighbor approach for secondary structure protein folding prediction, Clustering, Advanced clustering techniques.

Unit III

PREDICTIVE METHODS USING PROTEIN SEQUENCES: Introduction- Protein identity based on composition- AACompIdent and AACompSim, Propsearch, MOWSE, physical properties based on sequence- ComputepI/MW and ProtParam, PeptideMass, Motifs and Patterns, Conserved Domain Database.

Unit IV

GENETIC ALGORITHM: Single- objective genetic algorithms–method and example, Multi-objective genetic algorithms–method, Application guidelines, Genetic algorithms–bioinformatics applications.

Unit V

NEURAL NETWORK: Method- Supervised learning, Unsupervised learning, Application guidelines, Bioinformatics applications- Identifying protein subcellular location, Bioinformatics servers using neural network.

Text Book

1. Edward K and Ajit N, "Intelligent Bioinformatics- The Application of Artificial Intelligence techniques to Bioinformatics problems", John Wiley and Sons, USA, 2005.

Reference Book

1. Andreas D. B and Ouellette B. F. F, "Bioinformatics- A practical Guide to analyze Genes and Proteins", John Wiley and Sons, USA, 2001.

12BI205 INSTRUMENTAL METHODS OF ANALYSIS

Credits: 3:0:0

Course Objective:

- To study the definitions, preparations of buffering systems and its application,
- To explain the principles and applications of the important instruments used in biology.

Course Outcome:

- The student will learn about the definitions, preparations of buffering systems and its application.
- They will learn the principles and working condition of instruments and techniques to analyze biological samples.

Unit I

BUFFER SOLUTIONS: Definitions, preparations, derivation of Henderson-Hasselbalch equation and its application, buffering systems of blood, determination of pH using glass electrode, calibration of instruments, signal to noise ratio.

Unit II

COLORIMETER, FLOURIMETER, FLAME PHOTOMETER AND SPECTROPHOTOMETER: Beer - Lambert's law and its applications, Principle, description and application of Colorimeter, Flourimeter, Flame photometer and Spectrophotometer: UV and visible, FTIR, Raman spectroscopy.

Unit III

CHROMATOGRAPHY AND ELECTROPHORESIS: Chromatography – principles, types – paper, thin layer, adsorption, ion-exchange, affinity, gel filtration, GC and HPLC.

Electrophoresis – principles, types – disc, Isoelectric focussing, immuno-electrophoresis, supporting materials – paper, starch, agarose, polyacrylamide.

Unit IV
RADIO ACTIVE TECHNIQUES: Radioactive isotopes, radioactive decay and their types, radioactive techniques – RIA, GM counter, Scintillation counter and Autoradiography.

Unit V
THERMO ANALYTICAL TECHNIQUES: Theory of thermal analysis- Thermo gravimetry - Basic theory, construction and working of Differential Thermal Analysis (DTA) and Differential Scanning Calorimeter (DSC).

Text Book

1. Willard H. H, Merrit L.L., Dean J. A. and Settle F. A. "Instrumental Methods of Analysis". CBS Publishers and Distributors Pvt Ltd, New Delhi, 7th Edition, 1992.

Reference Book

1. Skoog D. A, Holler E. J. and Nieman T. A., "Principles of Instrumental Analysis", Harcourt Asia Pte Ltd, Delhi, 2000.

12BI206 ANALYTICAL BIOCHEMISTRY LAB

Credits: 0:0:2

1. Qualitative analysis of carbohydrates
2. Estimation of glucose by Glucose oxidase method
3. Qualitative analysis of amino acids
4. Estimation of protein by Lowry's method
5. Estimation of DNA
6. Estimation of amino acid by ninhydrin method
7. Assay of Acid phosphatase enzyme in potato extract
8. Estimation of cholesterol by Zak's method
9. Identification of amino acids by paper chromatography
10. Identification of sugars by paper chromatography
11. Conductometric titration
12. Determination of turbidity by nephelometry
13. Gas chromatography study (demo)
14. High Performance Liquid Chromatography Study (demo)

12BI207 CELL BIOLOGY AND MICROBIOLOGY LAB

Credits: 0:0:2

1. Culture Media – Types and Preparation of Agar medium and Nutrient Broth
2. Microscopy
3. Microscopical identification of cells in permanent fixed slides

4. Differentiation of blood cells using giemsa staining
5. Separation of peripheral blood mononuclear cells and trypan blue assay for live cells
6. Osmosis and tonicity studies using red blood corpuscles
7. Staining for various stages of mitosis in Allium cepa (Onion)
8. Sterilization and disinfection
9. Inoculation of microorganisms
10. Isolation of pure culture by streak plate technique
11. Gram staining
12. Spore staining
13. Negative staining
14. Phenol coefficient test
15. Motility test- Hanging drop method and soft agar inoculation

12BI208 BIOLOGICAL SEQUENCE ANALYSIS LAB

Credits: 0:0:2

1. Biological databases
2. EMBOSS.
3. Fasta analysis
4. BLAST analysis
5. Protein sequence analysis using GCG software
6. Pairwise comparison using GCG software
7. Gene finding and pattern recognition using GCG software
8. Multiple alignment using GCG software
9. Sequence utilities, Translation and nucleic acid secondary structure using GCG
10. Database reference searching and database sequence searching using GCG software
11. Evolutionary analysis using GCG
12. Enzyme analysis using GCG software.

12BI209 BASICS OF CHEMICAL ENGINEERING

Credits: 3:0:0

Course Objective:

- This course is intended to provide a clear overview of the field of chemical engineering.

Course Outcome:

- The students can gain basics of chemical engineering principles applied in Biotechnology and biochemical engineering.
- Throughout the course, students will develop basic skills in problem solving, computation, process design, and communication that will help them in all future engineering courses.

Unit I

PROCESS CALCULATIONS: Basic units and dimensions. Basics gas calculations-mole, mole percentage, weight, weight percentage, molarity, normality - Ideal gas laws - Material balance, energy balance.

Unit II

FLUID MECHANICS: Concept of fluid, types of fluid, properties of fluid, fluid flow, fluid flow pattern, flow control, fluid flow measurements and transportation of fluid.

Unit III

UNIT OPERATIONS: Concept of unit operations, heat transfer – modes of heat transfer, equipments – heat exchanger (double pipe, shell and tube, plate type), LMTD, heat transfer coefficients, basic concepts of filtration.

Unit IV

MASS TRANSFER OPERATIONS: Diffusion in fluids – molecular and eddy diffusion, concept of NTU and HTU, Distillation- concept, types, design calculation – Mc Cabe Thiele method, poncho savant method, Basic concepts of drying.

Unit V

CHEMICAL REACTION ENGINEERING: Law of mass action, rate equation, order of reaction, performance equation for CSTR, PFR. Types of reactions and reactors - definition of space time, mean residence time.

Text Books

1. Bhatt B.I. and Vora S.M. “Stoichiometry”, Tata McGraw-Hill Pub. Ltd., New Delhi, 2004.
2. Mccabe, W.L and Smith J.C., “Unit Operations in Chemical Engineering”, McGrawHill, New Delhi, 7th Edition, 2006.

Reference Books

1. Octave levenspiel, “Chemical reaction engineering”, John Wiley, New Jersey, 5th edition, 2006.
2. Himmelblau D.M., “Basic Principles and Calculations in Chemical Engineering”, Prentice-Hall of India Pvt. Ltd., New Delhi, 6th Edition, 2004.
3. Felder R.M. and Rousseau R.W., “Elementary Principles of Chemical Processes”, John Wiley and Sons, New Jersey, 3rd Edition, 2000.

12BI210 MOLECULAR BIOLOGY AND GENETIC ENGINEERING

Credits: 4:0:0

Course Objective:

- To understand the basics of Molecular Biology and Genetic engineering.

Course Outcome:

- Students understand the fundamental concepts in Genetics, Molecular biology and recombinant DNA technology.

Unit I

MOLECULAR GENETICS: DNA as genetic material - classical experiments – Hershey and chase; Avery McLeod and McCarty. Bacterial conjugation - transduction and transformation - Types of Mutation.

Unit II

REPLICATION AND TRANSCRIPTION: Replication in prokaryotes and eukaryotes – D loop and rolling circle mode of replication. Transcription: initiation – elongation - termination, features of promoters and enhancers - transcription factors – inhibitors - post-transcriptional modification - RNA splicing, RNA editing.

Unit III

TRANSLATION: Genetic code, Process of translation in prokaryotes and eukaryotes, Post-translational modifications, Regulation of gene expression - Lac and trp operons.

Unit IV

RECOMBINANT DNA TECHNOLOGY: DNA cloning, vectors, restriction enzymes**,** Construction of cDNA and genomic libraries. Screening of libraries with probes – Northern, Southern and Western blotting. PCR- Principle, application and types. RAPD, Site Directed Mutagenesis, Restriction mapping.

Unit V

APPLICATIONS OF RECOMBINANT DNA TECHNOLOGY: Cloning in plants-transgenic and knockout animals. Recombinant cytokines and antibodies, vaccines, gene therapy, stem cell therapy, Invitro fertilization, embryo transfer technology.

Text Books

1. Primrose S.B. and Twyman, "Principles Of Gene Manipulation, An Introduction To Genetic Engineering", Blackwell Science Publications, New Jersey, 2006.
2. David Freifelder, "Molecular Biology", Narosa Publishing House, New Delhi, 2000.

Reference Books

1. Sandhya Mitra, "Genetic Engineering Principles and Practice", Rajiv Beri for Macmillan India Ltd publications, Bangalore, 2008.
2. Gupta P.K., "Elements of biotechnology", Rastogi publications, Meerut, 2004.
3. Gardner, Simmons and Snustad, "Principles of Genetics", John Wiley, New Jersey, 8th Edition, 2000.

12BI211 BIOORGANIC CHEMISTRY

Credits: 3:0:0

Course Objective:

- This course provides a detailed view of the reactions and concepts used in modern organic chemistry. Reactions will be introduced for all common organic functional groups.

Course Outcome:

- Reason and think analytically in solving problems in bioorganic chemistry.
- Student will understand the reactions and synthesis of natural products.

Unit I

INTRODUCTION: Stereochemistry – R and S notation – E and Z isomerism - mechanism of SN1 and SN2 reactions, mechanism of E1 and E2 reactions. Enantiomers - Optical isomerism - optical activity and optical rotation polarimeter.

Unit II

CHEMICAL BONDING: Chemical Bonding in protein structure - specificity of enzymes, concept of free energy and its importance in protein structure - chemistry of active oxygen species, free radicals system.

Unit III

STEREOCHEMISTRY OF ENZYMES: Acid base and covalent catalysis - stereochemistry of amino acids - structure and mechanism of pyruvate dehydrogenase. Proteases – Ribonucleases – carboxy peptidase – lysozyme – NAD - dependent oxidization and reduction reactions.

Unit IV

BIMOLECULAR REACTION: Ester hydrolysis - amide hydrolysis - peptide synthesis - structure and mechanism of FAD, THF coenzymes - Application of enzymes in industry and medicine.

Unit V

PROTEIN FOLDING MECHANISM: Structure of protein - an overview of protein folding, two state kinetics, multistate kinetics in protein folding, and protein folding dynamics, stability of protein and molecular chaperones. Applications of NMR and circular dichorism to study protein structure.

Text Books

1. Dugas H., "Bioorganic chemistry", Springer Verlag publishers, New York, 3rd Edition 1999.
2. Mathew, Van Holde and Athwen., "Biochemistry" Pearson publishers Ltd, New Delhi, 2000.

Reference Books

1. Jain J.L. and Sunjay J., "Fundamentals of Biochemistry" Pearson publishers Ltd, New Delhi, 6th Edition, 2004.
2. Paula Y. B., "Organic chemistry", Pearson P LTD, New Delhi, 3rd edition, 2002.
3. Trevor P., "Enzymes", East West Press P Ltd, New Delhi, 2005.

12BI212 DATA STRUCTURE AND C++ PROGRAMMING

Credits: 3:0:0

Course Objective:

- To learn the fundamentals and abstract concepts of Data Structures.
- To learn basic concepts and features of object oriented programming.

Course Outcome:

- Ability to develop biological application using object oriented programming.
- Identify appropriate data structure for the given problem.

Unit I

INTRODUCTION TO DATA STRUCTURES: Information and Meaning, Linked list-Single linked list, Doubly linked list, Circular Linked list, Stack, Queue, Trees.

Unit II

SORTING AND SEARCHING TECHNIQUES: Bubble sort, Insertion Sort, Selection Sort, Quick Sort, Heap Sort, Merge Sort. Searching -Binary Tree Search, Linear Search, Binary Search.

Unit III

INTRODUCTION TO C++: Basic concepts, Object oriented Languages, Applications; Object oriented programming system, C++ - Key concepts, classes, features, functions, operators, variables, C++ program structure.

Unit IV

CLASSES AND OBJECTS: Tokens, expressions, control structures – tokens, keywords, Identifiers and constants, Data types, Functions, classes and objects, Constructors and Destructors, String manipulation – creating string objects, manipulation, relational operation, accessing character in strings.

Unit V

FILE HANDLING: Inheritance – Defining derived class, single inheritance, Multiple inheritance, Pointers – to objects, to derived classes, to virtual functions, Working with files – File stream operation, opening and closing a file.

Text Books

1. Balaguruswamy E, "Object oriented programming with C++", Tata Mc Graw Hill publications, New Delhi, 2nd edition, 2001.
2. Jean-Paul Tremblay and Sorenson P. G, "An Introduction to Data Structures with Applications", McGraw- Hill Publishing Company Limited, New Delhi, 2nd Edition reprint, 2001.

Reference Books

1. Robert L., "OOPS in C++", Galgotia publications, Noida, 4th Edition 2002.
2. Sartaj S., "Data Structures, Algorithms and Applications in C++", McGraw-Hill Publishing Company Limited, New York, 1st Edition, 2000.

12BI213 MOLECULAR BIOLOGY AND GENETIC ENGINEERING LAB

Credits: 0:0:2

1. Isolation of bacterial plasmid and genomic DNA
2. Isolation of plant cell and animal cell genomic DNA
3. Agarose gel electrophoresis
4. Restriction enzyme digestion
5. Competent cells preparation
6. Transformation and screening for recombinants
7. Preparation of plasmid DNA
8. Ligation of DNA into expression vectors
9. Optimisation of time of inducer for recombinant protein expression
10. SDS-PAGE
11. Western blotting
12. Hybridisation with anti-sera
13. PCR

12BI214 DATAMINING LAB

Credit: 0:0:1

1. Data Preprocessing
2. Importing Data
3. Storing Data
4. Retrieving data
5. Graphical representation of data
6. Applying Models for Prediction
7. Text mining
8. Mining sequence patterns in biological data.

12BI215 COMPUTATIONAL CHEMISTRY LAB

Credit: 0:0:1

1. Molecular Mechanics of Hydroxyl group, H_2O_2, Methanol
2. Amino acid studies using Insight/Charm.
3. Molecular Orbital Theory Application for Oxygen Molecule.
4. Electron Distribution in Allyl Ions
5. Ring Conformations of Dimethylhexanes
6. Free Energy Theory for Solvation.
7. Molecular Recognition in Cyclodextrins.
8. Study of binding and predict binding constants of activity.
9. 3-D Database Searching for Tight Binding Guests.
10. 3-D Sub-structure Spatial Relationships.
11. Design Drug that acts as Nicotinamide.
12. Conformational Energetics of Oligosaccharides.

12BI216 C++ PROGRAMMING LAB

Credits: 0:0:2

1. Fundamentals of C++
2. Operators and Control structures
3. Classes and Objects
4. Functions
5. Structures
6. Constructors
7. Inheritance
8. Pointers
9. Exceptions
10. Streams
11. File handling
12. C++ programs for Bioinformatics applications.

12BI217 BIOPHYSICS AND STRUCTURAL BIOLOGY

Credits: 4:0:0

Course Objective:

- To study the strategy and tactics of biophysical chemistry concepts of macromolecules and the conformational analysis and forces that determine the protein and nucleic acid structure.
- To study the size and shape of the macro molecules using different techniques.

Course Outcome:

- The students will learn the structures of biological macromolecules and their conformations, the forces stabilizing their structures.
- The students will learn the techniques used to analyze the conformations and forces.

Unit I

BONDS AND ENERGETICS OF MACROMOLECULES: Covalent bond – Disulphide bond. Charge interactions – Polar interactions: Hydrogen bond, Aromatic interactions. Non-polar interactions – Hydrophobic effect and Van Der Waals interactions. Enzyme active site and geometry.

Unit II

STRUCTURE AND CONFORMATION OF PROTEINS: Levels of protein structure – Primary, Secondary – Helical, Beta structure, Tertiary, Quaternary – Hemoglobin & Myoglobin. Polypeptide chains geometrics, Potential energy calculations, Observed values for rotation angles, Prediction of proteins structure.

Unit III

STRUCTURE AND CONFORMATION OF NUCLEIC ACIDS: Nucleic acid structure and types. Geometrics - Glycosidic bond, Rotational isomers and Puckering, Backbone rotational angles and Steric hindrances, Forces stabilizing ordered forms, Base pairing, Base stacking, Tertiary structure of RNA.

Unit IV

LIPIDS AND MEMBRANE STRUCTURE: Architecture of biological membrane – Lipid bilayer – Micelles and Liposomes – Lamellar structure – Lipid packing – Lipid domains and rafts. Structure of transmembrane helices – Bacteriorhodopsin.

Unit V

TECHNIQUES FOR THE STUDY OF BIOLOGICAL STRUCTURE AND FUNCTION: Size and shape of macromolecules, methods of direct visualisation, macromolecules as hydrodynamic particles, macromolecular diffusion, ultracentrifugation, viscometry, X-ray crystallography: X–ray diffraction, determination of molecular structures, electron microscopy, neutron scattering, light scattering.

Text Book

1. Cantor R., and Schimmel P.R, "Biophysical Chemistry", Freeman and Co., New York, 2004.

Reference Book

1. Anders L., Lars L., Jure P., Goran L., Poul N., and Morten K., "Text Book on Structural Biology", World Scientific Publishing Co., Singapore, 2009.

12BI218 GENOMICS AND PROTEOMICS

Credits: 3:0:0

Course Objective:

- To develop skills of the students in the area of genomics and proteomics.
- To provide knowledge on genome analysis through experimental and computational methods.
- To understand the various tools available for proteomics and their applications.

Course Outcome:

- Students may get interested in gene and genome analysis through experimental or computational methods.
- Students will learn the high-throughput technologies available for proteome research.

Unit I

OVERVIEW OF GENOMES: Introduction to Genomics- Genome organization of prokaryotes and eukaryotes- gene structure of bacteria, archaebacteria and eukaryotes- Human genome project.

Unit II

MAPPING AND SEQUENCING: Genetic and Physical Maps- Genetic Mapping, DNA markers- Physical Mapping and its types- Methodology for DNA sequencing, Contig assembly.

Unit III

FUNCTIONAL GENOMICS: Genome annotation - traditional routes of gene identification - detecting open-reading frames - software programs for finding genes - Identifying the function of a new gene - gene ontology.

Unit IV

ANALYTICAL PROTEOMICS: The Proteome, Genomics Vs Proteomics, Proteomics and the New Biology- Two-dimensional Polyacrylamide gel electrophoresis- Mass spectrometry for Protein and Peptide Analysis (MALDI-TOF, ESI-Tandem MS)- Designing Microarray Experiment, Types of Micorarrays.

Unit V

APPLICATIONS: Applications of Proteomics: Mining Proteomes, Protein expression profiling, Mapping, Post-translational Modification, Peptide Mass fingerprinting.

Text Books

1. Brown T.A., "Genomes", BIOS Scientific Publishers Ltd, Oxford, 2nd Edition, 2002.
2. Daniel C. Liebler, "Introduction to Proteomics: Tools for the New Biology", Humana Press, Totowa, New Jersey, 2002

Reference Books

1. Sandor Suhai, "Genomics and Proteomics- Functional and computational Aspects", Springer, NewYork, 2000.
2. Malcolm Campbell A. and Laurie J. Heyer, "Discovering genomics, proteomics and Bioinformatics", Pearson/Benjamin Cummings, New Delhi, 2006.
3. Mount, D. "Bioinformatics; Sequence and Genome Analysis", Cold Spring Harbor Laboratory Press, New York, 2004

12BI219 PERL PROGRAMMING

Credits: 3:0:0

Course Objective:

- To introduce Perl with basic concept like variables, arrays, control structure, subroutine, string manipulation, modules and packages etc. for beginners.

Course Outcome:

- Students will be able to appreciate the role of Perl in solving biological problems.

Unit I

PERL: Introduction to Perl, Variables and Data types, Perl variables, Scalar values, Calculations, Interpolation and Escapes, Arrays: Array manipulation, Push and Pop, Shift, Splice and other array function- List and scalar context.

Unit II

CONTROL STRUCTURES, SUBROUTINES, STRING MANIPULATION: Comparisons, Choices, Intermediate Loops, Loop exits. Subroutines: Creation, Arguments, Return and Scope, String Manipulations, Array based character manipulations, Regular expressions- Patterns.

Unit III
INPUT AND OUTPUT: Program parameters, File I/O, File handles, working with file handles, Built-in file handles, file safety, Inter process communications, Processes, Process pipes, Creating and monitoring processes.

Unit IV
PERL MODULES AND PACKAGES: Modules, packages, included modules, CPAN: setting, finding, installing, managing modules.

Unit V
BIOPERL: Sequences, Seqfeature, Annotation, Sequence I/O, Cool Tools, Bioperl Modules: availability and sources, installation and uses, Problems using bioperl

Text Book

1. D. Curtis Jamison, "Perl Programming for Bioinformatics and Biologists", Wiley-Dreamtech India Pvt. Ltd, New Delhi, 2009.

Reference Book

1. James D. Tisdall, "Mastering Perl for Bioinformatics", O'Reilly and Associates, New Jersey, 2003.

12BI220 IMMUNOLOGY AND IMMUNOINFORMATICS

Credits: 3:0:0

Course Objective:

- To introduce Immunological foundations and apply Informational technology to study immune systems

Course Outcome:

- This course gives a complete understanding of the concepts of Immunology and Immunotechniques.
- The course will help the students to understand Immunoinformatics and its applications.

Unit I
OVERVIEW OF IMMUNE SYSTEM: Types of Immunity - Innate and Adaptive. Cells and organs of the immune system, Antigens – epitopes, antigenicity, factors influencing antigenicity.

Unit II
IMMUNOGLOBULINS: Structure and types of Immunoglobulins, Biological activities. Monoclonal antibodies- productions and applications, Cytokines – types and immune response, Complement system.

Unit III

ANTIGEN ANTIBODY INTERACTIONS: Antibody affinity and activity, precipitation, agglutination, Radio Immuno Assay, ELISA, Western blotting, Immunoprecipitation, Immunofluorescence, Flow cytometry for separation of immune cells, Major Histocompatiblity Complex (MHC), Antigen processing and presentation.

Unit IV

T CELL AND B CELL ACTIVATION: T cell and B cell maturation, activation and differentiation, Leukocyte migration and inflammation, Hypersensitive reactions.

Unit V

IMMUNOINFORMATICS: Immunoinformatics - Introduction and Methods, Applications – Prediction of epitopes, Vaccine design, Web based tools for vaccine design.

Text Books

1. Richard A. G and Thomas J. K., "Kuby Immunology", W.H.Freeman and Company, New Jersey, 4th edition, 2000.
2. Ole Lund, "Immunological Bioinformatics", MIT Press, USA, 2005.

Reference Books

1. K. Chakravarthy, "Immunology and Immunotechnology", Oxford University Press, New Delhi, 2006.
2. Darren R.F., "Immunoinformatics: Predictive Immunogenicity *insilico*", Humana Press, New Jersey, 2007.

12BI221 DATABASE MANAGEMENT SYSTEM

Credits: 3:0:0

Course Objective:

- To have an overview of the functions of the Database Management System (DBMS), relational database design and SQL (Structured Query Language) used with relational databases.

Course Outcome:

- Ability to analyze, design and develop an effective database in some implementation.

Unit I

INTRODUCTION: Purpose of Database systems - overall system structure - Entity relationship model: entities and entity sets relationships - mappings constraints - primary keys - E.R diagram.

Unit II

QUERY LANGUAGES: Structure - Formal Query languages - Relational Algebra - Commercial Query languages – SQL: Basic structure, set operations, aggregate functions, nested sub queries, modification of the database, QUEL.

Unit III

NORMALIZATION: Pitfalls - Normalization using functional dependencies - Decomposition - Boyce-codd Normal form - third normal form - fourth normal form, normalization using join dependencies – domain key normal form.

Unit IV

QUERY PROCESSING AND OPTIMIZATION: Query processing - Overview, selection operation, sorting, join operation, Query optimization - Estimating statistics of expression, Transformation, materialized views.

Unit V

ORACLE: Database design and querying tool, SQL variation and extension, storage and indexing, concurrency control and recovery, system architecture, replication, distribution and external data.

Text Book

1. Abraham Silberschatz, Henry K Korth, and Sudarshan S, "Database concepts", McGraw Hill International publications, New Delhi, 4th edition, 2002.

Reference Book

1. Ramesh Elmasri, and Shamkant B. Navathe, "Fundamentals of Database systems", Addison –Wesley Publications, India, 4th edition, 2004.

12BI222 INTRODUCTION TO UNIX AND LINUX

Credits: 3:0:0

Course Objective:

- To understand the Operating System concepts with the help of Unix operating system and to have a good experience to work with the open source Linux operating system.

Course Outcome:

- Enable the students to install and work with Open source software.

Unit I

UNIX INTRODUCTION: Unix operating system – History - Understanding the unix command - General purpose utilities - Navigating the file system - Handling ordinary files - The shell - The Vi editor- The environment.

Unit II

UNIX ADMINISTRATION: Basic file attributes - More file attributes - System administration II - The file system revisited - Simple filters - Regular Expressions and the grep family.

Unit III

UNIX PROGRAMMING: The process - Communication and electronic mail - Shell programming - System administration I -The routine duties.

Unit IV

LINUX ADMINISTRATION: Introduction- GNOME and KDE - Managing users- The command line - Booting and shutting down - File systems.

Unit V

LINUX INTERNET AND INTRANET SERVICES: Linux internet services – DNS - Setting up web server using Apache - The secure shell - Intranet services in Linux - Network file system and Network information service - Network configuration.

Text Books

1. Sumitabha Das, "Unix – Concepts and Applications", Tata McGraw Hill, New Delhi, 2nd Edition, 2000.
2. Steven Graham and Steve Shah, "Linux Administration", Dreamtech, New Delhi, 3rd Edition, 2003.

Reference Books

1. Kenneth R., Douglas H., James F., and Richard R., "Unix-The Complete Reference", Mc-Graw Hill, New Delhi, 1st Edition, 1999.
2. Roderick W. S., "Linux in a Windows world", O'reilly's, USA, 1st Edition, 2005.
3. Yaswanth K., "Unix Shell Programming", BPB Publications, New Delhi, 2003

12BI223 DATABASE MANAGEMENT SYSTEM LAB

Credit: 0:0:1

1. Data Definition language
2. Data manipulation language
3. Data Control language and Transaction control language
4. Operators
5. Joins
6. View
7. Constraints
8. PL/SQL

12BI224 UNIX AND LINUX LAB

Credit: 0:0:1

1. Basic Unix Commands
2. General purpose Utilities
3. File Navigation
4. Vi editor
5. Shell
6. Simple filters
7. Changing terminal
8. Enviroment Variables
9. Shell script
10. Regular Expression

12BI225 PERL LAB

Credits: 0:0:2

1. Perl variables

2. Basic linux commands and text editors
3. Control and loop statements
4. Functions and subroutines
5. File handling
6. Regular expressions
7. Random sequence
8. Use of arrays
9. String manipulation
10. Biological sequence-I
11. Biological sequence-II
12. User administration commands
13. Perl web server
14. Modules: LWP and bioperl
15. Command line argument

12BI226 IMMUNOLOGY AND IMMUNOINFORMATICS LAB

Credits: 0:0:2

1. Blood group typing
2. Vidal Test
3. ELISA
4. Immunoelectrophoresis
5. Radial Immunodiffusion
6. Raising antibodies
7. B cell Epitope prediction
8. T cell Epitope prediction
9. MHC class 1 binding
10. MHC class 2 binding
11. Immunological databases
12. *Insilico* vaccine designing

12BI227 JAVA PROGRAMMING

Credits: 3:0:0

Course Objective:

- To learn basic concepts and Object oriented paradigm.
- Application of Java language in bioinformatics.

Course Outcome:

- Ability to develop Java application for biological problems.

Unit I

INTRODUCTION: Java evolution – History - Features of Java - Java and C - Java and C++ - Java and internet - Java environment - Program structure - Basic concepts of object oriented programming.

Unit II

ARRAYS AND VARIABLES: Java tokens – constants – variables - data types – operators - control statements- arrays.

Unit III

OBJECT ORIENTED PROGRAMMING: Introducing classes – objects – methods - method overloading – overriding – constructors – inheritance - packages.

Unit IV

MULTITHREADING AND EXCEPTION HANDLING: Interface- multithreading-Managing errors and exception handling - String handling.

Unit V

JAVA FOR BIOINFORMATICS: Applet Programming - managing input/output files in Java - Applications in bioinformatics - Sample Java programs for bioinformatics.

Text Book

1. Balagurusamy E, "Programming with Java: A primer", Tata McGraw-Hill, New Delhi, 2nd Edition, 2000.

Reference Books

1. Herbert S, "Java - The Complete Reference", Tata McGraw- Hill, New Delhi, 7th edition, 2008.
2. Ivor H, "Beginning Java 2 JDK", Wiley, New York, 5th Edition, 2004.

12BI228 MOLECULAR MODELING AND DRUG DESIGN

Credits: 4:0:0

Course Objective:

- To teach the critical relationship among bimolecular structure, function and force field models.
- To understand the basic modeling techniques to explore biological phenomena at the molecular level.
- To emphasize Modeling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

Course Outcome:

- Students are introduced to the principles and practice of Molecular modeling and modern drug discovery.
- An awareness of rational drug design, based on understanding the three-dimensional structures and physicochemical properties of drugs and receptors will be created.

Unit I

INTRODUCTION TO MOLECULAR MODELING: Introduction - Useful concepts in molecular modeling - Coordinate systems - Internal coordinates, Potential energy surfaces -

Molecular graphics – Surfaces - Computer hardware and software - The molecular modeling literature.

Unit II

FORCE FIELDS: Bond stretching, Angle bending, Torsional terms, Introduction to non-bonded interactions - Electrostatic interactions, Van der Waals interactions, Hydrogen bonding in molecular mechanics - Force field models for the simulation of liquid water.

Unit III

ENERGY MINIMISATION AND COMPUTER SIMULATION: Energy minimization and related methods for exploring the energy surface, Non-derivative methods and derivative methods, 1st and 2nd order minimisation methods - Computer simulation methods - Simple thermodynamic properties and phase space – Boundaries - Analyzing the results of a simulation and estimating errors - GROMACS and CNS.

Unit IV

MOLECULAR DYNAMICS AND MONTE CARLO SIMULATION: Molecular dynamics simulation methods – Simple models - Molecular dynamics with continuous potentials, constant temperature and pressure - Metropolis method - Monte Carlo simulation of molecules - Models used in Monte Carlo simulations of polymers - Molecular modeling software: BIOSUITE and DESMOND.

Unit V

STRUCTURE PREDICTION AND DRUG DESIGN: Protein structure prediction-Introduction to comparative modeling - Sequence alignment - Constructing and evaluating a comparative model, Predicting protein structures by 'Threading', Molecular docking methods and scores, GLIDE, AUTODOCK and HEX - Structure based De Novo ligand design, Drug discovery – ADMET - Chemoinformatics – QSAR.

Text Book

1. Leach A.R, "Molecular Modelling Principles and Application", Pearson – Prentice Hall, New Delhi, 2nd Edition 2001.

Reference Books

1. Satya Prakash G., "QSAR and Molecular Modeling", Springer - Anamaya Pub, New Delhi, 2008.
2. N. Claude C., "Molecular Modeling in Drug Design", Academic Press, California, 2006.

12BI229 MOLECULAR EVOLUTION AND PHYLOGENY

Credits: 3:0:0

Course Objective:

- This course aims to combine the concepts of molecular biology, evolutionary biology and population genetics to understand recent discoveries on the structure and function of nucleic acids and proteins. An important area within the study of molecular evolution is the use of molecular data to determine the correct biological classification of sequences and organisms called phylogenetics.

Course Outcome:

- The students would be able analyze the techniques and methods used in molecular evolution and phylogeny in processing the molecular data in building phylogenetic trees. They will also be able to study epidemiology based on molecular data.

Unit I

INTRODUCTION TO MOLECULAR EVOLUTION: Archaeology of the genome-fundamentals of Population genetics-The nature of molecular evolution- Driving forces in evolution, evolutionary changes in nucleotide sequences.

Unit II

MOLECULAR PHYLOGENETICS: Terminology of phylogenetic trees- Trees and distances-Molecular phylogenetic archaeology- Molecular phylogenetic examples- The universal phylogeny.

Unit III

MEASURING GENETIC CHANGE: Sequence alignment and homology- Genetic distance-Measuring evolutionary change on a tree- kinds of data- Methods of reconstruction- Distance matrix methods, Maximum parsimony methods, Maximum likelihood methods- analysis of true tree- Problems associated with phylogenetic reconstruction.

Unit IV

MODELS OF MOLECULAR EVOLUTION: Modes of evolutionary process- Functional constraints and the rate of substitution-Patterns of codon usage and base composition- Molecular clocks, evaluation of molecular clock hypothesis - Neutral theory- Genetic variation within species- Natural selection.

Unit V

APPLICATIONS OF MOLECULAR PHYLOGENETICS: Organismal phylogeny - Gene trees and species trees- Host parasite co- speciation - Age and rates of diversification - phylogeny in molecular epidemiology.

Text Book

1. Dan Graur and Wen-Hsiung Li, “Fundamentals of Molecular evolution”, Sinauer Associates, INC, USA, 2nd Edition, 2000.

Reference Book

1. Roderic D. M. Page and Edward C. Holmes Molecular evolution, “A phylogenetic approach”, Blackwell Science Inc, USA, 2nd Edition, 2000.

12BI230 BIOETHICS, IPR AND BIOSAFETY

Credits: 3:0:0

Course Objective:

- To understands the basics of Bioethics, IPR and Biosafety.

Course Outcome:

- Students will understand the concepts of ethical and environmental issues related to life sciences

Unit I

ENGINEERING ETHICS: Senses of Engineering Ethics- variety of moral issues - types of inquiry - moral dilemmas - moral autonomy - Kohlberg's theory - Gilligan's theory - consensus and controversy –Models of Professional Roles - theories about right action - Self-interest - customs and religion - uses of ethical theories.

Unit II

ENVIRONMENTAL ASPECTS OF BIOTECH APPLICATIONS: Use of genetically modified organisms and their release in environment Special procedures for r-DNA based product production, identification of directions for yield effect in agriculture, aquaculture etc, Bioremediation.

Unit III

INTELLECTUAL PROPERTY RIGHTS: TRIPS, International conventions patents and methods application of patents, Legal implications, Biodiversity and farmers rights. Beneficial applications and development of research focus to the need of the poor.

Unit IV

GLOBAL ISSUES: Multinational corporations - Environmental ethics - computer ethics - weapons development - engineers as managers-consulting engineers-engineers as expert witnesses and advisors - sample code of Ethics (Specific to a particular Engineering Discipline).

Unit V

LEGAL AND SOCIOECONOMIC IMPACTS OF BIOTECHNOLOGY: Informed decision making, Biosafety- National and International guidelines and regulation, r-DNA guidelines, Experimental protocol approvals, containment -levels of containment.

Text Book

1. Shaleesha A.S., “Bioethics”,Wisdom Educational service publications, Chennai, 2008.

Reference Book

1. Jeyakumar V, “Professional ethics and Human values”, Anuradha Publications, Chennai, 2006.

12BI231 SYSTEMS BIOLOGY

Credits: 3:0:0

Course Objective:

- To introduce the student to the systems approach of biology.
- Discover new knowledge in modeling of genome, proteome and metabolic pathways.

Course Outcome:

- These modeling techniques will enable the students to identify important target proteins and pathways for any disease.

Unit I

INTRODUCTION TO SYSTEMS BIOLOGY: Scientific challenges in systems biology, Bringing genomes to life; the use of genome-scale, *In silico* model, from gene expression to metabolic fluxes.

Unit II

LEVEL OF BIOLOGICAL SYSTEMS: System - level understanding of biological systems - Advanced measurement - Systems modeling - Genetic networks.

Unit III

EXPERIMENTAL TECHNIQUES FOR SYSTEMS BIOLOGY: Handling and interpreting gene groups, Reconstruction and structural analysis of metabolic and regulatory network, Methods for protein-protein interaction network.

Unit IV

THEORETICAL AND MODELING TECHNIQUES: Reconstructing transcriptional networks using gene expression profiling and Bayesian, Employing systems biology to quantify receptor, Tyrosine Kinase signaling in time and space. Application, representation and management of signaling pathway - Introduction to signaling pathway project.

Unit V

METHOD AND SOFTWARE PLATFORM FOR SYSTEMS BIOLOGY: SBML models and MATHSBML, Cell designer, Systematic detection of biological networks - Storing, searching and dissecting experimental proteomic data.

Text Book

1. Sang dun Choi, "Introduction to Systems Biology", Human Press, New Jersy, 6th Edition, 2007.

Reference book

1. Hiroaki K, "Foundations of Systems Biology", MIT Press, London, 1st Edition, 2001.

12BI232 MACHINE LEARNING IN BIOINFORMATICS

Credits: 3:0:0

Course Objective:

- This course will enable students to know about the informative yet accessible overview of the ways in which bioinformatics and Machine Learning borrow strength or motivation from each other.
- Understand main problems in bioinformatics and the fundamental concepts and algorithm of machine learning.

Course Outcome:

- Students will be able to explore how machine learning techniques can be applied to bioinformatics problems.
- Students will be able to extract knowledge from the deluge of information produced by

today's biological experiments using the innovative tools and techniques of machine learning.

Unit I

PROBABILISTIC AND MODEL BASED LEARNING: Probabilistic Learning, Basics of probability, Random variables and probability distributions, Basics of information theory, Basics of stochastic processes, Hidden Markov Models, Frequentist Statistical Inference, Some computational issues, Bayesian Inference.

Unit II

CLASSIFICATION AND UNSUPERVISED LEARNING TECHNIQUES: Introduction and problem formulation, The framework, Application of classification techniques to bioinformatics problems, Principal components analysis, Multidimensional scaling, Other dimension reduction techniques, Cluster analysis techniques.

Unit III

COMPUTATIONAL INTELLIGENCE IN BIOINFORMATICS: Fuzzy sets, Artificial neural networks, Evolutionary computing, Rough sets, hybridization, Application to bioinformatics - Sequence analysis, Analysis of high-throughput gene expression data, Network inference.

Unit IV

MACHINE LEARNING IN STRUCTURAL BIOLOGY: Introduction, Automated refinement procedure (ARP/WARP), RESOLVE, TEXTAL, Automatic crystallographic map Interpreter (ACMI).

Unit V

BAYESIAN MACHINE LEARNING METHODS: Classification using RKHS, Hierarchical classification model, Likelihoods of RKHS models, The Bayesian analysis, Prediction and model choice, some examples.

Text Book

1. Sushmita M., Sujay D., Theodore Perkins and George Michailidis, "Introduction to Machine Learning and Bioinformatics", CRC Press, New York, 2008

Reference Book

1. Ethem A., "Introduction to Machine Learning", MIT Press, London, 2nd Edition, 2010

12BI233 JAVA PROGRAMMING LAB

Credit: 0:0:1

1. Java Fundamentals
2. Control statements
3. Classes and objects
4. Methods
5. Arrays in java
6. Inheritance

7. Packages
8. Interface
9. Exception handling
10. Multithreading
11. File handling
12. Applet programming
13. Graphics programming
14. Java programs for bioinformatics.

12BI234 SYSTEMS BIOLOGY LAB

Credit: 0:0:1

1. Functional protein interaction network STRING
2. Mammalian protein interaction database
3. MINT
4. KEGG
5. BIOCYC
6. WIKIGENE
7. CELL DESIGNER
8. ECELL
9. CYTOSCAPE
10. CLUSTERONE
11. MiMI
12. CYTO HUBBA

12BI235 MOLECULAR MODELING LAB

Credits: 0:0:2

1. Biomolecular model building and small molecule modeling
2. Primary and Secondary Structural Analysis of Protein/Nucleic Acids
3. Conformational study of oligosaccharides/ polypeptides
4. Homology modeling using SWISS-PDB / MODELLER
5. Energy minimization for protein/ carbohydrates – TINKER/Schrodinger software
6. Molecular Dynamics for Protein/carbohydrates – TINKER/Schrodinger software
7. Docking and binding site analysis – ARGUS LAB / Schrodinger software
8. Combinatorial Screening of small molecules database – GOLD/ ZINC/ CombiGlide
9. Insilico ADME calculations – Qikprop
10. Quantitative structure activity relationship and QSAR equation - Schrodinger software
11. Bonded and non-bonded interaction for Protein-Lead complex - Schrodinger software
12. Pharmacophore based screening, shape based screening – Phase

12BI236 COMPUTATIONAL BIOLOGY LAB

Credits: 0:0:2

1. Structure determination in small molecules

2. Geometrical analysis
3. Methods in crystallization
4. Exercises in genome mapping
5. Comparative genome analysis
6. 2D PAGE (Demo)
7. Designing Microarray experiment (Demo)
8. X ray Diffraction – data collection (Demo)
9. Introduction to MATLAB.
10. Application of Fuzzy Logic concept.
11. Artificial Neural Network for Bioinformatics.
12. Practical Application of Bioinformatics Tools of MATLAB.

12BI237 CHEMINFORMATICS

Credits: 3:0:0

Course Objective:

- To introduce different methods of cheminformatics with particular emphasis on applications including modern drug discovery.

Course Outcome:

- The course will introduce the students preparing for professional work in chemistry and help to learn how to retrieve specific information from the enormous and rapidly expanding chemical literature.
- The course will provide a broad overview of the computer technology to chemistry in all of its manifestations
- The course will expose the student to current and relevant applications in QSAR and drug design.

Unit I

INTRODUCTION TO CHEMINFORMATICS: History and evolution of cheminformatics- Use of cheminformatics- Cheminformatics in lead identification - Molecular modeling and structure elucidation.

Unit II

REPRESENTATION AND MANIPULATION OF 2D AND 3D MOLECULAR STRUCTURE: Computer representation of chemical structure- Structure searching- Substructure searching - Reaction databases - Experimental 3D databases - 3D pharmacophore - Theoretical 3D databases and conformational search - Pharmacophore mapping and application.

Unit III

MOLECULAR DESCRIPTORS: Descriptors calculated from the 2D structure - Physiochemical properties - 2D descriptors - Descriptors based on 3D representations - 3D descriptors - Pharmacophore descriptors - Data verification and manipulation - Principle component.

Unit IV

CHEMINFORMATICS METHOD: Similarity searching - Diversity analysis - Finger prints - Shape based screening - self organized maps - Common substructure search - clustering heat maps - R group analysis.

Unit V

QSAR AND COMPUTATIONAL MODELS: Quantitative structure activity relationship-Ligand structure based 2D descriptor- Pharmacophore based 3D descriptors- Deriving a QSAR equation: simple and MLR - Square correlation coefficient - Leave one out method s- Cross validation - Partial least square.

Text Book

1. Andrew R. L and Valerie J. G. C, "Introduction to Chemo informatics", Academic Publisher, Netherlands, 2003.

Reference Book

1. Johann Gasteiger and Thomas Engel, "Cheminformatics: A textbook" WILEY VCH Publisher, Germany, 2003.

12BI238 PHARMACOGENOMICS

Credits: 3:0:0

Course Objective:

- To introduce the scientific knowledge of drugs that reacts with the biomolecules and to understand the novel concepts in Pharmacogenomics.

Course Outcome:

- To provide students with an understanding of the principles and applications of human genetics and genomics in drug therapy optimization, patient care, and counseling.

Unit I

INTRODUCTION TO PHARMACOGENOMICS: Promises, Opportunities and limitations. The human genome, Turning SNPs into useful makers of drug response, Association studies in pharmacogenomics, Genomics application that facilitate the understanding of drug action and toxicity.

Unit II

PHARMACOGENETICS IN DRUG DISCOVERY: The role of pharmacogenetics in drug discovery and therapeutics, Pharmacogenomics and drug design, The pharmacogenomics of human P-glycoprotein, Pharmacogenomics of drug transporters, Pharmacogenomics of asthma treatment.

Unit III

CELLS AS TARGETS FOR HYDROXY UREA: Relevance to the current therapeutic strategy in Sickle Cell disease, Pharmacogenomics and complex cardiovascular disease – Clinical studies in candidate genes, Pharmacogenomics of lipid-lowering agents - Pharmacogenomics of chemotherapeutic agents in cancer treatment - Pharmacogenomics of the Blood-brain barrier.

Unit IV

PHARMACOGENOMICS AND THE TREATMENT OF NEUROLOGICAL DISEASE: Pharmacogenomics of neurodegenerative diseases - examples and perspectives, Psychiatric pharmacogenetics - prediction of treatment outcomes in Schizophrenia, Pharmacogenomics of major depression and antidepressant treatment, Pharmacogenomics of bipolar disorder.

Unit V

PHARMACOGENOMICS OF ALCOHOLISM: Pharmacogenomics of tobacco addiction, pharmacogenomics of opioid systems, ethnicity and Pharmacogenomics, Pharmacogenomics - ensuring equity regarding drugs based on genetic difference - Translation of vascular proteomics into individualized therapeutics.

Text Books

1. Julio L and Ma-Li W, "Pharmacogenomics: The Search for Individualized Therapies", Wiley-VCH Publishers, Germany, 2nd Edition, 2002.
2. Mark A. R, "Pharmacogenomics: Social, ethical, and clinical dimensions", Humana press, USA, 3rd Edition, 2011

Reference Books

1. Werner K, Urs A, Mayer, Rachel Tyndale, "Pharmacogenomics", Taylor and Francis Publisher, UK, 2nd Edition, 2005.
2. Martin M., Zdanowicz. "Concept in Pharmacogenomics", ASHS Pharmacists Publishers USA, 1st Edition, 2010.

12BI239 BIOPHARMACEUTICAL TECHNOLOGY

Credits: 3:0:0

Course Objective:

- The course introduces students to disciplines of the pharmacy and health sciences fields. The course gives general view of topics related to pharmacy and the ethics and regulations of these areas.

Course Outcome:

- Develop an ability to integrate information to improve Drug synthesis skills. Develop an informal understanding of the role of science and technology in society.

Unit I

INTROUCTION TO PHARMACEUTICALS: History and definition of drugs, Sources of drugs - plant, animals, microbes and minerals, Different dosage forms, Routes of drug administration.

Unit II

PHARMACODYNAMICS: Physico-chemical principles, Pharmacodynamics - Mechanism of drug action, drug receptors, and physiological receptors - structural and functional families, Pharmacokinetics - Drug absorption, factors that affect the absorption of drugs, Distribution of drugs, Biotransformation of drugs, Bioavailability of drugs.

Unit III

DRUG MANUFACTURING PROCESSES: Good manufacturing practices, Good laboratory practices, manufacturing facilities, sources of biopharmaceuticals, Production and analysis of biopharmaceuticals.

Unit IV

PRODUCTION AND APPLICATION OF BIOPHARMACEUTICALS: Production of therapeutic proteins, Hormones, Cytokines - Interferons, Interleukins I and II, Tumor Necrosis Factor (TNF), Nucleic acids, Applications of biopharmaceuticals- Role of biopharmaceuticals in treatment of various health disorders.

Unit V

DRUG DELIVERY SYSTEMS, BIOMATERIALS AND THEIR APPLICATIONS: Controlled and sustained delivery of drugs, Biomaterial for the sustained drug delivery, Liposome mediated drug delivery, Drug delivery methods for therapeutic proteins.

Text Books

1. Sathoskar R.S, Bhandrkar S.D and Ainapure S.S "Pharmacology and Pharmacotherapeutics", Popular Prakashan publication New Delhi. 17th edition, 2001.
2. Remington, "The Science and Practice of Pharmacy", Lippincot Williams and Wilkins publications New York, 21st Edition, 2006.

Reference Books

1. Chetan D.M, Dinesh K.P, "Health and Pharmaceutical Biotechnology", Firewall Media Publications, New Delhi, 3rd Edition, 2006.
2. Vasant V. R, Mannfred A. H, "Drug Delivery Systems", CRC Press, New York, 2nd edition, 2003.
3. Rodney J. Y. Ho, Milo G, "Biotechnology and Biopharmaceuticals: Transforming Proteins and Genes into Drugs", Wiley-IEEE, New York, 2003.

12BI240 CLINICAL DATA MANAGEMENT

Credits: 3:0:0

Course Objective:

- The main objective of this course is to develop experts/skilled professionals to perform clinical data management tasks by having a correct spatial orientation of clinical research data management. Understand the regulatory perspectives on clinical research activities.

Course Outcome:

- Develop an ability to apply principles and generalizations already learned about science and technology to new problems and situations. Learn terms and facts of Clinical trials. Learn concepts and theories of Data management.

Unit I

INTRODUCTION: Audience and scope, other sources of knowledge, Fundamental concepts, Types of outcome measures and understanding clinical research analysis.

Unit II

CLINICAL TRIALS AS RESEARCH: Clinical reasoning based on the case history, Statistical reasoning emphasizes inference based on designed data production, Clinical and statistical reasoning converge in research, defining clinical trials- Formal analysis, Clinical trials as science, Practicalities of usage.

Unit III

CLINICAL TRIALS ETHICS: Introduction-science and ethics share objectives, Equipoise and uncertainty, Duality-clinical trials sharpen, the Issue, A gene therapy tragedy illustrates duality, The hippocratic tradition - Proscribe clinical trials, Historically derived principles of ethics, Contemporary foundational principles, methodologic reflections, professional conduct.

Unit IV

CONTEXTS FOR CLINICAL TRIALS: Introduction-ways to learn about trials in a given context, Issues of context, drugs, devices, prevention- The prevention versus therapy dichotomy is overworked, Vaccines and biologicals, A perspective on risk– benefit, Methodology and framework for prevention trials, Complementary and alternative medicine, A brief view of clinical trial contexts.

Unit V

STATISTICAL PERSPECTIVES: Introduction- differences in statistical perspectives, frequentist, bayesian, likelihood, afterthoughts, modeling longitudinal data, Evaluation of diagnostic tests.

Text Books

1. Piantadosi S, "Clinical Trials: a Methodologic Perspective", JohnWiley and Sons, New York, 2nd edition, 2007.
2. Allan H, "A Concise Guide to Clinical Trials", A John Wiley and Sons, Ltd., New York, 1st edition, 2009.
3. Partrick P, "Clinical Epidemiology practice and methods", Humana press, New York, 1st edition, 2009.

Reference Books

1. Friedman L.M, Furberg C, and DeMets D.L, "Fundamentals of Clinical Trials", Springer, New York, 3rd edition, 1998.
2. Chow S-C and Liu J-P, "Design and Analysis of Clinical Trials", JohnWiley and Sons, New York, 2nd edition, 2004.
3. Stephanie G, Jacqueline B, and John C, "Clinical Trials in Oncology", CRC press, USA 2nd edition, 2002.

12BI241 COMPUTER AIDED DRUG DESIGN LAB

Credits: 0:0:2

1. Small molecule search database
2. Preparation of compound Library
3. Optimization and minimization of small molecules
4. Calculation of physiochemical property

5. Overview of macromolecules and their interaction with micro molecules
6. Active site residue interactions with the binding site by using LIGPLOT
7. Introduction to Schrodinger, ligand preparation and protein preparation
8. Receptor Grid generation and protein-ligand docking using Glide and their refinement
9. 2D QSAR based upon physiochemical properties using LSBD and model generation
10. 3D QSAR based upon pharmacophore generation
11. Validation of QSAR model
12. Applications of QSAR

12BI242 CLINICAL DATA MANAGEMENT LAB

Credits: 0:0:2

1. Clinical data Set-Up
2. GLIBS – data extraction methods and analysis
3. Data Entry
4. Data Validations
5. Query Management
6. Database lock
7. Validation procedures
8. Data Clustering using Bayesian tool
9. Likelihood Test for data analysis
10. Modeling Longitudinal Data.
11. Medical Transcription data analysis
12. Clinical data management format design

12BI243 R PROGRAMMING

Credits: 3:0:0

Course Objective:
- Express fundamental programming constructs such as input and output, R function, loops, Graphics and OOP in R.
- Programs for Packages and Data technologies in R

Course Outcome:
- Write, compile, and run R programs, analyze the R function, OOP and mapping using R environment.
- Create R programs that make use of Packages and Data technologies

Unit I
FUNDAMENTALS: Introduction, Data structures, Managing R session, Language basics, Subscripting and sub setting.

Unit II
R FUNCTIONS: Vectorized, Replacement functions, Writing functions, Flow control, Exception handling, Evaluation , Lexical scope and graphics.

Unit III

OBJECT-ORIENTED PROGRAMMING IN R: Introduction, basics of OOP in R, S3 OOP, S4 OOP, Using classes and methods in packages, Debugging, Managing S3 and S4 together.

Unit IV

WORKING WITH CHARACTER DATA: Basic file handling, Connections, File input and output, Source and sink: capturing R output , Tools for accessing files on the Internet, Built-in capabilities , Regular expressions, Prefixes, suffixes and substrings, Matching patterns.

Unit V

PACKAGES AND DATA TECHNOLOGIES: Package basics, Package management, Package authoring, Initialization, Database technologies, DBI, XML, Bioinformatics resources on the WWW.

Text Book

1. Robert Gentleman, "R programming for bioinformatics" Taylor and Francis Group, USA, 1st Edition, 2009.

Reference Book

1. Sunil K. Mathur, "Statistical bioinformatics with R" Academic Press Elsevier, California,1st Edition, 2010.

12BI244 WEB PROGRAMMING

Credits: 3:0:0

Course Objective:

- Enabling the student to build and manage web applications.
- A working knowledge of HTML , DHTML and XML

Course Outcome:

- The students would learn to design, develop and manage web applications in bioinformatics.

Unit I

HTML: Introduction to internet and world wide web –Basic html document body -working with text-Hyperlinks-formatting – list- tables- using color and images - working with images – multimedia objects – working with frames – forms - XHTML.

Unit II

DHTML: Cascading style sheet – using styles – properties and values in styles – style sheets - Data Binding – Simple Data Binding – Moving with a record set – Sorting table data – Binding of an Image and table.

Unit III

XML: Basic XML – Defining data for web applications – Document type definition – XML schema – Document object model - Presenting XML - XSL – XML applications – XML with Perl.

Unit IV

WEB TECHNOLOGY: Internet protocols – Internet Applications and application protocols – Web browsers – Web servers – Web server scripting.

Unit V

CGI: Introduction – Building web application with Perl - Perl and CGI – CGI scripting – using RDBMS – creating and manipulating images – CGI environment variables – CGI.pm module – Debugging CGI applications and programs.

Text Books

1. Chris Bates, "Web Programming", Wiley India Ltd, New Delhi, 2nd edition, 2003.
2. Gopalan N.P, "Web Technology", Prentice - Hall of India Ltd, New Delhi, 1st edition, 2007.

Reference Books

1. Deitel and Deitel G, "Internet and World Wide Web – How to Program", Pearson Education Asia, 3rd Edition, 2006.
2. Simon Cozens and Peter Wainwright, "Beginning Perl", Shroff publishers, 1st Edition,2005.
3. Steven Holzner, "HTML", Dreamtech press , Reprint Edition, 2008
4. Elliotte Rusty Harold, "XML Bible", IDG Books India Ltd, Second Edition, 2003.

12BI245 KERNEL BASED DATA FUSION METHODS

Credits: 3:0:0

Course Objective:

- Provide specific introduction to data fusion problems using support vector machines.
- Understand novel kernel fusion algorithms and some real applications in supervised and unsupervised learning

Course Outcome:

- The students will be able to do a brief survey of additive models and Rayleigh quotient objectives in machine learning, and then will be able to apply fusion as the additive expansion of support vector machines in the dual problem.
- They will be able to understand the value of the proposed theories and algorithms in MerKator, open software to identify disease relevant genes based on the integration of heterogeneous genomic data sources in multiple species.

Unit I

INTRODUCTION: History of Multi-source Learning and Data Fusion, Rayleigh Quotient – Optimization, Type Problems in Machine Learning.

Unit II

MULTIPLE KERNEL LEARNING (MKL) AND SUPPORT VECTOR MACHINES (SVM): The Norms of Multiple Kernel Learning, One Class SVM MKL, and Support Vector Machine MKL for Classification, Least Squares Support Vector Machines MKL for

Classification, Weighted SVM MKL and Weighted LSSVM MKL, Numerical Experiments, MKL applied to Real Applications.

Unit III

TEXT MINING: Computational Gene Prioritization, Clustering by Heterogeneous Data Sources, Single View Gene Prioritization, Data Fusion for Gene Prioritization, Multi-view Text Mining for Gene Prioritization, Results of Multi-view Prioritization, Multi-view Text Mining for Gene Clustering, Results of Multi-view Clustering.

Unit IV

OPTIMIZED DATA FUSION: k-means: Objectives , Optimizing Multiple Kernels, Bi-level Optimization, Experimental Results, Combine Kernel and Laplacian for Clustering, Clustering by Multiple Kernels and Laplacians, Data Sets and Experimental Setup.

Unit V

WEIGHTED MULTIPLE KERNEL CANONICAL CORRELATION: Computational Issue, Learning from Heterogeneous Data Sources by WMKCCA, Candidate Gene Prioritization with MerKator - Data Sources, Kernel Workflow and Integration of Prioritization Scores, Software Structure and Interface.

Text Book

1. Shi Y, Leon-Charles T, Bart D. M and Yves M, "Kernel-based Data Fusion for Machine Learning: Methods and Applications in Bioinformatics and text Mining", Springer, Heidelberg, 1st Edition, 2011.

Reference Book

1. Guihai Chen, Yi Pan, Minyi Guo, Jian Lu, "Parallel and Distributed Processing and Application ISPA 2005", Springer, Heidelberg, 1st Edition, 2005.

12BI246 PYTHON PROGRAMMING

Credits: 3:0:0

Course Objective:

- Express fundamental programming constructs such as variables, arrays, loops, subroutines and input/output in Python.
- Understand several concepts of modules in Python and Biopython.

Course Outcome:

- Write, compile, and run Python programs, Analyze the effects of using Python structures that implement decisions, loops, and store arrays and use these structures in a well designed, OOP program.
- Create Python programs that make use of various modules and packages

Unit I

INTRODUCTION: Install and run Python program, System command lines and files, module imports and reloads. The IDLE user interface, Numeric types basis, Numbers in action, Comparision, Decimal and Fraction type, Sets, Booleans, Numeric extension.

Unit II
STRINGS: String literals, Strings in action, String methods, The original string module, String formatting expressions, String formatting method calls, General type categories.

Unit III
LISTS AND FILES: Lists, Lists in action, basic operations, comprehensions, Indexing, slicing, matrixes, Dictionaries, Dictionaries in action, Basic dictionary operations, Tuples: tuples in action, compare list and tuples, files and examples.

Unit IV
CONTROL STATEMENT IN PYTHON: If statement, Python syntax rules, truth test, while loop, break, continue, pass, for loops, loop coding techniques, examples.

Unit V
MODULES AND PACKAGE: Module creation, module usage, module namespaces, reloading modules, package import basics and examples, Biopython.

Text Book

1. Jason Kinser, "Python for bioinformatics" Jones and Bartlett Publishers, UK, 1st edition, 2009
2. Mark Lutz "Learning Python", O'REILLY Publication, USA, 4th Edition, 2009

Reference Book

1. Alex Martelli and David Ascher, "Python cookbook", O'Reilly, USA, 2nd Edition 2002.

12BI247 WEB PROGRAMMING LAB

Credits: 0:0:2

1. Creating a web page using HTML
2. Working with text
3. Working with hyperlinks
4. Working with list
5. Working with tables and frames.
6. Cascade style sheet using DHTML
7. Data binding using DHTML
8. Creating simple web page using XML.
9. Working with XML and XSL
10. XML with Perl
11. Web applications with perl
12. CGI Scripting.

12BI248 PYTHON PROGRAMMING LAB

Credits: 0:0:2

1. Basic programs
2. Program using Numbers
3. Strings
4. Lists
5. Dictionaries
6. Tuples
7. Files
8. If statement
9. while loop
10. for loops
11. Calculate the length of protein sequence (FASTA format)
12. Retrieve the PDB data from RCSB web page

12BI249 PROTEIN ENGINEERING

Credits: 3:0:0

Course Objective:

- To teach the principles of protein engineering, structural architecture of proteins and their functions.

Course Outcome:

- To understand the concept of Protein structure and function relationship and protein engineering.

Unit I

BONDS AND ENERGIES IN PROTEIN MAKEUP: Covalent, Ionic, Hydrogen, Coordinate, hydrophobic and Vander walls interactions in protein structure, Interaction with electromagnetic radiation (radio, micro, infrared, visible, ultraviolet, X-ray) and elucidation of protein structure.

Unit II

AMINO ACIDS AND THEIR CHARACTERISTICS: Amino acids – structure with three and single letter codes- molecular properties (size, solubility, charge, pKa), Chemical reactivity in relation to post-translational modification (involving amino, carboxyl, hydroxyl, thiol, imidazole groups) and peptide synthesis.

Unit III

PROTEIN ARCHITECTURE: Primary structure, Secondary structure - Alpha, beta and loop structures and Super-secondary structure (Alpha-turn-alpha, beta-turn-beta (hairpin), beta-sheets, alpha-beta-alpha, and TIM barrel structures), Tertiary structure - Domains, folding, denaturation and renaturation, Quaternary structure - Modular nature, formation of complexes.

Unit IV

STRUCTURE-FUNCTION RELATIONSHIP: DNA-binding proteins - prokaryotic transcription factors, Helix-turn-Helix motif in DNA binding, Trp repressor, Eukaryotic transcription factors, Zn fingers, helix-turn helix motifs in homeodomain, Leucine zippers, Membrane proteins and receptors bacteriorhodopsin and Photosynthetic reaction center, Immunoglobulins: IgG Light chain and heavy chain architecture.

Unit V

PROTEIN ENGINEERING: Advantages – Protein database analysis – methods to alter primary structure of proteins, examples of engineered proteins, thermal stability of T4-lysozyme, recombinant insulin to reduce aggregation and inactivation, *de novo* protein design – principles and examples.

Text Book

1. Voet D. and Voet G, "Biochemistry", John Wiley and Sons, New Jersey, 3rd Edition, 2001.

Reference Book

1. Sheldon J .P., and Jennifer R Cochran, " Protein engineering and design", Boca Raton: CRC Press, New York, 2010.

12BI250 PLANT TISSUE CULTURE

Credits: 3:0:0

Course Objective:

- To understand the concepts in plant tissue culture

Course outcome:

- To have clear understanding in methods and applications of plant tissue culture

Unit I

INTRODUCTION: Importance of Tissue culture techniques, Principles of plant tissue culture - Callus culture, Meristem culture, organ culture. Methods of culture– Media preparations, sterilization, isolation of plant material, Callus tissue and organogenesis, Micropropagation through organogenesis.

Unit II

PROTOPLAST CULTURE: Isolation of protoplast from various parts, Purification, Steps in Protoplast Culture, Protoplast fusion, Selection of fusion hybrids, Somatic cell Hybridization (r Cytoplast), Applications of protoplast fusion.

Unit III

MICROPROPAGATION AND SOMATIC EMBRYOGENESIS: Micropropagation-Advantages, Methods and Applications. Somatic embryogenesis – Genetic approach of somatic embryogenesis and Process, Obtaining embryos from culture, embryo maturation and development of germinablility, genetic control of embryo cloning, applications.

Unit IV

SOMACLONAL AND GAMETOCLONAL VARIATION: Genetic variation and crop improvement, mechanism of somaoclonal variation, Mutagenesis and somoclonal variation, Applications.

Unit V

BIOTECHNOLOGY AND CROP IMPROVEMENT: Plant breeding and concepts of crop improvement, methods for crop improvement, Gene transfer techniques, Transgenic plants.

Text Book

1. Purohit S.S, "Biotechnology- Fundamentals and Applications" Agrobios (India), Jodhpur, 3rd Edition, 2003.

Reference Book

1. Dubey, R.C, " A textbook of Biotechnology", S.Chand and Company Ltd, New Delhi, 2002.

12BI251 BIOPROCESS TECHNOLOGY

Credits: 3:0:0

Course Objective:

- To develop skills of the students in the area of Bio process technology with emphasis on Bioprocess principles.

Course Outcome:

- At the end of the course, the students would have learnt about fermentation processes, Kinetics of microbial growth etc. This will serve as an effective course to understand the basics of bioprocess related fields.

Unit I

OVERVIEW OF FERMENTATION PROCESSES: Overview of fermentation industry-Five groups of commercially important fermentation Process, Development of fermentation industry, general requirements of fermentation processes, Aseptic condition and containment.

Unit II

ISOLATION AND PRESERVATION OF INDUSTRIALLY IMPORTANT MICROBES: Isolation of industrially important microbes- selection of desired characteristics- Enrichment liquid culture, enrichment using solidified media, screening methods, Preservation of industrially important microbes- Storage at reduced temperature, dehydrated form.

Unit III

RAW MATERIALS AND MEDIA DESIGN FOR FERMENTATION PROCESS: Criteria for good medium, carbon, nitrogen, minerals, vitamins and other complex nutrients, oxygen requirements, medium formulation of optimal growth and product formation, examples of simple and complex media, medium optimization method - Plackett Burman Design, Response surface.

Unit IV

STERILIZATION KINETICS: Thermal death kinetics of microorganisms, batch and continuous heat sterilization of liquid media, filter sterilization of liquid media, air sterilization, design of sterilization equipment - batch and continuous.

Unit V

DEVELOPMENT OF INOCULUM FOR INDUSTRIAL FERMENTATION: Criteria for transfer of inoculum, development of inocula for yeast process - Brewing, Baker's yeast-development of inoculm for microbial processes, Effect of inoculum on morphology of filamentous organism in submerged culture.

Text Book

1. Peter F. Stanbury, Stephen J. Hall and A. Whitaker, "Principles of Fermentation Technology", Butterworth – Heinemann An Imprint of Elsevier India Pvt. Ltd., New Delhi, 2nd Edition, 2005.

Reference Book

1. Shuler, M.L. and Kargi, F. " Bioprocess Engineering - Basic concepts" Prentice Hall of India Pvt. Ltd., New Delhi, 2nd Edition, 2002.

12BI252 MEDICAL INFORMATICS

Credits: 3:0:0

Course Objective:

- To introduce students to the concepts and practices of health informatics

Course Outcome:

- Know the issues in health practices. Students are expected to gain insight in planning and building healthcare information systems; software design and human-computer interaction issues.

Unit I

INTRODUCTION TO MEDICAL INFORMATICS: Basic concepts in health informatics and its history, Definitions, Sub disciplines and professional organizations and activities.

Unit II:

MAJOR APPLICATIONS AND COMMERCIAL VENDORS: Major health informatics applications including electronic medical records (EHR) and computerized physician order entry (CPOE), Data interoperability of records, Medical controlled vocabularies and electronic data interchange standards, Commercial and open source applications.

Unit III

GOOD CLINICAL PRACTICES (GCP): GCP history and guidelines; India and the world in GCP, Standard operating procedure and guidelines, Current issues in India and abroad, Institutional review boards and protection of human health.

Unit IV

INFORMATION SYSTEMS DESIGN AND ENGINEERING: Planning and implementing issues of healthcare information systems, Software engineering principles, Human factors and human-computer interaction issues, and evaluation methods of end user acceptance and outcomes.

Unit V

NEW OPPORTUNITIES AND EMERGING TRENDS: Information technologies in healthcare; wireless and handheld devices, social computing paradigms, and eHealth applications, web-based tools.

Text Book

1. Taylor Paul, "From Patient Data to Medical Knowledge: The Principles and Practice of Health Informatics", Blackwell Scientific Publishing, UK, 2006.

Reference Book

1. Shortliffe and Cimino, "Biomedical informatics: computer applications in health care and biomedicine", Springer, NewYork, 3rd edition, 2006
2. Frank M. S. and Jeremy C. Wyatt, "ABC of health informatics", Blackwell publishing, Massachusetts, USA, 2006.

12BI253 PLANT TISSUE CULTURE LAB

Credits: 0:0:2

1. Preparation of media
2. Sterilization of media
3. Sterilization and inoculation of explants – plant 1
4. Sterilization and inoculation of explants – plant 2
5. Callus induction
6. Sub culturing from explants
7. Rooting media preparation, sterilization and rooting of explants
8. Micro grafting and hardening of explants
9. Genetic transformation by using Plasmid
10. Steps in micropropagation
11. Protoplast preparation methods
12. Protoplast fusion

12BI254 MEDICAL LAB TECHNOLOGY

Credits: 0:0:2

1. Blood Pressure and Pulse rate
2. Clotting time, Bleeding time
3. Haemoglobin estimation
4. Erythrocyte Sedimentation Rate
5. Packed cell volume
6. Prothrombin time
7. Differential count
8. Total Red Blood cell count
9. Total White blood cell count

10. Platelet count
11. Eosinophilic count
12. Reticulocyte count

12BI255 BIOLOGICAL DATABASES

Credits: 3:0:0

Course Objective:

- To provide the basic knowledge about the field of Bioinformatics.
- It highlights the need for the databases in the field of Bioinformatics.
- It provides knowledge about various Biological databases available and their diverse utilities to benefit the researchers.

Course Outcome:

- From this course the students would learn about the needs for biological databases and practical knowledge on retrieving various, yet useful information that would encourage them to take part in the research activities pertaining to the field of Bioinformatics and are motivated to use their knowledge and skills to solve biological problems.

Unit I

INTRODUCTION TO BIOINFORMATICS: Basic concepts: Cell - Gene- Genome- Genetic code – Central dogma – Nucleic acids and proteins – Biological sequence data – Need for biological databases.

Unit II

SEQUENCE DATABASES: Databanks – nucleotide databanks – Genbank, NCBI, EMBL, DDBJ – protein sequence databanks – PIR, SWISSPROT, TrEMBL.

Unit III

STRUCTURAL DATABASES: Protein secondary structure- Ramachandran plot- Tertiary and quaternary structure of proteins databases: - PDB, SCOP, CATH, SSEP, CADB, THGS, SMS, Pfam and GDB.

Unit IV

ENZYME AND PATHWAY DATABASES: Role of enzymes in Biochemical pathways- Enzyme databases- MEROPS, BRENDA. Pathway databases - CAZy. Disease databases and Literature databases.

Unit V

APPLICATIONS OF BIOLOGICAL DATABASESS: Biological databases in bioinformatics research – Essential prerequisites – Scope of bioinformatics – Useful sites – Bioinformatics in pharmaceutical industry – Bioinformatics orientation in IT industry.

Text Book

1. Orpita Bosu and Simminder Kaur Thukral, “BIOINFORMATICS Databases, Tools and Algorithms”, Oxford University Press, London, 2007

Reference Book

1. T.K.Attwood and D.Parry-Smith, "Introduction to Bioinformatics", Pearson Education, New Delhi, 2001.

12BI256 MOLECULAR SIMULATION AND ENGINEERING

Credits: 3:0:0

Course Objective:

- The aim of this course is to provide the student with the basic statistical mechanics principles behind current methods in molecular simulation and also introduce these simulation techniques. It is expected that the student will have a deeper understanding of the molecular basis of physical behavior.

Course Outcome:

- The course will introduce the student to the chemistry and physics behind the methods, accomplished through self-contained lectures on classical and quantum mechanics, and fundamentals of statistical mechanics.
- The course will provide a broad overview of the many different (both established and recent) simulation techniques.
- The course will expose the student to current and relevant applications in molecular simulation and modeling.

Unit I

INTRODUCTION: Useful Concepts in Molecular simulation - Coordinate systems - Computer hardware and software. Potential energy functions, Energy minimization, and Molecular Dynamics - Introduction to LINUX.

Unit II

COMPUTER SIMULATION METHODS: Force Fields. Hydrogen Bonding in Molecular Mechanics. Calculation of thermodynamic properties – Phase space – Practical aspects pf computer simulation – Boundaries monitoring equilibrium – Long range process – Analyzing result of simulation and estimating errors.

Unit III

MOLECULAR DYNAMICS SIMULATION METHOD: Molecular Dynamics using simple modules – Molecular Dynamics with continuous potentials – Running Molecular Dynamics simulation – Constant dynamics – Time dependent properties – Molecular Dynamics at constant temperature and pressure.

Unit IV

MONTE CARLO SIMULATION METHOD: Metropolis methods – Monte Carlo simulation of molecules – Monte Carlo simulation of polymers – Calculating chemical potentials – Monte Carlo or Molecular Dynamics-Models Used in Monte Carlo Simulations of Polymers - Molecular Modeling software.

Unit V

BIOMOLECULAR INTERACTION AND DRUG DESIGN: Molecular modeling in drug discovery – deriving and using 3D Pharmacores – Molecular docking – Structure Based methods to identify lead components- *De novo* ligand design.

Text Book

1. Leach A.R, "Molecular Modelling Principles and Application", Pearson – Prentice Hall, New Delhi 2nd Edition 2001.

Reference Book

1. Satya P.G., "QSAR and Molecular Modeling", Springer - Anamaya Pub, New Delhi 2008.
2. N. Claude C., "Molecular Modeling in Drug Design", Academic Press, California, 2006.

12BI257 COMPUTER AIDED DRUG DESIGN

Credits: 3:0:0

Course Objective:

- To understand the critical relationship among biomolecular structure, function
- To be able to utilize secondary structure prediction server.
- To understand the SNPs and Computer Aided Drug Design.

Course Outcome:

- Students are introduced to the principles and practice of protein structure prediction and modern drug discovery.

Unit I

INTRODUCTION: Computational biology application, Major databases, Data management, computational molecular biology, Central dogma, Data retrieval, Data mining, Sequence alignment

Unit II

PROTEIN STRUCTURE: Classification, Visualization, Protein structure database, Visualization tools, Tool for protein ligand interaction, Motif and domains, Protein – protein interaction.

Unit III

STRUCTURE PREDICTION: Methods of sequence based structure prediction, Ab initio approach for structure prediction, Methods of 2-D structure prediction, Protein function prediction, Homologous modeling.

Unit IV

DRUG DISCOVERY: Pharmacogenetic and pharmacogenomic application, SNPs, Important parameter for drug discovery. Drug and target discovery technology and strategy, Target validation.

Unit V

COMPUTER AIDED DRUG DESIGN: Drug design approaches, Structure based *de novo* Methods, ADME-Tox property prediction.

Text book

1. Rastogi, S. C., “Bioinformatics; Methods and applications; Genomics, Proteomics and Drug Discovery”, PHI Learning Publishers, New Delhi, 2010.

Reference books

1. Gautham N., “Bioinformatics”, Narosa Publishing Company, New Delhi, 2006.
2. Vasantha Pattabhi and N.Gautham, “Biophysics”, Narosa Publishing Company, New Delhi, 2001.
3. Lesk, A.M., “Introduction to Bioinformatics”, Oxford University Press, Oxford, UK, 1st Edition, 2001.

12BI301 MOLECULAR CELL BIOLOGY

Credits: 4:0:0

Course Objective:

- To provide an insight to molecular biology and techniques before stepping into the computational biology.

Course Outcome:

- To understand about cellular architecture, transport and signaling.
- To relate gene expression and its regulation with cell function.

Unit I

BIOMEMBRANES AND CELL ARCHITECTURE: Biomembranes: Lipid composition and structural organization, protein components and basic function. Cell: Organelles of eukaryotic cell, cytoskeleton components and structural functions. Overview of cell cycle and its control in eukaryotes.

Unit II

CELLULAR TRANSPORT: Cell-cell and cell-matrix adhesion, An overview of junctions and adhesion molecules, Extra cellular matrix. Membrane transport: ATP powered pumps, gated and nongated ion channels, action potential in nerve cells, signal transmission at synapses, symporters, antiporters, transepithelial transport.

Unit III

CELLULAR ENERGETICS AND CELL SIGNALING: Oxidation of glucose and fatty acids to CO_2, Electron transport and proton motive force, Synthesis of ATP. Signaling at cell surface: G Protein coupled Receptors (GPCR), TGFβ receptor, Receptor Tyrosine Kinase.

Unit IV

GENE EXPRESSION: Central dogma, DNA Replication and transcription in prokaryotes and eukaryotes, Post-transcriptional modification - RNA splicing. Process of translation in prokaryotes and eukaryotes, Post-translational modifications, Inhibitors of protein synthesis.

Unit V

REGULATION OF GENE EXPRESSION: Control in Bacteria and phages – Inducible and catabolite repression (Lac operon), Repressible and Attenuation (Trp operon), Lytic and Lysogenic cycles in Phage λ. Control in Eukaryotes: Cis and trans regulatory elements, Chromatin in gene regulation, transcriptional control, translational control, RNA interference in medical applications.

Text Book

1. Harvey Lodish, Arnold Berk, Paul Matsudaira, "Molecular cell biology", WH Freeman & Company, New York, 5th edition, 2004.

Reference Books

1. David R Hyde, "Genetic and Molecular Biology", Tata McGraw Hill Publications, New Delhi, 2010.
2. Bruce Alberts, Alexander Johnson and Julian Lewis, "Molecular Biology of the Cell", Garland Science, NY, 5th edition, 2008.

12BI302 COMPUTATIONAL GENOME AND PROTEOME ANALYSIS

Credits: 3:0:0

Course Objective:

- To provide the students with a foundation for application of available computational tools in genomics and proteomics

Course Outcome:

- To learn the principle and strategies of computational genome and proteome analysis and their applications.

Unit I

GENOME MAPPING: Genome sequencing and assembly, Human genome project, databases - nucleic acid and protein sequence, structural databases. Physical mapping of DNA. Experimental approaches to restriction mapping, Building contigs from cloned genome fragments, Minimal tiling clone sets and Finger printing.

Unit II

SEQUENCE ALIGNMENT METHODS: Global alignment, Local alignment, Scoring rules, Multiple alignment, Search strategies, Regions of similarity using FASTA, BLAST, Scoring matrices for protein sequences.

Unit III

GENE EXPRESSION ANALYSIS: Design of microarray experiments, Gene expression in human fibroblasts, Diffuse large B-cell lymphomas, MALDI-MS, SAGE, Protein microarrays.

Unit IV

PROTEIN INTERACTIONS AND METABOLOMICS: Methods to study Protein interactions- Genetic approaches, Biochemical methods, Yeast two-hybrid system, Protein interaction databases. Metabolomics- metabolite analysis, metabolomic studies in humans.

Unit V

COMPARATIVE GENOMICS: Compositional measures, Transposable elements, Sequence organization within chromosomes, Identifying conserved segments and segmental duplications, genome evolution by whole genome duplication, Gene content, Gene prediction from local sequence content, Comparative methods for identifying genes, Predicted proteome, Assigning gene function.

Text Book

1. Richard C. Deonier, Simon Tavare and M.S.Waterman, "Computational Genome Analysis – An introduction", Springer, 2005.

Reference Books

1. J. Pevzner, "Bioinformatics and functional genomics", 2nd Edition, John Wiley & Sons, NJ, USA, 2009.
2. A. D. Baxevanis and B. F. F. Ouellette, "Bioinformatics - A Practical Guide to the Analysis of Genes and Proteins", John Wiley & Sons Publication, NJ, USA, 2nd Edition, 2001.
3. S. B. Primrose and R. M. Twyman, “Principles of Gene manipulation and Genomics”, , Blackwell Publishings, USA, 7th Edition, 2006.

12BI303 BIOINFORMATICS ALGORITHMS

Credits: 3:0:0

Course Objective:

- To introduce the student to the biology of bioinformatics and to make them understand the algorithms to solve problems.

Course Outcome:

- To thoroughly describe and apply different algorithms for sequence analysis, analysis of gene expression data and molecular biological networks.
- To independently implement commonly used algorithms for sequence comparisons, analysis of gene expression data and graph theoretical problems relating to bioinformatics

Unit I

ALGORITHMS AND COMPLEXITY: Introduction, Biological algorithm versus computer algorithms, The change problem, Correct versus Incorrect algorithms, Recursive algorithm, Towers of Hanoi problem, Big O notation, Algorithm design techniques.

Unit II

EXHAUSTIVE SEARCH: Restriction Mapping, Impractical and practical restriction mapping Algorithm, Profiles, The motif finding problem.

Unit III

GRAPH ALGORITHMS: Introduction to Graphs, NP, Complete problem, Eulerian cycle, Hamiltonean cycle, Graphs and genetics, Shortest Superstring Problem, DNA array sequencing technique, Sequencing by Hybridization, SBH as a Hamiltonean path problem, SBH as a Eulerian path problem.

Unit IV

PATTERN MATCHING ALGORITHMS: Combinatorial pattern matching, Repeat finding, Hash tables, Exact pattern matching, Suffix trees, Heuristic similarity search Algorithms, Approximate Pattern matching.

Unit V

EVOLUTIONARY TREE ALGORITHMS: Introduction, Distance based tree Reconstruction, Reconstructing trees from additive matrices, Character based Tree Reconstruction, Sankoff Algorithm, Fitch Algorithm, Evolutionary trees and Hierarchical clustering, CG islands, Gibbs sampling.

Text Book

1. Neil Jones & Pavel Pevzner, "An Introduction to Bioinformatics Algorithms", MIT Press, USA, 2004.

Reference Book

1. M. Waterman, “Introduction to Computational Biology: Maps, Sequences & Genomes”, CRC Press, London, UK, 1995.

12BI304 ADVANCED PERL AND BIOPERL

Credits: 3:0:0

Course Objective:

- To focus on programming concepts such as variables, arrays, loops, subroutines and input/output in Perl.
- To make students to understand several concepts relatively idiosyncratic to Perl, such as associative arrays, Perl regular expressions, and system interfaces.

Course Outcome:

- Students will be able write Perl code for local biological problems.
- Students will work in Internet through programming.

Unit I

INTRODUCTION: History of Perl – Perl Benefits – Installing Perl - Running Perl Programs - Using Perl on Windows and UNIX – Data types – Operators – variables – Variable Interpolation, Control statements - Arrays.

Unit II

SUBROUTINES: Subroutines for calculation, Reference to subroutine, Passing arrays and hashes to subroutines. Regular Expression – Working with regular expression. File Handling –

Writing to Files.

Unit III

OOPs IN PERL: Perl standard modules. Object oriented Perl – Working with objects. Perl and Databases – Perl and DBM

Unit IV

GRAPHICS AND WEB APPLICATION: Web server and browsers; Common gateway interfaces, rebase; Computer graphics: GD, adding GD graphic to restriction map module, exercises.

Unit V

BIOPERL: Bioinformatics applications, 5 modules; Simple Perl application on motif, Genbank/file handling applications.

Text Book

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

Reference Book

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

12BI305 MOLECULAR CELL BIOLOGY LAB

Credits: 0:0:2

List of Practical

1. Exercises and problems in Mendelian Genetics
2. Exercises and problems in Linkage and mapping
3. Isolation of plasmid DNA
4. Isolation of genomic DNA from bacteria.
5. Isolation of genomic DNA from chloroplast.
6. Isolation of genomic DNA from human samples
7. Spectrophotmetric determination of Nucleic acid purity and concentration
8. Restriction enzyme digestion of DNA
9. Cloning: Preparation and transformation of competent *E. coli* cells
10. Agarose gel electrophoresis
11. *Invitro* amplification of DNA using PCR
12. Cell culture techniques (demo)

12BI306 COMPUTATIONAL GENOME AND PROTEOME ANALYSIS LAB

Credits: 0:0:2

List of Practical

1. Nucleotide Sequence databases
2. NCBI – Viral and Bacterial Genome analysis

3. Genome Browser Application
4. Heuristic Methods of biological sequence analysis – FASTA and BLAST
5. Pairwise and Multiple alignment - GCG
6. Comparative genomics
7. Gene finding and Pattern recognition – GCG
8. Sequence Utilities, Translation and Nucleic Acid Secondary Structure – GCG
9. Evolution Analysis and Hidden Markov Model (HMM) Alignment – GCG
10. Gene prediction methods
11. EMBOSS
12. *In silico* molecular biology techniques
13. PAGE
14. *In silico* protein interaction studies

12BI307 BIOINFORMATICS ALGORITHMS LAB

Credits: 0:0:2

List of Practical

1. Recursive problem
2. The change problem
3. Restriction mapping problem
4. Motif finding problem from a given sequence
5. Profile finding problem from a given sequence
6. Shortest superstring problem and DNA array sequencing techniques
7. Sequence by Hybridization as a Hamiltonian path problem
8. Sequence by Hybridization as a Eulerian path problem
9. Exact pattern matching
10. Approximate pattern matching
11. Distance based tree reconstruction
12. Character based tree reconstruction

12BI308 ADVANCED PERL LAB

Credits: 0:0:2

List of Practical

1. Control and loop statements
2. Functions and subroutines
3. Command line argument & File handling
4. Regular expressions
5. Perl web server
6. Use of arrays
7. String manipulation
8. Modules: LWP and BioPERL
9. DNA & Protein sequence analysis
10. PERL and DBI
11. PERL and CGI
12. PERL and Graphics

12BI309 STRUCTURAL BIOINFORMATICS AND INSTRUMENTAL TECHNIQUES

Credits: 3:0:0

Course Objective:

- To study the strategy and tactics of biophysical concepts of macromolecules and the conformational analysis and forces those determine the protein and nucleic acid structure and ligand interaction with macromolecules.
- To study the size and shape of the macro molecule using different techniques using various tools like X-ray crystallography and other techniques is explained.

Course Outcome:

- To enable the student to learn the different structural levels of biological macromolecules, their conformations and forces involved in stabilization and the tools needed for the analyses.

Unit I

INTRODUCTION: Levels of structures in biological macromolecules, basic strategies in biophysics, Principles and concepts used in biophysical analysis of life processes, biomolecules and their interactions, size and shape of macromolecules.

Unit II

AMINO ACIDS AND PROTEINS: Structure of proteins, Properties of amino acids, Ionization of amino and carboxyl groups in amino acids and peptides, Ionization of side chains, configuration of natural amino acids, polarity of amino acid side chains, composition of proteins, amino acid composition, predicting properties from amino acid compositions.

Unit III

CONFORMATIONAL ANALYSIS OF PROTEINS: Basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions, ionic interactions, disulphide bonds, prediction of proteins structure.

Unit IV

STRUCTURAL ANALYSIS OF NUCLEIC ACIDS: General characteristics of nucleic acid structure, geometrics, glycosidic bond, rotational isomers and those puckering, backbone rotational isomers and ribose puckering, forces stabilizing ordered forms, base pairing, base stacking tertiary structure of nucleic acids.

Unit V

INSTRUMENTAL TECHNIQUES: X–ray diffraction-X-ray crystallography, determination of molecular structures, electron microscopy, neutron scattering and light scattering.

Text Book

1. Cantor, R. and Schimmel, P. R., “Biophysical Chemistry”, Vol. I, II, W. H. Freeman & Co., 2004.

Reference Book

1. Gu, J. and Bourne, P. E., "Structural Bioinformatics", 2nd Edition, Wiley, 2009.

12BI310 MOLECULAR MODELING AND SIMULATION

Credits: 4:0:0

Course Objective:

- To understand the quantum mechanical concepts and advanced *ab initio* force field models.
- To provide knowledge in the principles of molecular mechanics and dynamics.
- To enable the students to practically apply modeling and simulation.

Course Outcome:

- To be empowered in the theoretical knowledge of molecular modeling and applications.
- To be skilled in the practical molecular simulation and analysis in computational biological problems.

Unit I

COMPUTATIONAL QUANTUM MECHANICS: Introduction to quantum mechanics – postulates – Operators - Schrodinger wave equation – Born-Oppenheimer approximation Molecular Orbital Theory – Hartree – Fock equations – Calculating molecular properties using *ab inito* quantum mechanics - Electron density distributions - Cartesian and internal coordinates.

Unit II

ADVANCED *ab initio* METHODS AND FORCE FIELD MODELS: Practical considerations when performing *ab initio* calculations – Density functional theory – Empirical force field models - molecular mechanics - United atom force fields – parametrisation and transferability of force fields – force fields for solid state systems – empirical potentials.

Unit III

METHODS FOR EXPLORING ENERGY SURFACE: Energy minimization methods - statement of the problem - Simplex and Sequential univariate methods – Steepest descent minimization – Conjugate gradient method - Newton-Raphson method – monitoring the equilibration – Long-range forces in Computer simulation methods.

Unit IV

MOLECULAR SIMULATION AND CONFORMATIONAL ANALYSIS: Introduction – Molecular Dynamics Simulation – Monte Carlo simulation – Random number generation – Difference in MD & MC – Systematic methods for exploring conformational space – model building and random search – simulated annealing – Comparison of different conformational search approaches.

Unit V

APPLICATIONS OF MOLECULAR MODELING AND CHALLENGES: Comparison of 3D structures – Steps in Homology modeling – tools – databases – side chain modeling – loop modeling – Free energy calculations – Entropy and enthalpy differences - threading – molecular docking - Structure based drug design – molecular descriptors – QSAR.

Text Book

1. Leach A.R, "Molecular Modelling Principles and Application", Pearson – Prentice Hall, New Delhi, 2nd Edition, 2001.

Reference Books

1. Alan Hinchliffe, "Molecular Modelling for Beginners", John Wiley – Thomson Press, Chennai, 2003.
2. Satya Prakash G., "QSAR and Molecular Modeling", Springer - Anamaya Pub, New Delhi 2008.
3. N. Claude C., "Molecular Modeling in Drug Design", Academic Press, California, 2006.

12BI311 PATTERN RECOGNITION AND MACHINE LEARNING

Credits: 4:0:0

Course Objective:

- To know the concepts and applications of machine learning.
- To provide an insight to machine learning technique before stepping into Artificial Intelligence and mathematical modeling.

Course Outcome:

- To understand and apply fundamental machine learning techniques from theory to practical.
- To develop enhanced critical and conceptual thinking and problem solving skills.

Unit I

INTRODUCTION: Example of machine learning application, Polynomial curve fitting, Probability theory, Model selection, The curse of dimensionality, Decision theory, Information theory.

Unit II

BAYESIAN DECISION THEORY: Introduction, Classification, Losses and risk, Discriminant functions, Utility theory, Association rules. Parametric methods: Introduction, Maximum likelihood estimation, Evaluating an estimator, The Bayes' estimator, Parametric classification, Regression, Tuning model complexity, Model selection procedures.

Unit III

MULTIVARIATE METHODS AND CLUSTERING: Multivariate data, Parameter estimation, Estimation of missing values, Multivariate normal distribution, Multivariate classification, Tuning complexity, Discrete features, Multivariate regression. Clustering: Introduction, Mixture densities, k-Means cclustering, Expectation-Maximization algorithm, Mixtures of latent variable models, Supervised learning after clustering, Hierarchical clustering, Choosing the number of clusters.

Unit IV

NEURAL NETWORK AND HIDDEN MARKOV MODEL: Feed-forward network Functions, Network training, Error back propagation, The Hessian matrix, Regularization in neural networks, Mixture density networks, Bayesian neural networks. Hidden Markov Models: Introduction, Discrete Markov processes, Hidden Markov Models, Three basic problems of HMMs, Evaluation problem, Finding the state sequence, Learning model parameters, Continuous observations, The HMM with input, Model selection in HMM.

Unit V

GRAPHICAL MODELS: Bayesian networks, Conditional independence, Markov random fields, Inference in graphical models. Approximate inference: Variational inference, Illustration: Variational mixture of Gaussians, Variational linear regression, Exponential family distributions, Local variational methods, Variational logistic regression, Expectation propagation.

Text Books

1. Ethem Alpaydin, "Introduction to Machine Learning", MIT Press, USA, 2nd Edition, 2004.
2. Christopher M. Bishop, "Pattern Recognition and Machine Learning", Springer, Heidelberg, First Edition 2006.

Reference Book

1. Sushmita Mitra, Sujay Datta, Theodore Perkins and George Michailidis, "Introduction to Machine Learning and Bioinformatics", CRC Press, London, UK, 2008.

12BI312 MICROARRAY AND IMAGE PROCESSING

Credits: 4:0:0

Course Objective:

- To explain how microarray technology works, including the various types, and analyze data sets that are produced by microarrays.

Course Outcome:

- To analyze microarray data sets and design simple gene regulatory networks for few genes and assess its performance.

Unit I

INTRODUCTION: Types of microarrays, Microarray technologies, Using microarray, Microarray standard databases: LIMS, MGED, MAGE, Microarray sequence databases - primary and secondary databases.

Unit II

OVERVIEW OF MICROARRAY EXPERIMENTS AND IMAGE ANALYSIS: Microarray chip manufacture, steps in microarray experiment, Image processing- Microarray data cleaning and preprocessing, Data normalization.

Unit III

IMAGE FEATURE EXTRACTION: Identifying the positions of the features – Identifying the background pixel normalization, Data cleaning and transformation – Linear and non linear regression of log ratio against average density.

Unit IV

ANALYSIS OF DIFFERENTIALLY EXPRESSED GENES: Statistical inference, Hypothesis test, fold change methods, parametric test- paired t- Test, Unpaired t-Test, Non-parametric tests- classical and bootstrap analysis, ANOVA- One way and Two way.

Unit V

GENE BASED ANALYSIS: Proximity measurement for gene expression data - Euclidean distance, Correlation Coefficient, Partition Based approaches - K-means and its variation, SOM and its Extensions, model based clustering, Hierarchical approaches.

Text Books

1. Dov Stekel, "Microarray Bioinformatics" Cambridge University Press, UK, 2005.
2. Aidong Zhang, "Advanced analysis of Gene expression microarray data", World Scientific Publishing House, New Delhi, 2006.

Reference Book

1. Pierre Baldiand and Wesley Hatfield, "DNA microarrays and gene expression from experiments to data analysis and modeling", Cambridge University Press, New York, 2002.

12BI313 GRAPH THEORY AND SYSTEMS BIOLOGY

Credits: 3:0:0

Course Objective:

- This course helps them to understand concept of graph theory and network studies.
- The different algorithm related to Systems Biology and software used will be discussed in the course.

Course Outcome:

- Students will understand the network properties and will be able to design their own network through systems biology software.

Unit I

GRAPH THEORY: Graphs as models - connected graphs – k-connected graphs -2 connected graphs - connectivity of digraphs - k-connected and k-edge-connected graphs.

Unit II

BASICS OF SYSTEMS BIOLOGY: Introduction - Basic concepts in system Biology - Metabolic Networks - Transcriptional Regulatory Networks - Signaling Networks.

Unit III

MODELING ALGORITHMS: Kinetic Modeling - Cellular Network reconstruction and Static Modeling - Construction and verification and verification of kinetic models - introduction to DBsolve - Enzyme Kinetics modeling.

Unit IV

MODELING AND SIMULATION ALGORITHMS: Kinetic models of biochemical pathways - Modeling biochemical network - Kinetic models of excitable membranes and synaptic interactions, Stochastic simulation of cell signaling pathways

Unit V

SOFTWARE'S APPLICATION IN SYSTEMS BIOLOGY: Statistical tools for gene expression analysis and system Biology- Software for modeling and simulation-The ERATO system biology work Bench, Cytoscape, Gepasi, and Cell Designer.

Text Books

1 Bernhard Palsson, "Systems Biology Properties of reconstructed networks", Cambridge University Press, UK, 2009
2 Oleg Demin and Igor Goryanin, "Kinetic Modelling in Systems Biology", CRC Press, London, 2009.

Reference Books

1 Hiroaki Kitano, "Foundations of Systems Biology", MIT Press, 2001
2 Douglas B.West, "Introduction to Graph Theory", Prentice-Hall, India, 2000.

12BI314 STRUCTURAL BIOINFORMATICS AND INSTRUMENTATION LAB

Credits (0:0:2)

List of Practical

1. The levels of protein structure
2. The properties and composition of amino acids for different proteins
3. The geometrical parameters for different proteins
4. The Ramachandran diagram (Phi-Psi map) for different proteins
5. Study and view the non-bonded interactions of proteins with/without ligands
6. Study the protein data bank text files of one or two protein molecules.
7. The structural characteristics of different RNA molecules with/without protein
8. The structural characteristics of different DNA molecules with/without protein
9. Crystallization process for small and macro molecules (demo)
10. The principle and working condition of X-Ray Diffractometer (demo)
11. Solving the structure of small molecules (demo)

12. The principle and working condition of Electron Microscope (demo)

12BI315 MOLECULAR MODELING AND SIMULATION LAB

Credits: 0:0:2

List of Practical

1. Molecular modeling – Small Molecule Databases
2. Molecular simulation of tripeptides and carbohydrate
3. *ab initio* structure prediction
4. Homology modeling
5. Nucleic Acids structural modeling
6. Energy minimization of biomolecules - 1st order
7. Energy minimization of biomolecules - 2nd order
8. Molecular Dynamics simulation
9. Monte Carlo simulation
10. Visualization of Molecular Dynamics
11. Molecular Docking studies
12. Protein structure function relationship activity

12BI316 MACHINE LEARNING IN BIOINFORMATICS LAB

Credits: 0:0:2

List of Practical

1. Exercise for making Hypothesis and Model based on Probability theory.
2. Application of Bayesian Theory on the designed Model.
3. Application of Graph Theory for refining the Model.
4. Exercise on the Best Model Selection Procedures.
5. Designing of Model Based on Single Die.
6. Exercise for writing algorithms for solving basic Bioinformatics Problem.
7. Introduction to MATLAB.
8. Application of Fuzzy Logic concept.
9. Artificial Neural Network for Bioinformatics.
10. Practical Application of Bioinformatics Tools of MATLAB.
11. Application of Genetic Algorithm in Bioinformatics.
12. Problem Solving based on Hidden Markov Model.

12BI317 MICROARRAY DATA ANALYSIS LAB

Credits: 0:0:2

List of Practical

1. Gene expression analysis by GEO of NCBI
2. Functional genomics experiments from ArrayExpress of EBI
3. Data analysis through SMD

4. Gene Expression Database
5. Data analysis and visualization
6. Normalization of data
7. Prediction Analysis for Microarrays
8. Supervised learning software for genomic expression data mining
9. Perform hierarchical clustering, self-organizing maps.
10. Correlation analysis
11. Analyzing gene co-expression networks built from microarray expression data
12. Gene expression experiments in the context of biological pathways

12BI318 SYSTEMS BIOLOGY AND SIMULATION LAB

Credits: 0:0:2

List of Practical

1. Genomic tools for analyzing transcriptional regulatory networks
2. Essential gene identification
3. Diseased gene identification through GeneCards and Entrez Gene
4. Database analysis for protein-protein interaction
5. Microarray dataset analysis
6. Designing protein interaction through cell designer
7. Pathway analysis
8. Network creation and analysis
9. K-core analysis of the protein
10. Protein network simulation
11. Whole cell simulation through E-cell/V-cell
12. Statistical tool for gene expression analysis

12BI319 CHEMINFORMATICS AND QSAR

Credits: 3:0:0

Course Objective:

- To introduce Cheminformatics with special emphasis on applications including modern drug discovery.

Course Outcome:

- To retrieve specific information from the enormous and rapidly expanding chemical literature.
- To provide a broad overview of the computer technology to chemistry in all of its manifestations
- To expose current and relevant applications in QSAR and Drug Design.

Unit I

INTRODUCTION TO CHEMINFORMATICS: The domain of Chemistry - The scope of Cheminformatics - Learning in Cheminformatics, Structure Elucidation - Quantitative Structure - Activity Relationships - Chemical Reaction and synthesis design

Unit II

DATABASES AND DATA SOURCES IN CHEMISTRY: Data, Information and Knowledge Data Preprocessing - Variable selection - Preparation of datasets for validation of the model quality - Databases in the Information system-Catalogs of Chemical Compound - ChemInform RX-Reaction Retrieval.

Unit III

CALCUALTION OF DESCRIPTORS: Empirical approaches to the Calculation of Properties - Drug Receptor Binding energies - Ways to Speed up the calculation - Properties from Quantum Mechanical Calculations - Classification of Structure Descriptor - Quantitative Descriptors of Chirality - BCUT Descriptors - HYBOT Descriptors - 4D QSAR

Unit IV

METHODS FOR DATA ANALYSIS: Chemometrics - Multivariate Statistics – Correlation - Multiple Linear Regression Analysis (MLRA) - Principle Component Analysis (PCA) - Principle Component Regression (PCR) - Partial Least Square Regression (PLS) - Selection of Relevant Descriptors in a Structure-Activity Study - Prediction and Regression - Leave One Out (LOO) Methods

Unit V

APPLICATIONS: Prediction of Properties of Compounds - Linear Free Energy Relationship (LFER) - Quantitative Structure-Property Relationship (QSAPR) model - Target Identification and Validation - Lead Finding and Optimization - Preclinical and Clinical Trials - Fields of Application of Chemiinformatics in Drug Design - Design of Combinatorial Libraries.

Text Book

1. Johann Gasteiger and Thomas Engel, "Cheminformatics: A textbook" WILEY VCH Publisher, Germany, 2003.

Reference Book

1. Andrew R. Leach and Valerie J. Gillet, "Introduction to Cheminformatics", Kluwer Academic Publisher, Netherlands, 2003.

12BI320 MEDICAL INFORMATICS

Credits: 3:0:0

Course Objective:

- To give an idea on the applications of information technology in medical field.

Course Outcome:

- To have an overview of medical informatics as a discipline.
- To develop skills and concepts fundamental to more advanced topics in health informatics.

Unit I

INTRODUCTION: Introduction - Hospital management and information system: functional area - pre-requisites - integrated hospital information systems - health information system - and disaster management plan.

Unit II

KNOWLEDGE BASED EXPERT SYSTEMS: Artificial intelligence - expert systems - materials and methods - computer based patient Records - computer assisted medical education, modern medical equipments (Digital X-ray etc.).

Unit III

MODULES: Hospital Management and Information systems - structure and functions - computer assisted patient education, computer assisted patient surgery.

Unit IV

COMPUTER ASSISTED SURGICAL TECHNIQUES:
Three-dimensional imaging: limitations of endoscopy and imaging - benefits of virtual endoscopy- materials and methods – limitations - applications - merits and demerits - surgical simulation - virtual environment.

Unit V

TELECOMMUNICATION BASED SYSTEMS: Tele-medicine – needs - materials and methods - Internet tele-medicine- controversial issues – reliability - cost analysis – applications - tele-surgery - the Internet, Database of medical informatics.

Text Book

1. Mohan Bansal, "Medical Informatics - a primer", Tata McGraw-Hill, New Delhi, 2003.

Reference Book

1. Hsinnchun Chen, "Medical Informatics: Knowledge Management and Data Mining in Biomedicine", Springer-Verlag, New York, 2005.

12BI321 ENZYME ENGINEERING

Credits: 3:0:0

Course Objective:

- To understand the concepts in enzymology and enzyme techniques.

Course Outcome:

- To have clear understanding in isolation, purification and characterization of enzymes
- To understand the enzyme engineering technologies

Unit I

APPLICATIONS OF ENZYMES: Classification of Enzymes; Purification and characterization of enzymes from natural sources, Comparison of chemical and enzyme catalysis.

Unit II

ISOLATION OF ENZYMES: Extraction and Purification of Crude Enzyme extracts from plant, animal and microbial sources-some case studies; methods of characterization of enzymes; development of enzymatic assays.

Unit III

MECHANISMS AND KINETICS OF ENZYME ACTION: Mechanisms of Enzyme Action; Concept of active site and energetics of enzyme substrate complex formation; Specificity of enzyme action; Kinetics of single substrate reactions; turnover number; estimation of Michaelis-Menton parameters. Multi-substrate reaction mechanisms and kinetics.

Unit IV

ENZYME INHIBITION: Types of Inhibition- kinetic models; Substrate and Product Inhibition; Allosteric regulation of enzymes; Deactivation kinetics.

Unit V

ENZYME IMMOBILIZATION: Physical and Chemical techniques for enzyme, Immobilization-adsorption, matrix entrapment, encapsulation. cross-linking. covalent binding – examples; Advantages and disadvantages of different Immobilization techniques. Overview of applications of immobilized enzyme systems.

Text Book

1. Trevor palmer, "Understanding Enzymes", East West Press Pvt. Ltd., New Delhi, 2004.

Reference Book

1. Colin Ratledge and Bjorm Kristiansen , "Basic Biotechnology", Cambridge University Press, UK, 3rd edition, 2002.

12BI322 CHEMINFORMATICS LAB

Credits: 0:0:2

List of Practical

1. Sketching the chemical reaction and calculate the properties
2. Sketching the small molecules
3. Physiochemical Descriptors Calculation
4. Structural Descriptor Calculations
5. Databases and datasources in Chemistry
6. Overview of macromolecules and their interaction with micro molecules
7. Binding affinities calculations of molecule
8. Prediction of binding activities
9. 2D QSAR based upon physiochemical properties
10. 3D QSAR based upon atomic orientation
11. 4D QSAR based upon geometric orientation
12. Validation of QSAR model

12BI323 MEDICAL INFORMATICS LAB

Credits: 0:0:2

List of Practical

1. General concepts in Medical Informatics
2. Collect the patient data through internet.
3. Analysis the data
4. Collect the new forms of clinical information
5. Electronic Health Record analysis
6. Find the doctor using of information sources
7. How to apply Probability in health informatics data.
8. Use truth tables in medical informatics data
9. Apply predicate calculus in medical bioinformatics
10. Hospital Management and Information systems
11. Statistical hypothesis testing in Medical informatics
12. Clinical data management (an overview)

12BI324 ENZYME ENGINEERING LAB

Credits: 0:0:2

List of Practical

1. Estimation of Acid Phosphatase from potato
2. Kinetic studies - Effect of pH on the activity of acid phosphatase
3. Kinetic studies - Effect of Temperature on the activity of acid phosphatase
4. Kinetic studies - Effect of substrate concentration on the activity of acid phosphatase
5. Kinetic studies - Effect of enzyme concentration on the activity of acid phosphatase
6. Estimation of Alkaline phosphatase from cucumber
7. Estimation of Urease from horse gram
8. Estimation of amylase from saliva
9. Estimation of serum SGPT (Kit method)
10. Estimation of serum SGOT (Kit method)
11. Isoenzyme analysis of Lactate Dehydrogenase
12. Enzyme immobilization- Entrapment in polyacrylamide gel

12BI325 PYTHON FOR BIOINFORMATICS

Credits: 3:0:0

Course Objective:

- To use Python as a programming language to automate routine data management tasks in biological research and to solve difficult data-related computational problems.

Course Outcome:

- To enable the students to analyze data within the python interpreter and write well-documented, well-organized programs.

Unit I
INTRODUCTION: Strings- Lists- Dictionaries-Tuples- Files- Numeric type basic- Numbers in Action- Number extensions- Dynamic typing interlude- Shared References.

Unit II
PYTHON IN STATISTICS AND PROBABILITY: Simple Statistics – average - standard deviation – distributions – normalization - multivariate statistics - Probabilities- Decisions from Distributions – correlations.

Unit III
SEQUENCE ALIGNMENT USING PYTHON: Alphabets – matching sequences- perfect matches - insertions and deletions - rearrangements - Global Vs. Local alignments- sequence length - simple alignment- direct alignment - statistical alignment, Brute Force alignment.

Unit IV
DYNAMIC PROGRAMMING USING PYTHON: Dynamic programming algorithm-the scoring matrix, the arrow matrix-extracting the Aligned sequences-Efficient programming-Global Versus Local alignments in Dynamic Programming-How Dynamic Programming can provide a good alignment.

Unit V
MICROARRAY ANALYSIS USING PYTHON: Gene expression array files-Raw data-GEL files - TIFF headers-the image file directory - reading the data - Spot finding – Intensity variations – block location - the coarse grid - fine-tuning the spot locations - spot measurement.

Text Books
1. Jason Kinse, "Python for bioinformatics" First edition, Jones and Bartlett Publishers, 2009.
2. Mark Lutz , "Learning Python", O'REILLY Publication, 4th Edition, 2009.

Reference book
1. Alex Martelli and David Ascher, "Python cookbook", O'Reilly, 2002.

12BI326 SUPPORT VECTOR MACHINE

Credits: 3:0:0

Course Objective:
- To know the concepts and applications of Support Vector Machine.
- To provide an insight to Support Vector Machine Technique before stepping into Artificial Intelligence and Mathematical Modeling.

Course Outcome:

- To understand and apply fundamental Support Vector Machines Techniques from theory to practical.
- To develop enhanced critical and conceptual thinking and problem solving skills.

Unit I

INTRODUCTION AND LOSS FUNCTION: Statistical learning, Support vector machines: an overview, History of SVMs and geometrical interpretation, Alternatives to SVMs, Loss functions: definition and examples, Basic properties of loss functions and their risks, Margin-based losses for classification problems, Distance-based losses for regression problems.

Unit II

SURROGATE LOSS FUNCTIONS: Inner risks and the calibration function, Asymptotic theory of surrogate losses, Inequalities between excess risks, Surrogates for unweighted binary classification, Surrogates for weighted binary classification, Template loss functions, Surrogate losses for regression problems, Surrogate losses for the density level problem, Self-calibrated loss functions.

Unit III

KERNELS AND REPRODUCING KERNEL HILBERT SPACES: Basic properties and example of kernels, The Reproducing Kernel Hibert Space of a kernel, Properties of RKHSs, Gaussian kernels and their RKHSs, Mercer's theorem, Large Reproducing Kernel Hilbert Spaces. Existence and uniqueness of SVM solutions, A general representer theorem, Stability of infinite-sample SVMs, Behavior for small regularization parameters, Approximation error of RKHSs.

Unit IV

BASIC STATISTICAL ANALYSIS OF SVMS: Notions of statistical learning, Basic concentration inequalities, Statistical analysis of Empirical Risk Minimization, Basic oracle inequalities for SVMs, Data-dependent parameter selection for SVMs, Need of refined analysis, A refined oracle inequality for ERM, Some advanced machinery, Refined oracle inequalities for SVMs, Some bounds on average entropy numbers.

Unit V

SUPPORT VECTOR MACHINES FOR CLASSIFICATION: Basic oracle inequalities for classifying with SVMs, Classifying with SVMs using Gaussian kernels, Advanced concentration results for SVMs, Sparseness of SVMs using hinge loss, Classifying with other margin-based losses. Support vector machine for regression: introduction, consistency, SVMs for quantile regression, Median regression with the EPS-insensitive loss.

Text Book:

1. Ingo Steinwart, Andreas Christmann, Support Vector Machines, 2nd Edition, Springer, 2008.

Reference Book:

Shi Yu, Leon-Charles Tranchevent, Bart De Moor and Yves Moreau, "Kernel-based Data Fusion for Machine Learning: Methods and Applications in Bioinformatics and text Mining", Springer, Heidelberg, 2011.

12BI327 WEB TECHNOLOGIES FOR BIOINFORMATICS

Credits: 3:0:0

Course Objective:

- Enabling the student to build and manage web applications.
- A working knowledge of HTML, XML & Scripting Languages

Course Outcome:

- The students would learn to design, develop and manage web applications in bioinformatics.

Unit I

HTML& ADVANCED HTML: Introduction – Web pages and html – Overview of html – Working with text – Working with images – Creating images – Link and lists – Creating hyperlinks - Creating lists – Creating a table - Working with frames - Working with style sheets - Advanced html – Optimizing web page for internet explorer – Embedding java script in html.

Unit II

XML-I: Introduction – Xml – Xml applications – Xml document - Life of an Xml document – Structuring data - Examining the data - Xmlizing the data – Advantages of Xml format – Attributes – Empty tags - XSL

Unit III

XML –II: Document type definition – Document type declaration – Validating against DTD – Element declarations – Entity declaration –Internal general entities – External general entities – Attribute declaration- Declaring attributes in DTD's –Declaring multiple attributes – Attribute types – Embedding non-Xml data.

Unit IV

JAVA SCRIPT & ASP: Java scripting fundamentals – Client side features of java script – Variables and literals – Expression and operators – Fundamentals of objects – Built-in objects and functions. ASP fundamentals – Handling request and response – Working with forms – Using server variables – Cookies – Creating a cookie – Modifying and removing a cookie.

Unit V

PERL, CGI: Introduction – Perl and CGI – Setting up GCI on Unix – Apache – Starting apache server - Stopping apache server – Writing CGI scripts – Basic CGI – Writing interactive CGI scripts.

Text Books

1. Steven Holzner, "HTML", Dreamtech press, Mumbai, India, Reprint Edition, 2008.
2. Elliotte Rusty Harold, "XML Bible", IDG Books India (P) Ltd, Mumbai, 2nd Edition, 2003.

Reference Books

1. Simon Cozens and Peter Wainwright, "Beginning Perl", Shroff publishers, Mumbai, A Press Reprint, 2005.
2. Eric A. Smith, "ASP 3 Programming Bible", Wiley-Dreamtech India (P) Ltd, Mumbai, 2002.
3. Greg Buczek , "ASP Developers", Guide, Tata McGraw-Hill India (P) Ltd, New Delhi, 2000.
4. Gopalan N.P and Akilandeswari, J., "Web Technology" , Prentice-Hall, India, 1st edition, 2007.

12BI328 PYTHON FOR BIOINFORMATICS LAB

Credits: 0:0:2

List of Practical

1. Write a program to open the SWISSPROT sequence and find the length of the sequence.
2. Write a program to retrieve the PDB file from RCSB.
3. Write a program to open a file and read the X,Y and Z coordinates using PDB.
4. Write a program to calculate the bond length between two atoms using PDB.
5. Write a program to converting DNA sequences to Protein sequences.
6. Write a program to draw the plot using GnuPlot to find the average and deviations of ten samples.
7. Write a program to align two sequences using Direct Alignment method.
8. Write a program to align two sequences using Brute Force method.
9. Write a program to find scoring matrix
10. Write a program to find arrow matrix.
11. Write a program to open the file for reading in a binary format using the function ReadRawFile.
12. Write a program to read the data using the function ReadGEL.

12BI329 SUPPORT VECTOR MACHINE LAB

Credits: 0:0:2

List of Practical

1. Introduction to SVM light.
2. Solving the classification problems.
3. Solving the regression problems.
4. Solving ranking problems.
5. Computing XiAlpha-estimates of the error rate, the precision, and the recall.
6. Computing Leave-One-Out estimates of the error rate, the precision, and the recall.
7. Training large transductive SVMs (TSVMs).
8. Training SVMs with cost models and example dependent costs
9. Assessing the generalization performance
10. SVM learning for multivariate and structured outputs like trees, sequences, and sets
11. Incorporating SVM light into MATLAB
12. Using the MATLAB Interface of SVM light

12BI330 WEB TECHNOLOGIES FOR BIOINFORMATICS LAB

Credits: 0:0:2

List of Practical

1. Design an interactive webpage with basic HTML tags
2. Web page - Presenting and arranging text/images.
3. Working with hyper link and lists.
4. Web page with tables and frames.
5. Creating simple web page using XML.
6. Working with XML and XSL
7. Creation of simple web pages using ASP.
8. Usage of scripting objects.
9. Usage of components in ASP
10. Usage of Cookies in ASP.
11. CGI scripting with Perl
12. Developing a web based tool for sequence analysis.