LIST OF COURSES

Sl. No.	Course Code	Name of the Course	Credits
1.	17BI2001	Analytical Bioinformatics	3:0:0
2.	17BI2002	Instrumental Methods of Analysis	3:0:0
3.	17BI2003	Molecular Biology and Genetic Engineering	3:0:0
4.	17BI2004	Data Structure and OOPs in C++	3:0:0
5.	17BI2005	Genomics and Proteomics	3:0:0
6.	17BI2006	Structural Biology and Biophysical Techniques	3:0:0
7.	17BI2007	PERL and PYTHON Programming	3:1:0
8.	17BI2008	Immunoinformatics	3:0:0
9.	17BI2009	Database Systems and Administration	3:0:0
10.	17BI2010	Linux and R Programming	3:0:0
11.	17BI2011	Java Programming	3:0:0
12.	17BI2012	Molecular Modeling and CADD	3:0:0
13.	17BI2013	Bioethics , IPR and Biosafety	3:0:0
14.	17BI2014	Computational Systems Biology	3:0:0
15.	17BI2015	Machine Learning Principles and Applications	3:0:0
16.	17BT2010	Metabolism and Bioenergetics	3:1:0
17.	17BI2016	Cell Biology and Microbiology	3:0:0
18.	17BI2017	Cell Biology and Microbiology Lab	0:0:2
19.	17BI2018	Instrumental Methods of Analysis Lab	0:0:2
20.	17BI2019	Analytical Bioinformatics Lab	0:0:2
21.	17BI2020	Molecular Biology and Genetic Engineering Lab	0:0:2
22.	17BI2021	Object Oriented C++ Programming Lab	0:0:2
23.	17BI2022	Database Systems and Administration Lab	0:0:2
24.	17BI2023	PERL and PYTHON Programming Lab	0:0:2
25.	17BI2024	Java Programming Lab	0:0:2
26.	17BI2025	Molecular Modeling and CADD Lab	0:0:2
27.	17BI2026	Computational Systems Biology Lab	0:0:2
28.	17BI2027	Linux and R Programming Lab	0:0:2
29.	17BI2028	Network Biology	3:0:0
30.	17BI2029	Data Science	3:0:0
31.	17BI2030	Next Generation Sequencing	3:0:0
32.	17BI2031	Pharmacogenomics	3:0:0
33.	17BI2032	Functional Genomics Technologies	3:0:0
34.	17BI2033	Pathway Modeling and Simulation	3:0:0
35.	17BI2034	Synthetic biology	3:0:0
36.	17BI2035	Microarray Technology and Statistical Analysis	3:0:0
37.	17BI2036	Kernel Based Pattern Recognition	3:0:0
38.	17BI2037	Cheminformatics and QSAR	3:0:0
39.	17BI2038	Cheminformatics and QSAR Lab	0:0:2
40.	17BI2039	Network Biology Lab	0:0:2
41.	17BI2040	Ruby Programming Lab	0:0:2
42.	17BI2041	Clinical Database Management	3:0:0
43.	17BI2042	Health Care Informatics	3:0:0
44.	17BI2043	Medical Coding and Transcription	3:0:0
45.	17BI2044	Scientific Writing	3:0:0
46.	17BI2045	Web Programming	3:0:0
47.	17BI2046	Clinical Practices and Regulations	3:0:0
48.	17BI2047	Drug Discovery and Clinical Trails	3:0:0
49.	17BI2048	Medical Coding and Transcription Lab	0:0:2
50.	17BI2049	Clinical Database Management Lab	0:0:2
51.	17BI2050	Ruby Programming	3:0:0
52.	17BI2051	Biological Big Data Analytics	3:0:0

53.	17BI2052	Python Programming	3:0:0
54.	17BI2053	Bimolecular Visualization	3:0:0
55.	17BI2054	Computer Aided Drug Design	3:0:0
56.	17BI2055	Molecular Simulation and Engineering	3:0:0

17BI2001 ANALYTICAL BIOINFORMATICS

Credits: 3:0:0

Course Objectives:

- To provide the necessary protocols about biological resources.
- To teach the tools used for biological sequential data analysis and phylogenetic.
- To understand the methods of analyzing and gene and promoter prediction.

Course Outcomes:

- The students are able to understand the basics of Bioinformatics resources.
- They can carry out pair-wise, multiple and phylogenetic alignment.
- They have learned the gene and promoter prediction concepts.
- 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 - Scope of Bioinformatics – Elementary commands and Protocols, ftp, telnet, http. Open access bibliographic resources– nucleotide databanks – Genbank, NCBI, EMBL, DDBJ – protein databanks –sequence databanks – PIR, SWISSPROT, TrEMBL- structural databases – PDB, SCOP, CATH.
Unit II - Introduction–Strings – Edit distance two strings – string similarity - local alignment - gaps – Parametric sequence alignments–suboptimal alignments – multiple alignment Multiple sequence alignment - CLUSTALW, PILEUP– common multiple alignment methods.
Unit III - Database search – Algorithms issues in database search – sequence database search. Dynamic programming, Needleman-Wunch algorithm, Smith-Waterman algorithm -FASTA and BLAST - Protein motifs and domain prediction.Gene Expression database - Derived Databases Protein-Protein interaction database.
Unit IV - Gene prediction methods and evaluation–Gene prediction in microbial genome and eukaryotes - Molecular predictions with DNA strings – Protein secondary structure prediction methods.
Unit V - 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.Gene prediction in prokaryotic genomes and in eukaryotes, promoter prediction in E.coli, and in eukaryotes.

Text Books:

1. Dan Gusfield, "Algorithms on Strings Trees and Sequences", Cambridge University Press, Cambridge, 2017.
2. David Mount W., "Bioinformatics sequence and genome analysis", CBS Publishers, New Delhi, 2nd Edition, 2013.

Reference Books:

1. D.W. Mount. Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbour Laboratory Press, New York, 2012.
2. Andreas D. Baxevanis, B. F. Francis Ouellette, Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 3rd Edition, Wiley and Sons, 2012
3. S.C. Rastogi and N. Mendiratla and P.Rastogi. Bioinformatics methods and applications- Genomics, Proteomics and Drug Discovery. Prentice Hall India, 2013
4. A.M. Lesk. Introduction to Bioinformatics. Oxford University Press India, 2017.

17BI2002 INSTRUMENTAL METHODS OF ANALYSIS

Credits: 3:0:0

Course Objectives:

- To develop skills of students in instrumentation and biological techniques.
- To expose to the principles of spectroscopy, Electrophoresis & Chromatography and their Bio techniques.

- To study the definitions, preparations of buffering systems and its application,

Course Outcomes:

- The student will infer about the definitions, preparations of buffering systems and its application.
- The student will identify the principles and working condition of instruments and techniques to analyze biological samples.
- The student will estimate the principles of buffering systems, its preparation and application.
- The student will evaluate the instruments and familiar with techniques to analyze biological samples
- To explain the principles and applications of the important instruments used in biology.
- The student will learn the different types of radioactive techniques and their precautionary measurement.

UNIT I - 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 - 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 – principles, types – paper, thin layer, adsorption, ion-exchange, affinity, gel filtration, GC and HPLC. Electrophoresis – principles, types – disc, Isoelectricfocussing, immuno-electrophoresis, supporting materials – paper, starch, agarose, polyacrylamide.

Unit IV : Radioactive isotopes, radioactive decay and their types, radioactive techniques – RIA, GM counter, Scintillation counter and Autoradiography.

UNIT V - 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 H. H, Merrit L.L., Dean J. A. and Settle F. A. "Instrumental Methods of Analysis". CBS Publishers and Distributors Pvt Ltd, New Delhi, 13th Edition, 2004.

Reference Books:

1. Skoog D. A, Holler E. J. and Nieman T. A., "Principles of Instrumental Analysis", Harcourt Asia Pte Ltd, Delhi, 2000.
2. Willard and Merrit, "Instrumental Methods and Analysis", CBS Publishers & Distributors, 6th edition, 2002.
3. Skoog.D, "Instrumental Methods of Analysis", Saunders College Pub., 2000.
4. Ewing GW, "Instrumental methods of Chemical Analysis", McGraw Hill Book Company, 2000.
5. Upadhyay, Upadhyay&Nath, Biophysical Chemistry: Principles and Techniques, Himalya publications, 2012

17BI2003 MOLECULAR BIOLOGY AND GENETIC ENGINEERING

Credits: 3:0:0

Course Objectives:

- To understand the basics of Molecular Biology and Genetic engineering.
- an ability to design and conduct experiments, as well as to analyze and interpret biological data
- To understand the applications of rDNA technology

Course Outcomes:

- Students will understand the fundamental concepts in Genetics, Molecular biology and recombinant DNA technology.
- an ability to identify, formulate, and solve problems in genetics
- an understanding of professional and ethical responsibility in genetic engineering
- to receive the broad education necessary to understand the impact of engineering solutions in global, economic, environmental, and societal context
- an ability to use the techniques, skills
- To use modern engineering tools necessary for molecular biology

UNIT I : DNA as genetic material - classical experiments – Hershey and chase; Avery McLeod and McCarty. Bacterial conjugation - transduction and transformation - Types of Mutation.

UNIT II - 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 - Genetic code, Process of translation in prokaryotes and eukaryotes, Post-translational modifications, Regulation of gene expression - Lac and trp operons.
UNIT IV - 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 - 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 MacmillanIndia 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.

17BI2004 DATA STRUCTURE AND OOPs IN C++

Credits: 3:0:0

Course Objectives:

- To learn the fundamentals and abstract concepts of Data Structures.
- To learn basic concepts and features of object oriented programming.
- To enable and understand students to differentiate between object oriented and procedural paradigm.

Course Outcomes:

- Ability to develop biological application using object oriented programming.
- Identify appropriate data structure for the given problem.
- Understand problem solving techniques.
- Understand object-oriented design and programming.
- Be able to develop, design and implement simple computer programs.
- Ability to write C++ programs to solve complex biological problems

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 Me Graw Hill publications, New Delhi , 2nd edition, 2001.

Reference Books

1. Robert L., "OOPS in C++", Galgotia publications, Noida, 4rd Edition 2002.
2. Jean-Paul Tremblay and Sorenson P. G, "An Introduction to Data Structures with Applications", McGraw-Hill Publishin g Company Limited, New Delhi , 2nd Edition reprint, 2001.
3. Sartaj S., "Data Structures, Algorithms and Applications in C++", McGraw-Hill

4. Publishing Company Limited, New York, 151 Edition , 2000.

17BI2005 GENOMICS AND PROTEOMICS

Credits: 3:0:0

Course Objectives:

- 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 Outcomes:

- Students will develop interest towards knowledge of various genomes
- Students will learn the high-throughput technologies available for proteome research.
- Students will identify latest tools for gene identification and gene ontology
- Students will learn to use software for 2DPAGE image analysis and relevant databases
- Students will gain knowledge about various microarray platforms
- To understand Mass Spectrometry data from MS databases

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, New York, 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

17BI2006 STRUCTURAL BIOLOGY AND BIOPHYSICAL TECHNIQUES

Credits: 3:0:0

Course Objectives:

- To introduce the strategy and tactics of Structural Biology
- 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 technique s i s explained.

Course Outcomes:

- Describe different structural levels of biological macromolecules, their conformations and forces involved in stabilization and the tools needed for the analysis.
- Understand the structures of biological macromolecules and their conformations

- Learn the forces stabilizing the macromolecular structures.
- The students can apply the biophysical techniques for structure determination
- The student would also learn about the ligand interaction with macromolecules.
- The course has emphasis on bioinformatics related to exploration of proteins and visualization and analysis of protein structures,

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 geometries, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions, ionic interactions, disulphide bonds, prediction of protein s structure.
UNIT IV - Structural analysis of nucleic acids: General characteristics of nucleic acid structure, geometries, glycosidic bond, rotational isomers and those puckering, backbone rotational isomers and ribose puckering, forces stabili zing 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 microscop y, neutron scatterin g and light scattering.

Text Book:

1. Cantor, R. and Schimmel , P. R., "Biophysical Chemistry ", Vol. I, II, W. H. Freeman & Co., 2013.

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 Prote in Architecture ",Oxford University Press UK. Mcpherson,A. (2003) "Introduction of Molecular Ctystallography ", John Wiley Publication, USA.

17BI2007 PERL AND PYTHON PROGRAMMING

Credits: 3:0:0

Course Objectives:

- To learn the fundamentals of the PERL and Python programming language and how it can be used to write codes related to biological applications.
- To discover how to use of modules files with PERL and python to build biological applications.
- Master the fundamentals of writing PERL and Python scripts and search text using regular expression.

Course Outcomes:

- Create effective, reusable scripts
- Parse and manipulate text with regular expressions
- Extract and arrange information from multiple files
- Master the principles of object-oriented programming and the interplay of algorithms and data structures in well-written modular code
- Solve problems requiring the writing of well-documented programs in the PERL and Python language, including use of the logical constructs of that language
- Demonstrate significant experience with the PERL and Python program development environment.

UNIT I - Basic of PERL**:** Introduction, Scalar Data, Lists and arrays, Input and output, Hashes, Control Structures.
UNIT II - PERL programming**:** Subroutines, Modules, Regular Expressions, Matching with Regular expressions, Processing Text with Regular Expressions.
UNIT III - Types and Operations in Python:Python object types, Numeric types, String fundamentals, Lists and Dictionaries, Tuples, Files.
UNIT IV - Statements and Syntax**:** Python Statements, Assignments, Expressions, Prints, if Tests and Syntax Rules, While and For loop, Iterations and Comprehensions
UNIT V - Functions and Modules**:** Function, Scopes, Arguments, Modules, Module coding, Packages.

Text Books:

1. Randal L. Schwartz, brian d foy, Tom Phoenix, "Learning Perl" O'Reilly Media, Inc., 2016
2. Mark Lutz, "Learning Python" "O'Reilly Media, Inc.", 2013

Reference Books:

1. Brown, "Perl: The Complete Reference", Tata McGraw-Hill Education, 2001
2. Wesley Chun, "Core Python Programming" Pearson Education, 2006.
3. Randal L. Schwartz, brian d foy, Tom Phoenix, "Learning Perl" O'Reilly Media, Inc., 2011
3. Brown, "Perl: The Complete Reference", Tata McGraw-Hill Education, 2001
4. Mark Lutz, "Learning Python" "O'Reilly Media, Inc.", 2013
5. Wesley Chun, "Core Python Programming" Pearson Education, 2006.

17BI2008 IMMUNOINFORMATICS

Credits: 3:1:0

Course Objectives:

- The Objectives are to introduce Immunological foundations
- To apply Informational technology to study immune systems
- To understand the latest software for predicting epitopes and designing vaccines insilico

Course Outcomes:

- This course gives a complete understanding of the concepts of Immunology and Immunotechniques
- The students will have knowledge of immune responses to various pathogens by integrating genomics and proteomics with bioinformatics strategies.
- The student will be proficient in computer aided vaccine design
- The course will help the students to understand Immunoinformatics and its applications
- The students will acquire skill set for insilico immunological studies
- The students will continue to acquire and explore sequence and structural databases relevant in the area of immunology

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.Freemanand Company, New Jersey, 4th edition, 2000.
2. Ole Lund, "Immunological Bioinformatics", MIT Press, USA, 2005.

Reference Books:

1. K. Chakravarthy, "Immunology andImmunotechnology", Oxford University Press, New Delhi, 2006.
2. Darren R.F., "Immunoinformatics: Predictive Immunogenicity *insilico*", Humana Press, New Jersey, 2007.

17BI2009 DATABASE SYSTEMS AND ADMINISTRATION

Credits: 3:0:0

Course Objectives:

- To understand the fundamental concepts of database management
- To introduce the concepts of database design, database languages, and database-system implementation
- To understand the role and functions of Database Administrator (DBA)

Course Outcomes:

- Ability to acquire the knowledge and ability to design a database for implementation
- Understand database concepts and structures.
- The students are able to describe database development process.
- Ability to develop data models related to biological database.
- Ability to handle, maintain and analysis of biological data effectively.
- Understand the issues related to database performance.

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 optimjzation: Query processing - Overview, selectionoperation, sorting, join operation, Query optimization - Estimating statistics of expression ,Transformation , materialized views.
UNIT V - Database administration - Data and System administration, Role of Database administrator –Installation, Up gradation, configuration, monitoring and maintenance of databases, DBA certification.

Text Book:

1. Abraham Silberschatz, Henry K Korth, Sudarshan S, Database concepts, Fourth edition, Me Graw Hill International publications , 2012.

Reference Books:

1. Craig S.Mullians, Database Administration, A complete guide to practices and procedures, Addison - Wesley Publications, 2002.
2. Ramesh Elmasri, Shamkant B. Navathe, Fundamentals of Database systems, Fourth edition, Addison - Wesley Publications, 2004.
3. P.S. Gill, Database Management Systems, I.K. International publishing house, 2010.

17BI2010 LINUX AND R PROGRAMMING

Credits: 3:0:0

Course Objectives:

- To study the fundamentals of Operating System Concepts.
- To express fundamental programming constructs such as input and output, R function, loops, Graphics and OOP in R.
- To understand statistical analysis for biological data set.

Course Outcomes:

- Ability to understand the basic commands of open source operating systems.
- Ability to handle biological dataset effectively in Linux environment.
- Knowledge in installation, configuration and custom partitioning of Linux operating system.
- Enable to write, compile, and run R programs.
- Analyse data from different data interfaces
- Ability to develop R script for various biological problems.

Unit I - Linux Administration: Introduction- GNOME and KDE -Managing users- Thecommandline-Bootingandshuttingdown-Filesystems.

UNIT II - Linuxinternetandintranetservices: Linux internet services –DNS-Setting up web server using Apache-These cure shell-Intranet services in Linux-Network file system and Network information service-Network configuration.

UNIT III - Introduction & R Objects: R console , CRAN , Installation , configuration, R studio environment setup, Basic syntax, Data types, Variables, Operators, Vectors - , Lists, Matrices, Arrays, Factors , Data frames, Control structures

UNIT IV - R Packages & Data interfaces: Installing a package from CRAN, Manual installation and configuration of a package, loading package to library, Exploring R packages for Bioinformatics applications, R data interface.

UNIT V - R Charts, Graphs &Statistics: Develop pie chart, 3D pie chart, Histograms, Bar Graph, Group bar chart, Box plots, Line graph, Multiline Graph, Scatterplots. Mean, Median, Mode, Regression models – Linear regression, Multiple regression, Logistic regression, Chi Square test, Normal distribution, Binomial distribution.

Text Books:

1. Steven Graham & Steve Shah, Linux Administration, Third Edition, Dreamtech, NewDelhi, 2003.
2. Robert Gentleman, "R programming for bioinformatics" Taylor and Francis Group, USA, 1st Edition, 2009.

Reference Books:

1. Sunil K. Mathur, " Statistical bioinformatics with R" Academic Press Elsevier, California,1st Edition, 2010
2. Mark Gardener, "Beginning R: The Statistical Programming Language", John Wiley & Sons, 2012
3. Norman Matloff, Norman S. Matloff, "The Art of R Programming: A Tour of Statistical Software Design", No Starch Press, 2011
4. Robert Love, Linux Kernel Development, Pearson Education India, 2010
5. Daniel P, Bovet, Marco Cesati, Understanding the Linux Kernel, 2006
6. Evi Nemeth, Garth Snyder, Unix and Linux System Administrator handbook, 2011

17BI2011 JAVA PROGRAMMING

Credits: 3:0:0

Course Objectives:

- To understand the fundamentals of Object Oriented concepts.
- To understand the format and use of classes and objects.
- To gain knowledge of Bio-Java modules.

Course Outcomes:

- Gain insight into concepts of object oriented programming.
- Understand the reusability of code within a program.
- The Students can work with Java-enabled browser and/or the applet viewer to execute Java applets
- Understand development of java applets and java applications.
- Ability to install and configure Bio-Java packages.
- Ability to solve complex biological problem using Bio-Java modules.

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 - Exception handling & applet programming: Interface- multithreading- Managing errors and exception handling- String handling- Applet Programming-managing input/output files in Java

UNIT V - Bio-JAVA: Facilitating Pubmed search , Blast Analysis, Gene prediction, Biological sequence Analysis, Grid program for cancer biomedical informatics.

Text Book:

1. E. Balaguruswamy, Programming with Java, second edition, Tata McGraw Hill Publications, 2000.

Reference Books:

1. Patrick Naughton and HerbertzSchildt, "Java-2 The Complete Reference", TMH, 2001
2. K. Arnold and J. Gosling, "The JAVA programming language", Third edition, Pearson Education, 2000.

3. Cay S. Horstmann, Gary cornel l - Core Java 2 Volume I – Fundamentals, 5th Edn, PHI, 2000.
4. HarshawardhanBal, Johnny Hujol, Java for Bioinformatics and Biomedical Applications, Springer 2007.

17BI2012 MOLECULAR MODELING AND CADD

Credit: 3:0:0

Course Objectives:

- To emphasize Modeling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.
- To understand the principles of Molecular modeling
- To demonstrate the Computer Aided Drug Design methods

Course Outcomes:

- Students are able to generate 3D structure from known raw sequence.
- Students are able to understand the three-dimensional structures and their physicochemical properties of drugs and receptors.
- Students are enabled to perform molecular simulations and molecular interaction.
- To utilize basic molecular modeling techniques to explore biological phenomena at the molecular level.
- Students will be able to build the molecular model for the biological response.
- Students will be able to design the drug based on known and unknown target.

UNIT I - Introduction to Computer Aided Drug Design: Introduction – How Drugs are Discovered – The Basic Mechanistic Drug Design – Important Technique of Drug Design – Conclusion and Future Perspective
UNIT II - Uses of Computer Graphics in Computer-Assisted Drug Design: Introduction – Computer Graphic Display – Computed Molecular Model – Molecular Modeling System for Drug Design – Uses of Computer Assisted Drug Design – Extending Molecular Modeling
UNIT III - Theoretical Aspects of Drug Design: Molecular Mechanics and Molecular Dynamics:
Introduction – Potential Energy Function – Non-bonded Energy Terms – Hydrogen Bonds – Energy Minimization – Application of Theoretical Techniques to Drug Design
UNIT IV - Role of Computer aided Molecular modeling in the Design of Novel Inhibitor:
Introduction – Modeling of the Receptor and Substrate – Working with Receptor-Inhibitor Model – Application and Example – Conclusion and Future Aspects
UNIT V - Approaches to Antiviral Drug Design:Introduction – Rhinovirus as a Drug Receptor – Designing Antiviral Drugs – Structure Activity Relationship for the uptake inhibition – Possible Application – Conclusion and Future Aspects

Text Book:

1. Leach A.R, "Molecular Modelling Principles and Application", Pearson – Prentice Hall, New Delhi, 2nd Edition 2001.

Reference Book:

1. R.K.Prasad, Quantum chemistry , Halsted Press, 2002 .
2. N. Claude C., "Molecular Modeling in Drug Design", Academic Press, California, 2006.
3. Computer Aided Drug Design – Methods and Application by Thomas J Perun and C. L. Propst, 2007

17BI2013 BIOETHICS, IPR AND BIOSAFETY

Credits: 3:0:0

Course Objectives:

- To understands the basics of Bioethics, IPR and Biosafety
- Students will understand the tools and approaches needed to make a bioethical decision and to communicate that decision in rationally informed way
- Students will understand the ethical and philosophical underpinnings of bioethics and to develop ethical intuitions on bioethical issues

Course Outcomes:

- Students will understand the concepts of ethical and environmental issues related to life sciences
- Students will understand the bioethical primary literature, to understand how to read case studies, and familiarity with the major issues being discussed in bioethics today.

- Students will learn the terminology, vocabulary, and Objectives of bioethics.
- Students will understand the tools and approaches needed to make a bioethical decision and to communicate that decision in rationally informed way
- Students will locate, analyze, interpret, critically evaluate, summarize and use appropriately information in the scientific literature.

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 andcontroversy –Models of Professional Roles - theories about right action - Self-interest - customs andreligion - uses of ethical theories.
UNIT II - Environmental aspects of biotech applications:Use of genetically modified organisms and their release in environment Special proceduresforr-DNA based product production, identification of directions for yield effect inagriculture, aquaculture etc, Bioremediation.
UNIT III - Intellectual property rights:TRIPS, International conventions patents and methods application of patents, Legalimplications, Biodiversity and farmers rights. Beneficial applications and development ofresearch 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.
2. Jeyakumar V, "Professional ethics and Human values", Anuradha Publications, Chennai, 2006.
3. ShaleeshaAS.,"Bioethics",WisdomEducationalservicepublications,Chennai, Edition 1, 2008
4. Lewis Vaughn, "Bioethics: Principles, Issues, and Cases", Oxford University Press, Edition 1, 2009
5. Thomas A. Shannon and Nicholas J. Kockler, **"**An Introduction to Bioethics", PaulistPr, Edition 4, 2009

17BI2014 COMPUTATIONAL SYSTEMS BIOLOGY

Credits: 3:0:0

Course Objectives:

- To introduce the student to the systems approach for biological application
- To explain the metabolic pathways using theoretical and Modeling techniques
- This is a pre-requisite for course 17BI2026-Network Biology, 17BI2031-Pathway modeling and Simulation

Course Outcomes:

- Students are equipped inmodeling techniques for biological pathways
- Students can identify important target proteins and pathways for any disease.
- Students can carry out network analysis for large data
- Students will be enabled to identify important and pathways for any disease.
- Students are able to develop different metabolic networks
- Students learn SBML language for genetic network development

UNIT I - Introduction to systems biology: Scientific challenges in systems biology, Bringing genomes to life; the use of genome-scale, *Insilco* 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,NewJercy, 6th Edition, 2012.

Reference books:

1. Sang dun Choi, Introduction to Systems Biology, Human Press, 2007
2. Hiroaki Kitano (Editor), Foundations of Systems Biology, MIT Press, 2001
3. Kindle Edition, Networks: An Introduction, Mark Newman, 2005
4. Uri Alon, An Introduction to Systems Biology: Design Principles of Biological Circuits (Chapman & Hall/CRC Mathematical & Computational Biology), Kindle Edition, 2011

17BI2015 MACHINE LEARNING PRINCIPLES AND APPLICATIONS

Credits: 3:0:0

Course Objectives:

- To introduce students to the basic concepts and techniques of Machine Learning
- To develop skills of using recent machine learning software for solving practical problems.
- To gain experience of doing independent study and research.

Course Outcomes:

- Familiarity with a set of well-known supervised, unsupervised and semi-supervised learning algorithms
- The ability to implement some basic machine learning algorithms
- Understanding of how machine learning algorithms are evaluated
- Develop an appreciation for what is involved in learning from data
- Understand a wide variety of learning algorithms
- Understand how to apply a variety of learning algorithms to data

UNIT I - Introduction to Machine Learning: Introduction, Supervised Learning, Bayesian Decision Theory.
UNIT II - Methods: Parametric Methods, Multivariate Methods, Non-Parametric methods
UNIT III - Dimensionality Reduction: Dimensionality reduction, Clustering, Decision Trees, Linear Discrimination.
UNIT IV - Perceptron: Multilayer perceptron, Bayesian Estimation, Hidden Markov Model
UNIT V - Application: Graphical Models, Design and Analysis of Machine Learning Experiments

Text Book:

1. SushmitaMitra, SujayDatta, Theodore Perkins and George Michailidis, "Introduction to Machine Learning and Bioinformatics", CRC Press, 2013.

Reference Books:

1. EthemAlpaydin, "Introduction to machine learning", MIT Press, 2010.
2. David Barber, "Bayesian Reasoning and Machine Learning", Cambridge University Press, 2012
3. Stephen Marsland, "Machine Learning: An Algorithmic Perspective", CRC Press, 2011

17BI2016 CELL BIOLOGY AND MICROBIOLOGY

Credits: 3:0:0

Course Objectives:

- To understand the structure and organization of cells.
- To get an overview of microbial systems.
- To give an account of the origin of life, from the abiotic world to multicellular organisms, including an account of endosymbiosis

Course Outcomes:

- Will get fundamental knowledge in microbiology.
- Give an account of the structure and functions of the plasma membrane and the major organelles that occur in eukaryotic cells
- Describe the major steps involved in how a complex organisms are formed

- Describe the structure and properties of prokaryotic and eukaryotic microorganisms and the structure and replication of viruses
- Describe the mechanisms of action of and resistance to antibiotics, how pathogens cause infection and host innate and induced immunity
- Carry out a range of laboratory exercises, demonstrating the development of practical scientific skills.

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.

17BI2017 CELL BIOLOGY AND MICROBIOLOGY LAB

Credits: 0:0:2

Course Objectives:

- To understand the structure and organization of cells.
- To get an overview of microbial systems.
- Carry out a range of laboratory exercises, demonstrating the development of practical scientific skills.

Course Outcomes:

- Will get fundamental knowledge in microbiology.
- Give an account of the structure and functions of the plasma membrane and the major organelles that occur in eukaryotic cells
- Describe the major steps involved in how a complex organisms are formed
- Describe the structure and properties of prokaryotic and eukaryotic microorganisms and the structure and replication of viruses
- Describe the mechanisms of action of and resistance to antibiotics, how pathogens cause infection and host innate and induced immunity
- Carry out a range of laboratory exercises, demonstrating the development of practical scientific skills.

1. Culture Media – Types and Preparation of Agar medium and Nutrient Broth
2. Microscopy
3. 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

17BI2018 INSTRUMENTAL METHODS OF ANALYSIS LAB

Credits: 0:0:2

Objectives:

- To impart technical knowledge about the principle and working of biochemical instruments
- To train in the applications of different equipments related to biological experiments.
- To do experiments related to the separation techniques of plant and food samples

Outcomes:

- The students gain the basic hands on training in media preparation and calculation.
- Students are able to conduct experiment in different equipments with variant technique.
- Students are able to perform purification and separation from plant and food samples.
- The students are expert to handle different types of radioactive techniques and their precautionary measurement.
- Students will identify the sugars by thin layer chromatography.
- Students will identify the amino acids by ascending paper chromatography.

Experimens:

1. Estimation of polyphenol by colorimetric method
2. Verification of Beer's law and construction of Beer's law plot
3. Preparation of buffer solution with Henderson Hasselbach equation and its verification with pH meter
4. Titration curves of acetic acid and citric acid using pH meter
5. Precision and validity of an experiment
6. Determination of analytical wave length for given sample [Calibration of colorimeter]
7. Identification of amino acids by ascending paper chromatography
8. Identification of sugars by thin layer chromatography
9. Determination of turbidity by nephelometry
10. Conductivity measures in titration
11. Gas chromatography
12. High Performance Liquid Chromatography

17BI2019 ANALYTICAL BIOINFORMATICS LAB

Credit: 0:0:2

Objectives:

- To provide the practical protocols about biological resources
- To gain hands-on experience on the tools used for biological sequential data analysis
- To execute the methods of analyzing genetic and protein information.

Outcomes:

- Students are enabled to practically carry out the protocols about Bioinformatics resources.
- Students have gained hands-on experience on pair-wise, multiple sequence alignment along with molecular phylogenetic.
- Students are practically trained in gene and promoter prediction.
- Students will be able to identify gene prediction strategies
- Students are enabled to search different databases for biomolecule sequences
- Students will be able to annotate novel sequences in terms of classification

Experiments:

1. Biological databases
2. EMBOSS.
3. Fasta analysis
4. BLAST analysis

5. Protein sequence analysis
6. Pairwise comparison
7. Gene finding and pattern recognition
8. Multiple alignment
9. Sequence utilities, Translation and nucleic acid secondary structure
10. Database reference searching and database sequence searching
11. Evolutionary analysis
12. Enzyme analysis

17BI2020 MOLECULAR BIOLOGY AND GENETIC ENGINEERING LAB

Credits: 0:0:2

Objectives:

- To understand the structure and organization of cells.
- To get an overview of microbial systems.
- Carry out a range of laboratory exercises, demonstrating the development of practical scientific skills.

Outcomes:

- Will get fundamental knowledge in microbiology.
- Give an account of the structure and functions of the plasma membrane and the major organelles that occur in eukaryotic cells
- Describe the major steps involved in how a complex organisms are formed
- Describe the structure and properties of prokaryotic and eukaryotic microorganisms and the structure and replication of viruses
- Describe the mechanisms of action of and resistance to antibiotics, how pathogens cause infection and host innate and induced immunity
- Carry out a range of laboratory exercises, demonstrating the development of practical scientific skills.

Experiments:

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. Optimization of time of inducer for recombinant protein expression
10. SDS-PAGE
11. Western blotting
12. Hybridization with anti-sera
13. PCR

17BI2021 OBJECT ORIENTED C++ PROGRAMMING LAB

Credits: 0:0:2

Course Objectives:

- To learn object oriented programming concepts.
- To learn the data structures
- To write programs in C++ for solving biological problems.

Course Outcomes:

- Ability to understand the practical concepts of data structures.
- Acquire practical knowledge in object oriented programming.
- Ability to write their own programs using C++.
- Able to understand the use of program for analytical bioinformatics
- Solving complex biological problems using OOPs module.
- Able to identify patterns in Bio-Sequences using features of C++ program.

Experiments:

1. Fundamentals of OOP's
2. Control structures
3. Classes and Objects
4. Inheritance
5. Polymorphism
6. Constructors
7. Data type conversion
8. Virtual functions & Friend functions
9. Exception handling
10. Fileopertions
11. C++ programs for Biological problems
12. Sequence analysis using OOP's module.

17BI2022 DATABASE SYSTEMS AND ADMINISTRATION LAB

Credits: 0:0:2

Course Objectives:

- To understand the fundamental concepts of database management.
- To teach the concepts including aspects of database design, database languages, and database-system implementation.
- To understand the role of the DBMS.

Course Outcomes:

- Ability to perform basic functions of DBMS.
- Analyze database models.
- Ability to Query database using DDL and DML commands.
- Declare and enforce integrity constraints on a database.
- Familiarity with database development process.
- Develop database for any biological dataset.

Experiments:

1. Data Definition Language
2. Data Manipulation Language
3. Data control and Transaction control language
4. Multiplesub-queries
5. Correlatedsub-queries
6. Arraysmanipulation
7. Usageofexplicitcursors&implicitcursors
8. Usageoffunctions
9. Usageofprocedures
10. Exceptionhandling
11. Usageofdatabasetriggers
12. Develop sample database for biological data set.

17BI2023 PERL AND PYTHON PROGRAMMING LAB

Credits: 0:0:2

Course Objectives:

- Programming competency in the PERL and Python programming language
- Know how to use common PERL and Python development tools
- Be able to write moderate programs utilizing common UNIX/LINUX system calls

Course Outcomes:

- Demonstrate the proper use of syntax, including control structures and expressions
- Properly use of scalars, arrays and associative arrays
- Demonstrate how to write and properly use regular expressions
- Demonstrate the use of built-in Perl functions

- Design and write Perl functions
- Use of the various types of Input and Output.

Experiments:

1. Programming of Mathematical Function
2. Creation of Pyramid and Pattern
3. Decision making and Loop
4. File Handling I
5. File Handling II
6. Identification of Transmembrane region in a protein
7. Python Programming on Mathematical Function
8. Creation of pyramid and pattern using python
9. Decision making and looping using python
10. Modules
11. File Handling in Python
12. Creation of GUI

17BI2024 JAVA PROGRAMMING LAB

Credits: 0:0:2

Course Objectives:

- To focus on core Java language and explore Java's role in common domains.
- To perform java applet programs in graphics.
- Programs for data manipulation file maintenance and sequence manipulation.

Course Outcomes:

- Write, compile, and run Java programs.
- Ability to understand the features and effect of object oriented programming.
- Ability to understand fundamental programming constructs such as variables, arrays, loops, subroutines and input/output in Java.
- Understand the reusability of code within a program.
- Write java programs for analysis of biological dataset
- Solving complex biological problems using java modules.

Experiments:

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.

17BI2025 MOLECULAR MODELING AND CADD LAB

Credits: 0:0:2

Course Objectives:

- To observe molecular behavior in three dimensional approach.
- To perform the simulation based on molecular mechanics and molecular dynamics approach.
- To study the computer aided drug design through target structure prediction and drug-receptor interactions.

Course Outcomes:

- Students are able to generate 3D structure from 1D sequence.

- Students are able to perform comparative modeling of different approaches..
- Students will be executing the Molecular modeling concept in Computer Aided Drug Design methods.
- Students are to build the Model of Tri-Peptide molecule Ala-Ala-Ala and to analyze its conformational parameters
- Students are able to design the computer aided drug against target based on MDS approach
- Students are able to design the computer aided drug against target based on MCS approach

Experiments:

1. Molecular modeling of a peptide and a carbohydrate – using chem sketch 11.0
2. Analysis of protein primary and secondary structure
3. Molecular visualization and movie making using visual molecular dynamics (vmd)
4. Homology modeling and structure visualization using swisspdb viewer
5. Molecular mechanics and energy minimization of a peptide – using tinker force field explorer
6. Structure prediction and analysis of DNA (gi:145579321) and RNA (rd1140)
7. Monte-carlo energy minimization and conformational transition of cyclohexane – using tinker FFE.
8. Structural analysis of zn finger protein using rasmol, pdbsum and q-site finder
9. Molecular dynamics simulation of biomolecules – using tinker and ammp software.
10. Hyperthyroidism *ab initio* structure prediction for the related protein structure
11. Docking Studies Using Argus
12. *Abinitio* Structure Prediction

17BI2026 COMPUTATIONAL SYSTEMS BIOLOGY LAB

Credits: 0:0:2

Course Objectives:

- To impart the knowledge in modeling of genomics, proteomics
- To perform the metabolic pathways for biological process
- To train in the use of different software on computational modeling

Course Outcomes:

- The students are enabled to identify important target proteins
- Students are able to analyze pathways for any disease using the databases and software
- Students are able to execute different plug-ins in network analysis
- Students will be able to model their own chemical reactions for modeling
- Students will be able to produce their own biological plugins
- Students will be able to analyze protein protein interactions

Experiments:

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

17BI2027 LINUX AND R PROGRAMMING LAB

Credits: 0:0:2

Course Objective:

- To get an introduction to the R programming language
- To have hands-on R programming skills.
- To demonstrate R programming applications

Course Outcome:

- Ability to understand the basic commands of open source operating systems.
- Students will able to gain in- depth knowledge of Linux environment.
- Insight into knowledge on operators for calculations on arrays, lists, vectors and matrices.
- Generate different graphical representations and plots for given data set.
- Ability to apply R language in today's scientific context
- Trained to execute R programming for any biological data set.

Experiments:

1. Linux Administration
2. File Manipulation
3. File System
4. Memory Management
5. Factors
6. Data frames
7. Packages
8. Data Re-shapping
9. Charts & Graphs
10. Regression Models
11. Data interfaces
12. R – Database

17BI2028 NETWORK BIOLOGY

Credits: 3:0:0

Course Objectives:

- Students will be introduced to different computational approaches to understand large biological data using network biology
- Students will understand interactive networks and models
- Students will learn Omics data analysis

Course Outcomes:

- Students have learned transcriptomics data interpretation
- Students can carry out the application of protein interaction networks
- Students are able to evaluate the centrality properties
- Students are equipped in modeling techniques for biological pathways
- Students can identify important target proteins for any disease.
- Students can carry out network analysis for large data

UNIT I - Computational approaches - Data analysis - Experimental approaches - Gene isoforms - Gene sequences - National Resource for Network Biology, Protein–protein interaction networks

UNIT II - Gene regulatory networks (DNA–protein interaction networks) Gene co-expression networks (transcript–transcript association networks) Metabolic networks, Signaling networks, Neuronal networks

UNIT III - Between-species interaction networks, Within-species interaction networks Complex Diseases- Interaction networks - Metabolite concentrations –

UNIT IV - Models of complex networks- statistical testing of network properties- Network clustering- Next-generation sequencing - Protein complexes - Quantitative 'omic' datasets

UNIT V - mRNA transcripts- Quantitative modeling and analysis- signal transduction and gene regulation networks- Phylogenetic networks.

Text Book:

1. Network Biology: Methods and Applications, Cagney, Gerard; Emili, Andrew, A product of Humana Press Vol. 781, 2011

Reference Books:

1. Analysis of Biological Networks, Björn H. Junker, Falk Schreiber, John Wiley and Sons, 2011
2. AlpanRaval, Animesh Ray, Introduction to Biological Networks, Chapman and Hall/CRC publisher, 2013
3. Networks: An Introduction, Mark Newman, Kindle Edition, 2005

17BI2029 DATA SCIENCE

Credits: 3:0:0

Course Objectives:

- To learn the basics of Big Data Analytics
- To understand the storage and process of big data using Hadoop framework.
- Fundamental concepts of cloud computing and its architecture.

Course Outcomes:

- Ability to understand the fundamentals of big data technologies.
- Ability to handle variety of big data analytics.
- Understand the working of Hadoop Distributed File System.
- Explore use of R platform for biological big data analysis.
- Perform next generation sequencing data analysis.
- Understand the working of various types of cloud computing models.

UNIT I – INTRODUCTION TO BIG DATA: Big data overview, Big data technologies, Operational and Analytical systems, Benefits and challenges in Big data, Big data solutions – Traditional enterprise approach.
UNIT II – HADOOP: Installation and configuration of Hadoop, Operation modes, Hadoop Architecture, Mapreduce, Distributed file system, Working of Hadoop, Advantages of Hadoop.
UNIT III – HADOOP FILE SYSTEM: Features of HDFS, HDFS Architecture, Goals of HDFS, HDFS operations - Listing Files in HDFS, Inserting Data into HDFS, Retrieving Data from HDFS, Shutting Down the HDFS
UNIT IV – BIG DATA FOR BIOINFORMATICS: Big data analysis using R, Next generation DNA sequencing data analysis – Genome sequence data analysis, RNA sequence data analysis, Microbiome sequence data analysis,miRNA data analysis, Methylome data analysis and Chip data analysis.
UNIT V – INTRODUCTION TO CLOUD COMPUTING: Public cloud model, Private cloud model, Hybrid cloud model, Community cloud model, Cloud computing management and data storage.

Text Books:

1. Parag Kulkarni, Sarang Joshi,, Meta S. Brown, Big Data Analytics, PHI Learning,July 2016.
2. Shui Qing Ye, Big Data Analysis for Bioinformatics and Biomedical Discoveries, CRC Press, Jan 2016.

Reference Books:

1. Michael Minelli, Michele Chambers, AmbigaDhiraj, Big Data, Big Analytics: Emerging Business Intelligence and Analytic Trends for Today's Businesses, John Wiley & Sons,2012.
2. Wang, Baoying, Big Data Analytics in Bioinformatics and health care, IGI Global, 2014
3. Thomas Erl, Ricardo Puttini, Zaigham Mahmood, Cloud Computing: Concepts, Technology & Architecture, Prentice Hall, Prentice Hall, 2013

17BI2030 NEXT GENERATION SEQUENCING

Credits: 3:0:0

Course Objectives:

- To give the knowledge of the NGS technology with the focus on the data analysis
- To understand NGS data and analyze these in an UNIX/Linux working environment.
- To analyze computational genomics using advanced statistical methods for solving bioinformatics problems.

Course Outcomes:

- Describe the applications of the different NGS technologies, including the weakness and strengths of the approaches.
- Explain the steps involved in a general NGS data analysis.
- Explain key theoretical concepts of alignment and de novo assembly.
- Synthesize and formulate a project and relevant question within the field.
- Independently perform a basic NGS data analysis.
- Apply analytical and reflective skills in analyzing results from individual steps and the final project.

UNIT I - Introduction: The cellular system and code of life, DNA sequence, The transcribed sequence

UNIT II - Next Generation Sequencing: NGS Technologies, Early Stage NGS data analysis, Computing needs for NGS data management and analysis
UNIT III - Application specific NGS data analysis:Transcriptomics by RNA-seq, Small RNA sequencing, Genotyping and Genomic Variation discovery by whole genome resequencing
UNIT IV - Epigenomics data analysis:*De novo* genome assembly from NGS reads, Mapping Protein-DNA interactions with ChIP-seq, Epigenomics and DNA methylation analysis by NGS
UNIT V - Metagenome analysis:Metagenome analysis by NGS, changing landscape of NGS

Text Book:
1. Xinkun Wang, "Next-Generation Sequencing Data Analysis" CRC Press 2016

Reference Books:
1. Next-Generation DNA Sequencing Informatics [Kindle Edition] by Stuart Brown, Cold Spring Harbor Laboratory Press Newyork, 2013.
2. Tag-based Next Generation Sequencing by Matthias Harbers and GuenterKahl (Wiley Blackwell Germany 2012
3. Wong, Lee-Jun C., Next Generation Sequencing- Translation to Clinical Diagnostics, Springer, 2013

17BI2031 PHARMACOGENOMICS

Credits: 0:0:3

Course Objectives:
- To introduce the scientific knowledge of drugs that reacts with the biomolecules
- To understand the novel concepts in Pharmacogenomics
- To understand the novel drug discovery process

Course Outcomes:
- Students have an understanding of the principles and applications of human genomics
- Students have an understanding the concepts in Pharmacogenomics
- Students have an understanding of the concepts in drug therapy optimization & patient care
- Students with an understanding of the principles and applications of human genetics
- Students with an understanding of the principles and applications of genomics in drug therapy and optimization
- Students have an understanding of the 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,2012.
2. Mark A. R, "Pharmacogenomics: Social, ethical, and clinical dimensions",Humana press, USA, 3rd Edition, 2014

Reference Books:

1. Werner K, UrsA,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.

17BI2032 FUNCTIONAL GENOMICS TECHNOLOGIES

Credits: 3:0:0

Course Objectives:

- To provide an introduction to functional genomics
- To emphasize applications of genomics technologies, data analysis and experimental design
- To learn about the cutting edge technologies such as advanced array technologies

Course Outcomes:

- Students learn the application of High throughput data for genome-wide analysis
- Students acquire an understanding of the emerging technologies in functional genomics.
- Students are able to design experiments, interpret and analyze biological data.
- Students will demonstrate an understanding of the emerging technologies and how they can be applied to address biological questions.
- Students will design experiments, interpret &analyse data generated from key technologies
- Students can assess the strengths and weaknesses of each technology and apply this knowledge when interpreting and analysing data

UNIT I - Finding protein-coding genes within genomes: How many are there? How are they distributed along chromosomes? How do you find out what function they have?

UNIT II - Finding genes that do not code for proteins: How much of the genome is transcribed? Do they produce stable noncoding RNAs? What roles do they play in the cell (regulatory and enzymatic)?

UNIT III - Finding evolutionary signatures of function: Do protein-coding genes account for all or most of the functional sequences? How can you use genome comparisons between species to estimate the amount of functional sequence – and to identify it? This noncoding DNA inferred to be functional can be considered "dark matter" of the genome.

UNIT IV - Finding non-genic functional sequences: How can we illuminate the dark matter? How do you use high throughput genomics to find DNA sequences likely to be involved in gene regulation? This section will emphasize genomic approaches to mapping epigenetic features associated with gene regulation, such as histone modifications, DNase hypersensitive sites, and transcription factor occupancy. Again students will be encouraged to examine and analyze these data according to their interests.

UNIT V - Finding function by phenotype: Genetic association studies are currently identifying with high precision and statistical support loci that contribute to complex traits, such as disease susceptibility. How can you find these results easily? How can you use the data and insights from the earlier topics to develop testable hypotheses about how variation among humans at these loci lead to increased susceptibility to disease?

Textbook:

1. Microbial Functional Genomics, Jizhong Zhou, Dorothea K. Thompson, Ying Xu, James M. Tiedje, 2004, John Wiley & Sons, Inc.
2. Functional Genomics (Methods in Molecular Biology), Michael J. Brownstein , ArkadyKhodursky, 2003, Humana Press

Reference Books:

1. Functional Genomics: Methods and Protocols (Methods in Molecular Biology), Michael Kaufmann , Claudia Klinger, 2011, 3rd Edition, Humana Press
2. Functional Genomics: A Practical Approach (Practical Approach Series), Stephen Hunt, Frederick Livesey**,** 2000, OUP Oxford

17BI2033 PATHWAY MODELING AND SIMULATION

Credits: 3:0:0

Objectives:

- To express fundamental constructs in relation to pathway modelling
- To explain the simulation techniques involved in pathway identification
- To learn the process of identification of targets and small molecules

Outcomes:

- Knowledge of simulation principles
- The ability to create simulation models of various types
- Students are able to apply the programming skills in pathway modelling and simulations
- They can learn to stand alone tools for modelling biological pathways
- They can do the whole cell simulations using varied tools
- Basic knowledge of simulation system principles

UNIT I - Computational Methods and Intelligence in Modelling Genetics:Bayesian based wavelet package, Petri Nets-Based biological network reconstruction, Online Anomaly detection

UNIT II - Computational Methods and intelligence in organism modelling: Hemodynamic comparison, plant morphology modelling system

UNIT III - Design of synthetic biological system: Numerical simulation, dynamic analysis, Real time hand gesture.

UNIT IV - Societies and collective behavior: Agent based simulation, Human cognitive modelling, Modelling method of artificial society, Kinetic modelling for radiotherapy mechanisms

UNIT V - Systems Modelling and Simulation: MIMO Neuro Fuzzy, Damage imaging algorithm, DES Algorithm, Integrated Neuro-Fuzzy

Text Book:

1. Shiwei Ma, Li Jia, Xin Li, Ling Wang, Huiyu Zhou, Xin Sun "Life System Modeling and Simulation: International Conference on Life System Modeling and Simulation" Springer, 2014

Reference Books:

1. George Bekey, Boris Ja. Kogan "Modeling and Simulation: Theory and Practice" Springer Science & Business Media, 2012
2. Ina Koch, Wolfgang Reisig, Falk Schreiber "Modeling in Systems Biology: The Petri Net Approach" Springer London, 2012
3. Dokholyan, Nikolay, Computational Modeling of Biological Systems: From Molecules to Pathways, Springer, 2012

17BI2034 SYNTHETIC BIOLOGY

Credits: 3:0:0

Course Objectives:

- To expose the new field of systems and synthetic biology
- To expose some of the interesting theories that have helped to make systems biology a remarkably interdisciplinary field
- To understand the design and operation of natural and synthetic circuits to design new biology based systems.

Course Outcomes:

- The students are enabled to design simple cellular circuitry to meet engineering specification.
- They are enabled to design experiments to characterize and diagnose operation of natural and synthetic bimolecular network
- They can apply the knowledge in scientific, safety and ethical issues of synthetic biology
- Modern techniques in DNA assembly and regulation of gene expression and protein activity
- To design basic biological circuits
- Principles for scaling up and creating large-scale biological circuits and regulatory networks

UNIT I - Programming Biology: Expanding the tool set for engineering of transcriptome, Novel DNA and RNA elements

UNIT II - Methods of synthetic biology: Genome engineering and DNA assembly, Protein building blocks and the expansion of the genetic code
UNIT III - Cellular remodeling: Industrial relevant microbial phenotypes, Microbial Platform cells
UNIT IV - Engineering: Metabolic pathway engineering, Application in protein engineering
UNIT V - Application: Synthetic Biopolymers, Xenobiotic Life

Text Book:

1. Anton Glieder, Christian P. Kubicek, DiethardMattanovich, Birgit Wiltschi, Michael Sauer "Synthetic Biology" Springer International Publishing, 2015

Reference Book:

1. Geoff Baldwin, Travis Bayer, Robert Dickinson, Tom Ellis, Paul S Freemont, Richard I Kitney, Karen Polizzi, Guy-Bart Stan "Synthetic Biology" World Scientific, 2015

17BI2035 MICROARRAY TECHNOLOGY AND STATISTICAL ANALYSIS

Credits: 3:0:0

Course Objectives:

- To explain how microarray technology works, including the various types
- To understand how data is retrieved in different formats produced by microarrays
- To understand biological data normalization

Course Outcomes:

- Students can demonstrate the working of microarray by different technologies
- Students can carry out different algorithms for normalization
- Students are able to do different statistical analysis of normalized and preprocessed data
- 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.
- Students can imply clustering methods in expression data

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 AffymetrixGeneChipTM
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 Gene ChipTM 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 Books:

1. Mark Schena, Microarray Analysis, John Wiley and Sons ltd, America, 2003
2. Aidong Zhang, "Advanced analysis of Gene expression microarray data", World Scientific Publishing House, New Delhi, 2006.
3. DovStekel, "Microarray Bioinformatics" Cambridge University Press, UK, 2005.
4. Müller, Uwe R.; Nicolau, Miguel, Microarray Technology and Its Applications, Springer, 2005

17BI2036 KERNEL BASED PATTERN RECOGNITION

Credits: 3:0:0

Course Objectives:

- To introduce pattern recognition problems using support vector machines.
- To understand novel kernel fusion algorithms and applications in supervised and unsupervised learning
- To apply support vector machines in literature mining.

Course Outcomes:

- The students are able to apply fusion and pattern recognition methods.
- They are able to understand the pattern recognition algorithms in to identify disease relevant genes
- They are able to implement kernel based software
- Understand a wide variety of learning algorithms.
- Understand how to apply a variety of learning algorithms to data.
- Understand how to perform evaluation of learning algorithms and model selection.

UNIT I - Introduction and basic concept: Pattern recognition, graph and subgraph, graph matching
UNIT II - Graph Edit Distance: Properties, computation of exact graph edit distance, pattern recognition
UNIT III - Bipartite Graph Edit Distance: Quadratic distance problem, Bipartite Graph Edit Distance, Experimental evaluation, pattern recognition application
UNIT IV - Improving the distance accuracy: Change of notation, improvement via search strategies, improvement via integration
UNIT V - Learning Algorithm: Predicting exact graph distance, predicting the correctness, suboptimal assignment algorithm

Text Book:

1. KasparRiesen "Structural Pattern Recognition with Graph Edit Distance: Approximation Algorithms and Applications" Springer, 2016

Reference Books:

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
2. Patrick S. P. Wang, "Pattern Recognition, Machine Intelligence and Biometrics", Springer, 2012

17BI2037 CHEMINFORMATICS AND QSAR

Credits: 3:0:0

Course Objectives:

- To introduce different methods of cheminformatics with particular emphasis on applications including modern drug discovery.
- To provide an overview of computer aided drug design by Cheminformatics approach
- To acquire an understanding of Quantitative Structure Activity Relationship

Course Outcomes:

- The students are able to retrieve specific information from the enormous and rapidly expanding chemical literature and databases.
- The students will be able to use computer technology to chemistry in all of its manifestations.
- The students will be able to apply the Cheminformatics and QSAR technique in computer aided drug design.
- Students are able to build the 2D QSAR and 3D QSAR model for the biological response.
- Students are able to predict the biological activity based on experimental analysis.
- Students are able to find the structural features for the biological activity.

UNIT I - Introduction to Chemoinformatics: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

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; Design of Combinatorial Libraries

Text Book:

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

Reference Books:

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

17BI2038 CHEMINFORMATICS AND QSAR LAB

Credits: 0:0:2

Course Objectives:

- To introduce different methods of cheminformatics with particular emphasis on applications including modern drug discovery.
- To provide an overview of computer aided drug design by Cheminformatics approach
- To acquire an understanding of Quantitative Structure Activity Relationship

Course Outcomes:

- The students are able to retrieve specific information from the enormous and rapidly expanding chemical literature and databases.
- The students will be able to use computer technology to chemistry in all of its manifestations.
- The students will be able to apply the Cheminformatics and QSAR technique in computer aided drug design.
- Students are able to build the 2D QSAR and 3D QSAR model for the biological response.
- Students are able to predict the biological activity based on experimental analysis.
- Students are able to find the structural features for the biological activity.

Experiments:

1. Preparation of compound library
2. Small Molecule pathway database
3. overview of protein and their interaction with ligand preparation
4. Finding the Similar Molecules using Toxread
5. Computing the physiochemical parameter using MOPAC
6. Biological activity prediction using moleinspiration
7. 2D QSAR based on physiochemical descriptor using MiniTab
8. Introduction to Schrodinger, ligand preparation and protein
9. Receptor Grid generation and protein-ligand docking using Glide and their refinement
10. Active site residue interactions with the binding site by using LIGPLOT
11. 2D QSAR based upon physio-chemical descriptors by using ligand structure based descriptors (LSBD) and model-generation
12. Molecular Modeling of a Peptide and a Carbohydrate – Using CHEMSKETCH 11.0

17BI2039 NETWORK BIOLOGY LAB

Credits: 3:0:0

Course Objectives:

- To provide practical exercises related to biological networks
- To learn hands on skills on biological systems and their subunits
- To apply network based approach in biological context.

Course Outcomes:

- The students gain practical skills related to biological networks
- They have learned social and ecological network data analysis
- They are able to apply network biology algorithms in software applications
- Students are able to build the network model for the biological response.
- Students are able to predict the biological activity based on experimental analysis.
- Students are able to find the structural classification for the biological network entity.

Experiments:

1. Types of graph for network building
2. SBML
3. Cytoscape
4. Centiscape
5. MiMI
6. Virtual Biology Lab
7. COMBINE
8. MIRIAM
9. URN
10. MIASE
11. NETWORK ANALYZER
12. CENTRAILTY PARAMETERS

17BI2040 RUBY PROGRAMMING LAB

Credits: 0:0:2

Course Objective:

- Analyse requirements of software systems for the purpose of determining the suitability of implementing in Perl or Python;
- Analyse and model requirements and constraints for the purpose of designing and implementing software systems in Perl and Python;
- Evaluate and compare designs of such systems on the basis of specific requirements and constraints.

Course Outcome:

- Develop server-side Ruby scripts for publishing on the Web
- Employ control structures, methods, procs, arrays and hashes to create Ruby programs
- Explain object-oriented programming and input/output processing and apply these concepts to develop dynamic interactive Ruby applications.
- Discuss Model-View-Controller architecture and its relationship to Ruby on Rails applications
- Use SQL commands and the MySQL database together with Ruby
- Create an advanced project using MySQL, Ruby and the Ruby on Rails framework.

Experiments:

1. Write Ruby applications using variables, data types, strings and methods.
2. Write Ruby applications using loops, arrays. hashes, blocks and sorting.
3. Build Rails applications using Rails best practices.
4. Manage a database with migrations.
5. Build complex models using ActiveRecord, including associations, validations and callbacks.
6. Programming projects to upgrade the UI using Rails' built-in support for JavaScript and Ajax.
7. Programming project to add functionality and extend a Rails application using third-party plugins and gem libraries.
8. Employ TDD (Test Driven Development) and use Rails to write tests to validate an application's behaviour.
9. Classes and Objects
10. Web Interaction and File Access
11. SQL and the MySQL Database

17BI2041 CLINICAL DATA MANAGEMENT

Credits: 3:0:0

Course Objectives:

- The main Objectives 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.
- Understand the principles of clinical data management

Course Outcomes:

- 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.
- Describe analytics and decision support, including the capabilities of dashboards and data capture tools.
- Utilize enterprise-wide information assets in support of organizational strategies and Objectives.
- Explain concepts of database architecture and design.
- Differentiate the roles and responsibilities of various providers and disciplines, to support documentation requirements, throughout the continuum of healthcare.

UNIT I - Introduction: Audience and scope, other sources of knowledge, Fundamental concepts, Types of Outcomes 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, Thehippocratic tradition - Proscribe clinical trials, Historically derived principles of ethics, Contemporary foundational principles, methodologicreflections, 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 Son, 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 Son, New York, 2nd edition, 2004.
3. Stephanie G, Jacqueline B, and John C, "Clinical Trials in Oncology", CRC press, USA2nd edition, 2002.

17BI2042 HEALTH CARE INFORMATICS

Credits: 3:0:0

Course Objectives:

- To introduce students to the concepts and practices of health informatics
- To enable the students to understand patient- physician interaction
- To enable the students to understand the patient profile documentation

Course Outcomes:

- Students gain insight in planning and building healthcare information systems
- Students learn software design and human-computer interaction issues

- Develop a better understanding of current and emerging issues in healthcare information technology management
- Develop an understanding of meaningful use and its implications for clinical and administrative purpose in healthcare management
- Develop an understanding of the IT architecture for healthcare information management, including sourcing, security and governance decisions
- Develop appropriate performance measurement and reporting mechanisms to plan and evaluate the impact of IT initiatives in healthcare settings

UNIT I - Healthcare Informatics Definition Health Informatics Medical Informatics Clinical Informatics Biomedical Informatics Nursing Informatics Public Health Informatics Information Science,

UNIT II - Basic concepts in health informatics and its history, Definitions, Sub disciplines and professional organizations and activities, Major health informatics applications including electronic medical records (EHR) and computerized physician order entry (CPOE), good clinical practices (gcp)

UNIT III - Information systems design and engineering, new opportunities and emerging trends**:** Information technologies in healthcare; wireless and handheld devices, social computing paradigms, and eHealth applications, web-based tools.

UNIT IV - Introduction to the discipline of human factors with a particular focus on human attention and mental workload, a concept derived from applied cognitive psychology. Analysis of human error as well as usability evaluation methods to evaluate the design of the Electronic Health Record and medical devices to prevent user errors and enhance patient safety, are also addressed.

UNIT V - The module will introduce the concept of decision making and the role of Clinical Decision Support Systems in providing cognitive support as well as perpetuating unintended consequences with recommendations for redesign considerations based upon Human Factors analysis, Telemedicine and technologies to set up telemedicine unit, Telemedicine in India.

Text Book:

1. Taylor Paul, "From Patient Data to Medical Knowledge: The Principles and Practice of Health Informatics", Blackwell Scientific Publishing, UK, 2006.
2. Shortliffe and Cimino, "Biomedical informatics: computer applications in health care and biomedicine", Springer, NewYork, 3rd edition, 2006

Reference Books:

1. Frank M. S. and Jeremy C. Wyatt, "ABC of health informatics", Blackwell publishing, Massachusetts, USA, 2006.
2. Perry, S., Hockenberry, M., Lowdermilk, D., & Wilson, D. . Maternal child nursing care (4th ed.), 2010.
3. Silvestri, L.A. . Saunders comprehensive review for the NCLEX-RN examination (5th ed.). St. Louis, MO: Saunders, 2011.
4. Townsend, M.C. Essentials of psychiatric mental health nursing: Concepts of care in evidence-based practice (5th ed.). Philadelphia: FA Davis, 2011

17BI2043 MEDICAL CODING AND TRANSCRIPTION

Credits: 3:0:0

Course Objectives:

- To understand medical coding in health sector
- To understand the guidelines for specific transcription mechanics and techniques
- To be trained for a minimum entry level medical coding positions normally available in medical offices, hospitals and insurance companies

Course Outcomes:

- Students understand the basic systems and processes in billing, reimbursement and insurance coverage.
- Students are able to gain knowledge from the medical information system.
- Student are able to analyze medical records (charts) and codes for indexing diagnosis

UNIT I - Medical coding history, diagnosis coding, procedure coding, codes used for reimbursement, solving health care coding problems, coding as a career. Word Dynamics, Body Dynamics, Medical Instruments & Equipment, Medical Specialties & Specialists, Diagnostic Medicine, Abbreviations, Anatomy and Physiology,

Diagnostic Medicine, Abbreviations, Anatomy and Physiology, Pharmacology, Drug listing – generic alpha, name brand cross-reference, plus 200 of the most commonly prescribed drugs.

UNIT II - Health Insurance Specialist Job Description & Knowledge, Medical Care,Reimbursement, Health Organizations (MCO), Insurance Claims, Payer Processing, Laws, Rules, and Regulations, Private Insurers, Medicare, Medicaid, TriCare

UNIT III - Basics of Medical Transcription, Analysis of Sample Medical Reports, Understanding Medical Reference Library, Ethics and Confidentiality/ HIPAA Laws, Legal Aspects of Healthcare Records, Proper Ergonomics for the Medical Transcriptionist, Importance of Quality MT Education

UNIT IV - Introduction to medical transcription, medical transcription transcribing tools, telecommunication tools in medical transcription, Medical transcription formats, medical transcription mechanics, Medical Transcription skills, Consultation Reports, History and Physical Examination Reports, Special Procedures Reports, Operative Reports, SECTION VH Discharge Summary Reports, Challenge Reports

UNIT V - Introduction to FTP (File Transfer Protocol) Clients, The Future of Medical Transcription, Hospital Medical Reports, Preparation of a History & Physical, Clinic Medical Reports, Formats, Organizing the Information, Proofreading and Editing, Basic Formatting Guidelines, Flagging and Blanks, Transcribing Foreign Dictators, Methods of Line Counting.

Text Book:

1. Sandra Johnson, Robin Linker, "Understanding Medical Coding: A Comprehensive Guide", Cengage Learning, 2012

Reference Books:

2. Donna Avila-Weil, Rhonda Regan, "Independent Medical Coding: The Comprehensive Guidebook for Career Success as a Medical Coder", Rayve Productions, 2007.
3. Patricia Aalseth, "Medical Coding: What it is and How it Works", Jones & Bartlett Learning, 2005.
4. Lois Burns, Florence Maloney, "Medical Transcription & Terminology: An Integrated Approach", Cengage Learning, 2003

17BI2044 SCIENTIFIC WRITING

Credits: 3:0:0

Course Objectives:

- To understand the guidelines for style, grammar, specific writing and skills of scientific writing.
- To understand software tools relying on Natural Language Processing
- To focus on their research and still get published in top journals.

Course Outcomes:

- Ability to understand the fundamentals of scientific writing.
- Insight into the art of writing a research article.
- Students understand the six qualities of unique writing techniques, i.e. fluid, organized, clear, concise, convincing and interesting.
- Understand the effect of team-work in scientific writing.
- Acquire knowledge about different methods of publication
- Ability to follow various conventions of writing style.

UNIT I - The reading Toolkit, Sustain Attention to ensure continuous reading, Reduce reading time, Keep the reader motivated, bridge the knowledge gap.

UNIT II - Set the reader's expectations, set progression tracks for fluid reading, detect sentence fluidity problems, control reading energy consumption.

UNIT III - Paper structure and purpose, Abstract, headings – subheadings, Introduction, visuals, conclusions.

UNIT IV - Additional resources, Maximizing Chances of Publication, Essential Steps Before Writing a Paper, Drafting Papers.

UNIT V - Complex Studies, Linguistic Points, Covering Letters and Referees Objections.

Text Books:

1. Jean-Luc Lebrun, "Scientific Writing 2.0: A Reader and Writers Guide", World Scientific, 2011.

Reference Books:

1. David Lindsay, "Scientific Writing", Csiro Publishing, 2011.
2. Jennifer Ouellette, "The Best Science Writing Online 2012", Macmillan, 2012

3. John Blackwell, Jan Martin, "A Scientific Approach to Scientific Writing", Springer, 2011

17BI2045 WEB PROGRAMMING

Credits: 3:0:0

Course Objectives:

- To enable the student to build and manage web applications.
- To impart knowledge of HTML , DHTML and XML
- To introduce web technologies in clinical data management

Course Outcomes:

- Analyze a web page and identify its elements and attributes.
- Create web pages using XHTML and Cascading Styles sheets.
- Build web applications using PHP
- Create XML documents
- Create XML Schema
- Build and consume web services.

UNIT I - Introduction: Using PHP, Storing and retrieving data, using array, string manipulation and regular expressions, reusing code and writing function, object oriented PHP, Error and exception handling
UNIT II - MySQL: Designing web database, creating web database, working with MySQL database, Accessing MySQL database from the web with PHP, Advanced MySQL administration, Advanced MySQL Programming
UNIT III - Web application security: Web application security risks, building a web secure application, implementing authentication methods with PHP
UNIT IV - Advanced PHP Techniques: Interacting with the file system and server, using network and protocol function, managing the date and time, Internationalization and localization, generating images, using session control in PHP, integrating JavaScript and PHP
UNIT V - Building Practical PHP and MySQL projects: Using PHP and MySQL for large projects, debugging and logging, building user authentication and personalization, building a web based email service with laravel, social media integration sharing and authentication web edition, building a shopping cart web edition

Text Book:

1. Luke Welling, Laura Thomson "PHP and MySQL Web Development" Addison-Wesley Professional, 2016

Reference Books:

1. Larry Ullman "PHP and MySQL for Dynamic Web Sites" Peachpit Press, 2011
2. Marty Matthews "PHP and MySQL Web Development: A Beginner's Guide" McGraw Hill Professional, 2015
3. Janet Valade "PHP and MySQL Web Development All-in-One Desk Reference For Dummies" John Wiley & Sons, 2011

17BI2046 CLINICAL PRACTICES AND REGULATIONS

Credits: 3:0:0

Course Objectives:

- To emphasize on the delivery of safe and evidence based healthcare for clients
- To focus on the evaluation of healthcare Outcomes in individuals and groups with varied levels of acuity across the lifespan.
- To lay emphasis on complicated disease, injury and various degrees of disability

Course Outcomes:

- The student is able to implement evidence-based collaborative interventions in the care of clients with complicated illnesses.
- They are able to apply legal and ethical principles in the care of clients with complicated disease, injury, and disability.
- The students are able to apply knowledge in drug safety and regulations.
- Students are able to analyze the epidemiological effect on clinical practices
- Students are able to estimate the risk factor in clinical practices and regulations
- Students are able to understand the different phases of drug trials and ethics.

UNIT I - Introduction to Clinical practices and regulations: Basic epidemiology and observational methods, interventional and randomized controlled trials, and Clinical epidemiology and evidence-based medicine.
UNIT II - Standard epidemiological concept:Concepts of association and Outcomes, standard epidemiological concepts of incidence and prevalence.
UNIT III - Risk factor in clinical practices: Define and describe relative risk, absolute risk, attributable risk and the various methods for calculating those quantities in different observational research designs.
UNIT IV - Drug trials: Methods for reducing bias and confounding, Interventional trials, including the four phases of drug trials.
UNIT V - Analysis and interpretation of controlled trials: The importance and effects of randomization, analysis and interpretation of controlled trials.

Text Book:

1. Designing Clinical Research: An Epidemiologic Approach, Third Edition. SB Hulley, SR Cummings, WS Browner, D Grady, and TB Newman. 2007

Reference Books:

1. Clinical Trials: A Methodologic Perspective. S Piantadosi. Wiley Interscience, 2001
2. Clinical Trials: Design, Conduct and Analysis (Monographs in Epidemiology and Biostatistics Vol 8. CL Meinert. Oxford University Press, 2000
3. Seidel, HM, et al. Mosby's Guide to Physical Examination. Sixth Edition. Elsevier Science, St. Louis, 2006

17BI2047 DRUG DISCOVERY AND CLINICAL TRAILS

Credits: 3:0:0

Course Objectives:

- To provide a systematic application of information science and technology to support patient care
- To lay emphasis on the use of information systems/technology to evaluate health care systems for quality improvement
- To provide leadership skills within health care systems and/or academic settings.

Course Outcomes:

- The students are able to identify terminology and concepts in drug discovery informatics.
- They are able to demonstrate informatics skills in complex decision making in clinical trails
- They are able to evaluate technical and scientific health care information.
- Students and able to perform he operational executions in clinical trials
- Students are able to understand the phramcological and toxilogical effect to design clinical and therapeutic trials
- Students are able to understand the ethical issues before bringing and drug to the market.

UNIT I - Introduction to Drug Dsicovery: Terminology, concepts, technology, and systems used in drug discovery, Pharmacodynamics and pharmacokinetics
UNIT II - Phamacology and Toxicology: Present and future role of technology in revolutionizing/transforming advanced clinical trials. Design clinical trials and therapeutic trails.
UNIT III - Clinical Trial Operations: Experimental methodology and operational execution in clinical trials.
UNIT IV - Applications of Clinical Trials: Use of health care technologies in clinical decision making, quality improvement, patient education, and practice management- Analysis of evolving issues in the field of drug discovery informatics
UNIT IV - Ethical implications: Legal and ethical implications of health care technology- sample size estimation and safety assessment

Text Book:

1. J. Rick Turner, New Drug Development: An Introduction to Clinical Trials, Springer, 2010

Reference Books:

1. SK Gupta, Drug Discovery and Clinical Research, Jaypee digital. Pub, 2011
2. Epidemiology, Fourth Edition. L Gordis, 2008
3. Fundamentals of Clinical Trials, 3rd edition. Friedman, Furberg ad Dements. Spring Publisher, 2000

17BI2048 MEDICAL CODING AND TRANSCRIPTION LAB

Credits: 0:0:2

Course Objectives:

- To resolve diagnostic questions and medical codes
- To learn referring to comprehensive code books such as the International Classification of Diseases (ICD)
- To teach how to convert voice-recorded reports as dictated by physicians or other healthcare professionals, into text format.

Course Outcomes:

- Students understand the basic systems and processes in billing, reimbursement and insurance coverage.
- Students are able to gain knowledge from the medical information system.
- Student are able to analyze medical records (charts) and codes for indexing diagnosis
- Students have learned medical terminology and codes
- They are trained in medical insurance processing and coding
- They have gained ability to manage the flow of medical records.

Experiments:

1. Analyze Medical Codes: ICD 10 and CPT codes basics
2. Build Medical Codes: Practice how to build codes efficiently and effectively
3. CPT: Radiology Codes
4. CPT: Pathology and Laboratory Codes
5. CPT: Medicine Codes
6. HCPCS
7. Capstone Cases
8. Medical terminology (Anatomy, physiology, disease processes)
9. Medical dictation types
10. Express Scribe Transcription Playback Software
11. Medical report typing
12. MT record maintenance and transcription log

17BI2049 CLINICAL DATABASE MANAGEMENT LAB

Credits: 0:0:2

Course Objectives:

- To teach important practical exercises related to clinical data management plan
- To learn clinical data retrieval process
- To teach clinical data analysis exercises

Course Outcomes:

- Students understand the role of clinical data management in clinical trials
- They gain experience in clinical data retrieval process
- They gain ability to design and analyze database consideration
- Perform database/procedure testing, data validation, SAE reconciliation and medical coding.
- Have a thorough insight on project management in data management domain.
- Understand how a Pharmacovigilance and medical affairs team function and their dependency on data management

Experiments:

1. General Components in Clinical Data Management
2. Collection of Public Health Data from World Health Organization
3. WebMD and Vpsim – virtual Patient Simulator
4. Case Report Form Design
5. Entrypoint i4
6. SNOMED CT Browser
7. Repository of clinical data set using Server concepts
8. Developing database for clinical data
9. Research Electronic Data capture
10. Identifying patterns from clinical data using data mining techniques

11. Population studies for clinical data using statistical techniques
12. Castor Electronic Data Capture

17BI2050 RUBY PROGRAMMING

Course Objective:

- understand the syntax and semantics of the Ruby language and their similarity and differences from Java
- understand how to develop and implement various types of programs in the Ruby language
- understand various forms of data representation and structures supported by the Ruby language

Course Outcome:

- Proficient programming in the Ruby language and programming in general
- Design and revision of Ruby scripts
- Debugging techniques appropriate for the Ruby language
- Apply the Ruby programming language to build program conditions, loops, if-else statements, methods, and classes
- Build a simple web application using Ruby and the Ruby on Rails framework
- Connect a Ruby on Rails web application to a database

Unit I (Foundations and Scaffolding): Installing Ruby, Programming, Ruby's Building Blocks: Data, Expressions and Flow control
Unit II (First Ruby Application): Working with source code files, A text analyser, Ruby ecosystem, Classes, objects and modules
Unit III (Projects and Libraries): Using code from other files, Documentation, Error Handling, Debugging and testing, files and databases
Unit IV (Code and Libraries): Distributing Basic Ruby programs, detecting Ruby's runtime environment, distributing Ruby libraries as Gems, Deploying Ruby applications as remote services, Advanced Ruby Features, Developing larger Ruby Application
Unit V (Ruby Online): Web application, Ruby and internet- HTTP and the web, E-Mail, File Transfers with FTP, Networking and Sockets.

Text Book

1. Peter Cooper, "Beginning Ruby: From Novice to Professional" Apress, 2016

Reference Book:

1. David Flanagan, Yukihiro Matsumoto, "The Ruby Programming Language: Everything You Need to Know" "O'Reilly Media, Inc.", 2008

17BI2051 BIOLOGICAL BIG DATA ANALYTICS

Credits: 3:0:0

Course Objectives:

- To give the knowledge of the biological data with the focus on the analysis
- To understand NGS data and analyze these in an UNIX/Linux working environment.
- To analyze computational genomics using advanced statistical methods for solving bioinformatics problems.

Course Outcomes:

- Describe the applications of the different high throughput techniques, including the weakness and strengths of the approaches.
- Explain the steps involved in a general big data analysis.
- Explain key theoretical concepts of alignment and de novo assembly.
- Synthesize and formulate a project and relevant question within the field.
- Independently perform a basic NGS data analysis.
- Apply analytical and reflective skills in analyzing results from individual steps and the final project.

UNIT I - UNIX Operating System; General purpose utilities; Navigating the Filesystem; Handling ordinary files; The Shell; The Vi Editor; The Environment-Basic File Attributes; Introduction:
UNIT II - More File Attributes; System Administration-The Routine Duties; The Regular Expressions and The grep family-The Process; Communication and Electronic mail; Shell Programming;

UNIT III - The cellular system and code of life, DNA sequence, The transcribed sequence, Next Generation Sequencing: NGS Technologies, Early Stage NGS data analysis, Computing needs for NGS data management and analysis

UNIT IV - Application specific NGS data analysis:Transcriptomics by RNA-seq, Small RNA sequencing, Genotyping and Genomic Variation discovery by whole genome resequencing

UNIT V - Metagenome analysis:Metagenome analysis by NGS, changing landscape of NGS, Epigenomics data analysis:*De novo* genome assembly from NGS reads, Mapping Protein-DNA interactions with ChIP-seq, Epigenomics and DNA methylation analysis by NGS.

Text Book:

1. Xinkun Wang, "Next-Generation Sequencing Data Analysis" CRC Press 2016
2. Sumitabha Das, Unix – Concepts and Applications, Tata McGraw Hill, 2ndEdition.

Reference Books:

1. Next-Generation DNA Sequencing Informatics [Kindle Edition] by Stuart Brown, Cold Spring Harbor Laboratory Press Newyork, 2013.
2. Tag-based Next Generation Sequencing by Matthias Harbers and GuenterKahl (Wiley Blackwell Germany 2012
3. Wong, Lee-Jun C., Next Generation Sequencing- Translation to Clinical Diagnostics, Springer, 2013
4. Steven Graham & Steve Shah, Linux Administration, Third Edition, Dreamtech, NewDelhi, 2003.

17BI2052 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
- Parse and manipulate text with regular expressions
- Extract and arrange information from multiple files
- Master the principles of object-oriented programming and the interplay of algorithms and data structures in well-written modular code
- Solve problems requiring the writing of well-documented programs in the Python language, including use of the logical constructs of that language

UNIT I - 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, Bio-python.

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 Books

1. Alex Martelli and David Ascher, "Python cookbook", O'Reilly,USA, 2ndEdition 2002.

17BI2053 BIOMOLECULAR VISUALIZATION

Credits: 3:0:0

Course Objectives:

- To teach the principles and visualization of biomolecules, structural architecture of proteins, nucleic acids and their functions.

Course Outcomes:

- Develop an ability to integrate information to tools and databses.
- Develop an informed understanding of the role of science and technology in biological society.
- The students learnt different Graphical User Interphase components of biomolecule visualization tools.
- Students will be enabled to perform different simulation techniques.
- The course will expose the student to current and relevant applications in molecular simulation and modeling.
- To understand the concept of Protein structure and function relationship and protein engineering.

UNIT I - Biomolecules, Levels of structure in proteins, DNA, RNA, 3D structure function relationships, Major structural features, Domains, Customized molecular views, PDB, SCOP, CATH, SSEP, CADB, THGS, SMS, Pfam and GDB.
UNIT II - High quality animations, Browser plugins, Multiple structure visualization, MEROPS, BRENDA. Pathway databases - CAZy. Disease databases and Literature databases
UNIT III - Colouring sequence alignment, phylogeny and structure alignment, investigation of specific interaction motifs
UNIT IV - studies of protein-protein and protein-DNA interactions, and protein super-families
UNIT V - Jmol, Proteopedia, Rasmol, Pymol, Friend, and VMD tools

Text Book:

1. Gautham N., "Bioinformatics", Narosa Publishing Company, New Delhi, 2012.

Reference Books:

1. VasanthaPattabhi and N.Gautham,"Biophysics", Narosa Publishing Company, New Delhi, 2001.

17BI2054COMPUTER AIDED DRUG DESIGN

Credits: 3:0:0

Course Objectives:

- 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 Outcomes:

- Students are introduced to the principles and practice of protein structure prediction and modern drug discovery.
- Students are able to understand the pharmacological effect to design clinical and therapeutic trials
- Students are able to predict the biological activity based on experimental analysis.
- Students are able to find the structural features for the biological activity.
- Students are able to understand the toxicological effect to design clinical and therapeutic trials
- Students are able to identify the SNP among the biomolecules.

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. VasanthaPattabhi 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.

17BI2055MOLECULAR SIMULATION AND ENGINEERING

Credits: 3:0:0

Course Objectives:

- 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 Outcomes:

- The course will introduce the student to the chemistry and physics behind the methods, accomplished through self-contained lectures on classical and quantum mechanics
- Students will be enabled to perform different simulation techniques.
- The course will expose the student to current and relevant applications in molecular simulation.
- The course will expose the student to fundamentals of statistical mechanics for small molecules.
- The students learn the modeling techniques for the biomolecules.

Unit I : Useful Concepts in Molecular simulation - Coordinate systems - Computer hardware and software. Potential energy functions, Energy minimization, and Molecular Dynamics - Introduction to LINUX.

UNIT II - Force Fields.Hydrogen Bonding in Molecular Mechanics.Calculation of thermodynamic properties – Phase space – Practical aspects pf computer simulation – Boundaries monitoringequilibrium – Long range process – Analyzing result of simulation and estimating errors.

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

Text Book

1. Leach A.R, "Molecular Modelling Principles and Application", Pearson – Prentice Hall, New Delhi and 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.

LIST OF COURSES

Sl.No	Course Code	Name of the Course	Credits
1	16BI3001	Structural Bioinformatics	3:0:0
2	16BI3002	Health Informatics and Analytics	3:0:0
3	16BI3003	NGS and Data Analysis Lab	0:0:2

16BI3001 STRUCTURAL BIOINFORMATICS

Credits: 3:0:0

Course objectives:

- To teach the application of the principles and basic knowledge of the larger field of bioinformatics to questions focusing on macromolecular structure
- To understand the prediction of protein structure and how proteins carry out cellular functions
- To teach the application of bioinformatics by accelerating drug discovery and development

Course outcomes:

- The students learnt the three dimensional macromolecular structure and their function.
- The students understand the theories and associated algorithms, resources of macromolecular structure.
- The students are exposed to the tools used in the analysis, prediction, and theoretical underpinnings of DNA, RNA, and proteins

Description:

Databases for protein sequences and structures, protein sequence analysis- amino acid properties, protein structure analysis – solvent accessibility, residue-residue contacts, contact potentials, free energy calculations, amino acid properties derived from structural data, Protein folding kinetics, Protein secondary and tertiary structure prediction- Physiochemical parameters, HMM, Neural Networks, Multiple sequence alignments, Protein stability- Determination of protein stability, Thermodynamic databases for proteins and mutants, Contribution of non-covalent interactions to protein stability, Protein Interactions- Databases, prediction of binding sites, solvent accessibility studies, Protein- DNA Interactions, Protein- RNA interactions,

References:

1. M. Michael Gromiha, Protein Bioinformatics- From Sequence to Function, Press Publisher Elsevier Pvt. Ltd., 1st Edition, 2010
2. Dongqing Wei , Qin Xu , Tangzhen Zhao , Hao Dai “Advance in Structural Bioinformatics “ Springer, 2014
3. Jenny Gu, Philip E. Bourne “Structural Bioinformatics” Wiley Blackwell Publication, 2nd edition, 2009.
4. Carl-Ivar Branden and John Tooze “Introduction to Protein Structure” Garland publishing, 1999.
5. Chris Calladine, Horace Drew, Ben Luisi, and Andrew Travers “Understanding DNA” Elsevier 2004.

16BI3002 HEALTH INFORMATICS AND ANALYTICS

Credits: 3:0:0

Course Objectives:

- Focus on general health informatics, development, management
- Health data analytics that stresses the impact of technology on outcomes and quality of healthcare services
- Use of information systems in clinical healthcare settings

Course Outcomes:

- Students shall be able to collect and manage data related to public health disorders and infectious diseases
- Students shall learn to handle healthcare data integration and exchange, and management of health information systems
- Students shall learn the use of IT and health data in clinical and administrative settings

Description:

Overview of Healthcare Analytics, Problems in Healthcare Motivating Biomedical and Health Informatics, Resources for Field – Organizations, Information, Education, Electronic and Personal Health Records (EHR, PHR), Hospital Management Information Systems, Standards and Interoperability, Meaningful Use of the EHR, Protection and Analytical Use of Data, Information Retrieval and Digital Libraries, Imaging Informatics and Telemedicine, Research Informatics, Importance of data and data analytics to a healthcare organization.

References:

1. Mohan Bansal, "Medical Informatics- a primer", Tata McGraw-Hill , New Delhi, 2003.
2. Edward H. Shortliffe, "Medical Informatics: Computer Applications in Health Care and Biomedicine", Second Edition, Springer, 2001
3. Taylor Paul, "From Patient Data to Medical Knowledge: The Principles and Practice of Health Informatics", Blackwell Scientific Publishing, UK, 2006.
4. Shortliffe and Cimino, "Biomedical informatics: computer applications in health care and biomedicine", Springer, NewYork, 3rd edition, 2006

16BI3003 NGS AND DATA ANALYSIS LAB

Credits: 0:0:2

Co-Requisite: 15BI3013

Course Objectives:

- To teach computational genomics
- To teach them normalization and data analysis
- To demonstrate the different integrated methods with significant genes

Course Outcomes:

- Understand the format of NGS data sets
- Apply normalization techniques in different data sets
- Perform different types of algorithms for removing noise from NGS-Seq data

LIST OF SUBJECTS

Sub. Code	Name of the Subject	Credits
15BI2001	Introduction to Bioinformatics Algorithms	3:0:0
15BI2002	Medical Informatics	3:0:0
15BI3001	Structural Bioinformatics	3:0:0
15BI3002	Computational Genome and Proteome Analysis	3:0:0
15BI3003	Bioinformatics Algorithms	3:0:0
15BI3004	Cheminformatics and QSAR	3:0:0
15BI3005	Microarray and Image Analysis	3:0:0
15BI3006	Systems Biology	3:0:0
15BI3007	Computational Genome and Proteome Analysis Lab	0:0:2
15BI3008	Bioinformatics Algorithms lab	0:0:2
15BI3009	Microarray Data Analysis Lab	0:0:2
15BI3010	Systems Biology Lab	0:0:2
15BI3011	Cheminformatics and QSAR Lab	0:0:2
15BI3012	Health Informatics and Analytics	2:0:0
15BI3013	Next Generation Sequencing	3:0:0
15BI3014	R Programming	3:0:0
15BI3015	Pattern Recognition and Machine Learning	3:0:0
15BI3016	R Programming Lab	0:0:2
15BI3017	Pattern Recognition and Machine Learning Lab	0:0:2
15BI3018	Scientific Writing	2:0:0
15BI3019	Drug Design and Discovery	3:0:0
15BI3020	Pharmacoinformatics	3:0:0
15BI3021	Computational Chemistry	3:0:0
15BI3022	Drug Design and Discovery Lab	0:0:2
15BI3023	Microbial Genomics	3:0:0

15BI2001 INTRODUCTION TO BIOINFORMATICS ALGORITHMS

Credits: 3:0:0

Course Objectives:

- To understand the basic concept of various algorithms used in Bioinformatics
- To teach different algorithms used for prediction of protein secondry structure
- To discuss algorithms to find significant patterns in protein and nucleotide Sequences

Course Outcomes:

- Students will apply the application of algorithms in different areas of Bioinformatics
- Predicting secondary and tertiary structures using different algorithms
- To analyse conserved regions in DNA sequence

Description:

Artificial intelligence and computer science - Search algorithms, Heuristic search methods, Optimal search strategies, Problems with search techniques, Complexity of search, nearest neighbor and clustering approaches– Nearest neighbor approach for secondary structure for protein folding prediction, Clustering, predictive methods using protein sequences- Protein identity based on composition, Motifs and Patterns, Genetic algorithm - objective genetic algorithms, Multi-objective genetic algorithms, Neural network- Supervised learning, Unsupervised learning, Bioinformatics servers using neural network.

References:

1. Andreas D. B and Ouellette B. F. F, "Bioinformatics- A practical Guide to analyze Genes and Proteins", John Wiley and Sons, USA, 2001.
2. Edward K and Ajit N, "Intelligent Bioinformatics- The Application of Artificial Intelligence techniques to Bioinformatics problems", John Wiley and Sons, USA, 2005.
3. David W. Mount., Bioinformatics: Sequence and Genome Analysis., Cold Spring Harbor Laboratory Press,U.S.,2nd edition, 2004

15BI2002 MEDICAL INFORMATICS

Credits: 3:0:0

Course Objectives:

- To give an idea on the applications of information technology in medical field.
- To teach them biological databases for sequence and structure retrieval
- To help them to understand hospital management system

Course Outcomes:

- Students will have an overview of medical informatics as a discipline.
- Develop skills and concepts fundamental to more advanced topics in health informatics.
- Learnt about the medical databases

Description :

Databases - nucleic acid and protein sequence, structural databases, Regions of similarity using FASTA, BLAST, Multiple sequence alignment, Hospital management and information system: functional area - pre-requisites - integrated hospital information systems - health information system, Artificial intelligence - expert systems, computer based patient Records - computer assisted medical education, Three-dimensional imaging: limitations of endoscopy and imaging - benefits of virtual endoscop, surgical simulation - virtual environment, tele-medicine- tele-surgery - the Internet, Database of medical informatics.

References :

1. Mohan Bansal, "Medical Informatics - a primer", Tata McGraw-Hill, New Delhi, 2003.
2. J. Pevzner, "Bioinformatics and functional genomics", 2nd Edition, John Wiley & Sons, NJ, USA, 2009.
3. 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.
4. Hsinnchun Chen, "Medical Informatics: Knowledge Management and Data Mining in Biomedicine", Springer-Verlag, New York, 2005

15BI3001 STRUCTURAL BIOINFORMATICS

Credits : 3:0:0

Course objectives:

- To teach the application of the principles and basic knowledge of the larger field of bioinformatics to questions focusing on macromolecular structure
- To understand the prediction of protein structure and how proteins carry out cellular functions
- To teach the application of bioinformatics by accelerating drug discovery and development

Course outcomes:

- The students learnt the three dimensional macromolecular structure and their function.
- The students understand the theories and associated algorithms, resources of macromolecular structure.
- The students are exposed to the tools used in the analysis, prediction, and theoretical underpinnings of DNA, RNA, and proteins

Description:

Introduction to structural bioinformatics, Fundamental principles of protein/DNA/RNA structure, Experimental methods for structure determination, Data collection analysis and visualization, Data representation and databases, Data integrity and comparative features, structural and functional assignment, macromolecular interaction, Structure prediction, Structure comparison and alignment, Prediction of structure of biopolymers, Prediction of protein function from structure and other types of data, Principles of molecular recognition and docking, Therapeutic Discovery.

References:

1. Jenny Gu, Philip E. Bourne "Structural Bioinformatics" Wiley Blackwell Publication, 2nd edition, 2009.
2. Dongqing Wei , Qin Xu , Tangzhen Zhao , Hao Dai "Advance in Structural Bioinformatics " Springer, 2014
3. Carl-Ivar Branden and John Tooze "Introduction to Protein Structure" Garland publishing, 1999.
4. Chris Calladine, Horace Drew, Ben Luisi, and Andrew Travers "Understanding DNA" Elsevier 2004.

15BI3002 COMPUTATIONAL GENOME AND PROTEOME ANALYSIS

Credits : 3:0:0

Course Objectives:

- To provide the students with a foundation for application of available computational tools in genomics
- Provide insight into Biological Mass Spectrometry and 2D PAGE technologies
- To inculcate the knowledge about the software for image/mass spectrum analysis

Course Outcomes:

- Students understand the principle and strategies of computational genome and proteome analysis and their applications.
- Students will understand the significance of the emerging fields of genomics and proteomics.
- Students will be able to skillfully apply image analysis and MS spectra analysis in research.

Description:

Databases - nucleic acid and protein sequence, structural databases, Genome sequencing and assembly, Human genome project, Bioinformatics of genome annotation, current status of genome sequencing projects, Genomic browsers and databases, Comparative Genomics, Types of Microarray experiments, The proteome, Genomics Vs. Proteomics, 2D PAGE and Image analysis with Melanie, Biological Mass Spectrometry, Mascot, SEQUEST, OpenMS.

References :

1. D.W. Mount. Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbour Laboratory Press, New York, 2001.
2. Andreas D. Baxevanis, B. F. Francis Ouellette, Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 3rd Edition, Wiley and Sons, 2004
3. Brown T.A., "Genomes ", BIOS Scientific Publishers Ltd, Oxford, 2nd Edition, 2002
4. Daniel C. Liebler, "Introduction to Proteomics: Tools for New Biology", Humana Press, Totowa, New Jersey, 2002

15BI3003 BIOINFORMATICS ALGORITHMS

Credits : 3:0:0

Course Objectives:

- To introduce the student with bioinformatics algorithm for solving biological problems
- To understand unique balance between rigorous mathematics and practical techniques, emphasizing the ideas underlying algorithms rather than offering a collection of apparently unrelated problems
- To learn new knowledge in genomics, proteomics, metabolomics, transcriptomics, and other omics.

Course Outcomes:

- Apply different algorithms for sequence analysis, analysis of gene expression data and molecular biological networks.
- Implement commonly used algorithms for sequence comparisons and graph theoretical problems relating to bioinformatics
- Test the ability of students programming skills in algorithm design

Descriptions :

Algorithms and Complexity: Biological algorithm versus computer algorithms-The change problem-Correct versus Incorrect algorithms-Recursive algorithm- Towers of Hanoi problem- Big O notation- Algorithm design techniques; 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; Graph Algorithms: 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; Combinatorial Pattern matching: Repeat finding-Hash tables-Exact pattern matching-Suffix trees-Heuristic similarity search Algorithms-Approximate Pattern matching-BLAST; Evolutionary trees, Reconstructing trees from additive matrices

References:

1. M. Waterman, “Introduction to Computational Biology: Maps, Sequences & Genomes”, CRC Press, 1995.
2. Neil Jones & Pavel Pevzner An Introduction to Bioinformatics Algorithms, MIT Press, 2004.
3. Wing-Kin Sung, Algorithms in Bioinformatics: A Practical Introduction (Chapman & Hall/CRC Mathematical and Computational Biology), 2012
4. Phillip Compeau & Pavel Pevzner Bioinformatics Algorithms: An Active Learning Approach, 2014

15BI3004 CHEMINFORMATICS AND QSAR

Credits : 3:0:0

Course Objectives:

- To emphasis on applications including modern drug discovery
- To study the process of mechanistic approach on computer aided drug design
- To learn a deep understanding of the molecular basis of physiochemical behavior

Course Outcomes :

- Test how to retrieve specific information from the enormous and rapidly expanding chemical literature.
- Analyse broad overview of the computer technology to chemistry in all of its manifestations
- Develop current and relevant applications in QSAR and Drug Design.

Description :

Introduction to cheminformatics, History and Evolution of cheminformatics, Use of cheminformatics, Prospects of cheminformatics, Molecular Modeling and Structure Elucidation- Structure of Molfiles and Sdfiles; Different electronic effects; Reaction classification- CoMFA and related methods, such as CoMSIA; the basic principles of modeling and statistical tools routinely required in QSAR methodologies, including optimization methods, strengths and weaknesses of 3D-QSAR approaches; Biological activity of chemicals to their structure, encompassing both their 2D structural formulae and 3D geometry; Pharmacophore QSAR modeling

References :

1. Thomas J Perun and C. L. Propst, Computer Aided Drug Design – Methods and Application, 2007
2. Andrew R. Leach, Valerie J. Gillet Cluwer , Introduction to Chemoinformatics, Academic Publishe, Netherlands, 2003
3. Lisa B, Combinatorial Library Methods and Protocols, English. Humana Press Inc, Volume:201, 2002
4. Frank Jensen, Introduction to Computational Chemistry, Wiley Publisher, Second Edition, 2006
5. R. K. Prasad, Quantum chemistry, Halsted Press, 2002

15BI3005 MICROARRAY AND IMAGE ANALYSIS

Credits: 3:0:0

Course Objectives:

- To explain how microarray technology works, including the various types
- To understand how data is retrieved in different formats produced by microarrays
- To understand biological data normalization

Course Outcomes:

- Students can demonstrate the working of microarray by different technologies
- Students can carry out different algorithms for normalization
- Students are able to do different statistical analysis of normalized and preprocessed data

Description :

Microarray technologies- Using microarray, Microarray standard databases-LIMS, MGED, MAGE, Microarray sequence databases, Microarray chip manufacture, Image processing- Microarray data cleaning and preprocessing, Data normalization, 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, 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, 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

References :

1. Dov Stekel, "Microarray Bioinformatics" Cambridge University Press, UK, 2013.
2. Aidong Zhang, "Advanced analysis of Gene expression microarray data", World Scientific Publishing House, New Delhi, 2006.
3. Pierre Baldiand and Wesley Hatfield, "DNA microarrays and gene expression from experiments to data analysis and modeling", Cambridge University Press, New York, 2002.

15BI3006 SYSTEMS BIOLOGY

Credit: 3:0:0

Course Objectives:

- This course helps them to understand the basic concept of graph theory in netwoks of proteins
- The different algorithm related to Systems Biology and software used will be discussed in the course
- To teach regulatory networks

Course Outcomes:

- Students will understand the network properties
- Will be able to design regulatory network through systems biology software
- Will apply the algorithms for biochemical network construction

Description :

Basic concepts in systems Biology - Metabolic Networks- Transcriptional Regulatory Networks- Signaling Networks, modeling algorithms-Kinetic Modeling - Cellular Network reconstruction and Static Modeling - Construction and verification of kinetic models- introduction to dbsolve - Enzyme Kinetics modeling, 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, 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.

References:

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.
3. Hiroaki Kitano, "Foundations of Systems Biology", MIT Press, 2001
4. Douglas B.West, "Introduction to Graph Theory", Prentice-Hall, India, 2000

15BI3007 COMPUTATIONAL GENOME AND PROTEOME ANALYSIS LAB

Credits: 2:0:0

Co-Requisite: 15BI3002

Course Objectives:

- To demonstrate the applications of computational tools in genome analysis
- Analysis of proteins with Mass Spectrometry software using mass spectrum data
- Analysis of 2D PAGE data with image analysis software

Course Outcomes:

- Students shall learn the strategies of computational genome and proteome analysis
- Students will be able to skillfully learn the analysis of MS spectra
- Students shall be able to demonstrate 2D PAGE image analysis using databases and software.

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3008 BIOINFORMATICS ALGORITHMS LAB

Credits: 0:0:2

Co-Requisite: 15BI3003

Course Objectives:

- To offers a clear exposition of the algorithmic principles driving advances in bioinformatics
- To provide an in-depth introduction for algorithm design using graph based approach
- To demonstrate and design algorithms for solving practical problems in biology

Course Outcomes:

- To strike a unique balance between practical challenges in modern biology and fundamental algorithmic ideas, thus capturing the interest of biology and computer science students alike.
- Students will explore applications of the phylogenetic tree, methods for comparing phylogenetic trees,
- Analyse problems of genome rearrangement and motif findings

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3009 MICROARRAY DATA ANALYSIS LAB

Credits: 0:0:2

Co-Requisite: 15BI3005

Course Objectives:

- To teach analysing expression data using NCBI
- To teach them normalization and data analysis
- To demonstrate the clustering algorithms

Course Outcomes:

- Understand the format of different expression data sets
- Apply normalization techniques in different data sets
- Perform different types of algorithms for removing noise from expression data

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3010 SYSTEMS BIOLOGY LAB

Credits: 0:0:2

Co-Requisite: 15BI3006

Course Objectives:

- To teach Genomic tools for analysing transcriptional regulatory networks
- To teach Essential gene identification
- To demonstrate the Network creation and analysis

Course Outcomes:

- Understand the Diseased gene identification through GeneCards and Entrez Gene
- Execute protein interaction through cell designer
- Perform Protein network simulation and pathway modelling

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3011 CHEMINFORMATICS AND QSAR LAB

Credit: 2:0 0

Co-Requisite: 15BI3004

Course Objectives:

- To introduce different methods of Cheminformatics with particular emphasis on applications including drug design and discovery
- To provide an overview of the process of mechanistic, computer aided drug design
- To study a deep understanding of the molecular basis of physical behavior

Course Outcomes:

- To retrieve specific information from the enormous and rapidly expanding chemical literature
- Test the skills of computer technology to chemistry in all of its manifestations
- To execute current and relevant applications in computer aided drug design

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3012 HEALTH INFORMATICS AND ANALYTICS

Credits: 2:0:0

Course Objectives:

- Focus on general health informatics, development, management
- Health data analytics that stresses the impact of technology on outcomes and quality of healthcare services
- Use of information systems in clinical healthcare settings

Course Outcomes:

- Students shall be able to collect and manage data related to public health disorders and infectious diseases
- Students shall learn to handle healthcare data integration and exchange, and management of health information systems
- Students shall learn the use of IT and health data in clinical and administrative settings

Description:

Overview of Healthcare Analytics, Importance of data and data analytics to a healthcare organization, Basic statistical skills for data analysis, Principles of Predictive Analytics, Basic concepts in health informatics and its history, Definitions, Sub disciplines and professional organizations and activities, Major health informatics applications including electronic medical records (EHR) and computerized physician order entry (CPOE), good clinical practices (gcp)**,**
information systems design and engineering, new opportunities and emerging trends**:** Information technologies in healthcare; wireless and handheld devices, social computing paradigms, and eHealth applications.

References:

1. Mohan Bansal, "Medical Informatics- a primer", Tata McGraw-Hill , New Delhi, 2003.
2. Edward H. Shortliffe, "Medical Informatics: Computer Applications in Health Care and Biomedicine", Second Edition, Springer, 2001
3. Taylor Paul, "From Patient Data to Medical Knowledge: The Principles and Practice of Health Informatics", Blackwell Scientific Publishing, UK, 2006.
4. Shortliffe and Cimino, "Biomedical informatics: computer applications in health care and biomedicine", Springer, NewYork, 3rd edition, 2006

15BI3013 NEXT GENERATION SEQUENCING

Credits : 3:0:0

Course Objectives:

- The course exposes students to active research in NGS, computational genomics and introduces advanced statistical methods for solving bioinformatics problems.

Course Outcomes:

- Understand and critique existing methodology for the analysis of DNA sequencing, massively parallel sequencing,
- Know the current challenges and open issues in computational genomics,
- Obtain skills to develop novel statistical approaches to study NGS data

Description:

DNA sequencing, Visualization of Next Generation Sequencing Data, Genome assembly, Short Sequence reads, ChIP-Seq, Genome annotation, Sequence variants, RNA sequencing with Next Generation Sequence, Metagenomics, High Performance Computing in Next Generation Sequencing data.

References:

1. Stuart Brown, "Next-Generation DNA Sequencing Informatics", Kindle Edition, Cold Spring Harbor Laboratory Press Newyork, 2013.
2. Matthias Harbers and Guenter Kahl, Tag-based Next Generation Sequencing, Wiley Blackwell Germany, 2012

15BI3014 R PROGRAMMING

Credits: 3:0:0

Course Objectives:

- To understand the fundamentals of R programming
- To get a broad insight into analytics and acquire skills in methodologies and techniques
- Get familiar with R Analytics as a career option with practical knowledge of some of the most in-demand techniques like Predictive Analytics and Data Visualisation to plot

Course Outcomes:

- The students will gain an understanding of the programming syntax
- Develop programming skills in R
- Students will be able to use R in MatLab

Description:

Using the R console, Data Structures, Variables, Control Flow, Functions, Getting Data into the R environment, Overview of Statistics in R, Descriptive statistics, Inferential statistics, Linear Regression, Classification, Clustering, Time series, Dimensionality reduction, Machine Learning, Object Oriented R, Sophisticated Graphics in R, R for Mapping and GIS, BIOCONDUCTOR, Case Study through SRA database.

References :

1. Mark Gardener. Beginning R: The Statistical Programming Language. John Wiley & Sons, 2012.
2. Robert Gentleman. R Programming for Bioinformatics. CRC Press, 2008.
3. John Chambers. Software for Data Analysis: Programming with R. Springer, 2010.
4. Michael J. Crawley. The R Book. John Wiley & Sons, 2012.
5. Norman Matloff. The Art of R Programming: A Tour of Statistical Software Design. Starch Press, 2011.

15BI3015 PATTERN RECOGNITION AND MACHINE LEARNING

Credits: 3:0:0

Course Objectives:

- To know the concepts and applications of Machine Learning.
- To provide an insight to Machine Learning Technique before stepping into Artificial Intelligence
- To teach for applying mathematical modeling in biological applications.

Course Outcomes:

- To understand and apply fundamental Machine Learning Techniques from theory to practical.
- To develop enhanced critical and conceptual thinking and problem solving skills in large biological data sets
- To apply different algorithms in protein structure prediction.

Description

Machine learning application, polynomial curve fitting, probability theory, model selection, i
bayesian decision theory: introduction, classification, losses and risk, discriminant functions, utility theory, multivariate methods and clustering: multivariate data, parameter estimation, estimation of missing values, multivariate normal distribution, multivariate classification, tuning complexity, discrete features, multivariate regression. neural network- 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, graphical models: bayesian networks, conditional independence, markov random fields, inference in graphical models. approximate inference: variational inference.

References:

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.
3. Sushmita Mitra, Sujay Datta, Theodore Perkins and George Michailidis, "Introduction to Machine Learning and Bioinformatics", CRC Press, London, UK, 2008.

15BI3016 R PROGRAMMING LAB

Credits: 0:0:2

Co-Requisite: 15BI3014

Course Objectives:

- To discover how to install R packages
- To use vectorized calculations and write R functions
- To understand basic R graphics and be familiar with advanced graphics

Course Outcomes:

- Master the use of the R Console
- Learn R flow control and data structures and write R statistical models
- Write R functions and use R for descriptive statistics, confirmatory/inferential statistics

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3017 PATTERN RECOGNITION AND MACHINE LEARNING LAB

Credits: 0:0:2

Co-Requisite: 15BI3015

Course Objectives:

- To be fluent in the use of procedural statements--assignments, conditional statements, loops, function calls--and arrays.
- To be able to design, code, and test programs for image analysis
- To have a working familiarity with graphics tools in different tools

Course Outcome:

- Translate mathematical methods to programming code
- Break a complex task up into smaller, simpler tasks using logic methods
- Tabulate results and represent data visually for large data sets

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3018 SCIENTIFIC WRITING

Credits: 2:0:0

Course Objectives:

- To understand software tools relying on Natural Language Processing
- To understand the guidelines for style, grammar, specific writing and skills of scientific writing.
- To focus on their research and still get published in top journals

Course Outcomes:

- Students understand the six qualities of unique writing techniques, i.e. fluid, organized, clear, concise, convincing and interesting
- They acquire knowledge about different methods of publication
- They are able to follow various conventions of writing style

Description:

The reading Toolkit, Sustain Attention to ensure continuous reading, Reduce reading time, Keep the reader motivated, bridge the knowledge gap, set the reader's expectations, set progression tracks for fluid reading, detect sentence fluidity problems, control reading energy consumption, paper structure and purpose, Abstract, headings – subheadings, Introduction, visuals, conclusions, Additional resources, Maximizing Chances of Publication, Essential Steps Before Writing a Paper, Drafting Papers, Complex Studies, Linguistic Points, Covering Letters and Referees Objections.

References:

1. Jean-Luc Lebrun, "Scientific Writing 2.0: A Reader and Writers Guide", World Scientific, 2011.
2. David Lindsay, "Scientific Writing", Csiro Publishing, 2011.
3. Jennifer Ouellette, "The Best Science Writing Online 2012", Macmillan, 2012
4. John Blackwell, Jan Martin, "A Scientific Approach to Scientific Writing", Springer, 2011

15BI3019 DRUG DESIGN AND DRUG DISCOVERY

Credits: 3:0:0

Course Objectives:

- To provide an overview of the comprehensive information on all aspects of drug design and discovery. .
- To teach the conversion of new insight into lead structures and subsequently into drug candidates.
- To emphasize Modeling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

Course Outcomes:

- Learn the principles and practice of Molecular modelling and modern drug discovery.
- Understand to integrate a number of related scientific disciplines, including structural biology, and molecular pharmacology
- Solve Structure Activity Relationship for uptake inhibition

Description:

Introduction – how drugs are discovered – the basic mechanistic drug design – important technique of drug design; ligand based drug design, structure based drug design, molecular modeling system for drug design – uses of computer assisted drug design – extending molecular modeling; potential energy function – non-bonded energy terms – hydrogen bonds – energy minimization – application of theoretical techniques to drug design; modeling of the receptor and substrate – working with receptor-inhibitor model – application and example – rhinovirus as a drug receptor – designing antiviral drugs – structure activity relationship for the uptake inhibition – possible application – conclusion and future aspects

References :

1. Thomas J Perun and C. L. Propst, Computer Aided Drug Design – Methods and Application by, 2007
2. A.R.Leach, Molecular Modeling Principles and Application, Longman, 1996
3. R.K.Prasad, Quantum chemistry , Halsted Press, 2002 .
4. Satya Prakash Gupta, QSAR and Molecular Modeling, Springer - Anamaya Publishers, 2008.

15BI3020 PHARMACOINFORMATICS

Credits: 3:0:0

Course Objectives:

- To explain the use of information systems and technologies for the provision of decision support tools necessary for improved drug.
- To introduce the novel concepts in Pharmacoinformatics.
- To teach the novel drug discovery process

Course Outcomes:

- Learnt the principles and applications of human pharmacy physiology
- Demonstrate the concepts in Drug passage and bioavailability.
- Students have an understanding of the concepts in drug therapy optimization & patient care

Description:

Pharmacoinformatics- advanced information system for improved pharmaceutical care, methodologies, technologies and application of pharmacoinformatics- targeting drug related problems, reference models for the improvement of hospitals. Methodologies and genetic basis of Pharmacogenomics, drug metabolism, pharmacodynamics and pharmacokinetics, Identification of pharmacophore features. Building pharmacophore hypothesis; Searching databases using pharmocophores. Design & Analysis of combinatorial libraries; R eagent and product base combinatorial library generation; Focus library and HTS library. Case study on *In- silico* paharmaco-gene informatics- Identification of insulin like protein from plants.

References:

1. Tagelsir Mohamed Gasmelseid, "Pharmacoinformatics and Drug Discovery Technologies: Theories and Applications". Idea Group,U.S., 1 edition (15 March 2012)
2. Julio Licinio & Mali Wong, "Pharmacogenomics: The Search for Individualized Therapies," Thomas Edition, 2002.
3. Ingelman-Sundberg, M. Human drug metabolising cytochrome P450 enzymes: properties and polymorphisms. Archives of Pharmacology 369, 89-104, 2004

15BI3021 COMPUTATIONAL CHEMISTRY

Credits: 3:0:0

Course Objectives:

- To provide an overview of the computational aspect in biomoleculae
- To teach the concepts related to molecular simulation.
- To emphasize algorithms related to energy minimization

Course Outcomes:

- Learnt the principles and application for biolomolecule design
- Apply the knowledge for dynamics studies using suitable algorithm
- Solve Structure using molecular mechanics or Monte Carlo approach

Description:

Structure representation systems, 2D and 3D structures; General introduction to chemical structure-hybridization, tetrahedron geometry etc.; The degeneracy of isomeric SMILES and
introduction to unique SMILES; Reaction transformations notation like SMIRK, Chemical properties 2D and 3D; Introduction to adjacency, distance matrix and use of these matrices for calculating Weiner Index, Hosoya Index, Balban Index, Shultz Index, Randic Index. Introduction to shape indices-Kappa Shape index and calculation of molecular shape, Molecular Mechanics- potential energy functional forms, Bond is stretching, Angle Blending, Vanderwall Interaction, Force field energies and thermodynamics- Force Fields and docking, Molecular dynamics-Monte Carlo, ensemble and dynamical properties.

References :

1. Christopher J. Cramer, Essentials of Computational Chemistry: Theories and Models, John Willy and Sons, 2006
2. Frank Jensen, Introduction to Computational Chemistry, John Willy and Sons, 2007
3. Thomas Heine, Jan-Ole Joswig, Computational Chemistry, John Willy and Sons**,** 2009

15BI3022 DRUG DESIGN AND DISCOVERY LAB

Credit: 0:0:2

Co-Requisite: 15BI3019

Course Objectives:

- To discuss various computational techniques and its application related with drug discovery and design
- To provide comprehensive overviews of all the major modern techniques, tools and technologies used in drug design and development
- To provide key techniques to investigate biomedical applications for drug developments based on computational chemistry

Course Outcomes:

- Students will have the concepts and computer-based methodologies in drug discovery.
- Solve binding sites prediction to the accurate inclusion of solvent and entropic effects, from high-throughput screening
- Will be able to perform computational protein-protein inhibition, toward quantitative free-energy approaches

The faculty conducting the Laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

15BI3023 MICROBIAL GENOMICS

Credits: 3:0:0

Course Objectives:

- This course is framed to provide students an in depth knowledge of biological data analysis using computational tools.
- It is also useful for investigating molecular biology problems from computational perspective
- To teach them various components related to microbial genome

Course Outcomes:

- At the end of the course, the students would gain expertise tools and resources for computational analysis of biological data.
- They develop an understanding of large scale data analysis related to genomics and proteomics
- They will be able to perform computational genomics study using microbial database

Description: Bioinformatics and its applications- Types of biological databases, NCBI, Nucleotide and Protein databases, Conventional sequencing (Sanger, Automated sequencing Methods), Mapping (Genetic and Physical), Sequence analysis- Computational methods, Comparative Genomics, DNA Microarray- principle, working and microarray databases, Proteome analysis, 2D PAGE and Mass spectroscopy, The Human microbiome: process of infection, Microbial Genome Database.

References:

1. Higgins D and Taylor W. Bioinformatics: Sequence, Structure and Databanks: A Practical Approach, OUP Oxford, 2000.
2. Teresa Altwood and David Parry-Smith. Introduction to Bioinformatics, First edition, Benjamin Cummings, 2001.
3. Stephen Pennington and Michael J Dunn. Proteomics from Protein Sequence to Function, Second edition, Viva Books Ltd, 2002.

LIST OF SUBJECTS

Code	Name of the subject	Credits
14BI2001	Analytical Bioinformatics	3:0:0
14BI2002	Instrumental Methods of Analysis	3:0:0
14BI2003	Molecular Biology and Genetic Engineering	3:0:0
14BI2004	Genomics and Proteomics	3:0:0
14BI2005	Structural Biology and Biophysical Techniques	3:0:0
14BI2006	PERL and PYTHON Programming	3:0:0
14BI2007	Immunoinformatics	3:1:0
14BI2008	Molecular Modeling and CADD	3:0:0
14BI2009	Bioethics , IPR and Biosafety	3:0:0
14BI2010	Computational Systems Biology	3:0:0
14BI2012	Instrumental Methods of Analysis Lab	0:0:2
14BI2013	Analytical Bioinformatics Lab	0:0:2
14BI2015	PERL and PYTHON Programming Lab	0:0:2
14BI2016	Molecular Modeling and CADD Lab	0:0:2
14BI2017	Computational Systems Biology Lab	0:0:2
14BI2018	Network Biology	3:0:0
14BI2019	R Programming	3:0:0
14BI2020	Next Generation Sequencing	3:0:0
14BI2021	Pharmacogenomics	3:0:0
14BI2022	Functional Genomics Technologies	3:0:0
14BI2023	Pathway Modeling and Simulation	3:0:0
14BI2024	Synthetic Biology	3:0:0
14BI2025	Microarray Technology and Statistical Analysis	3:0:0
14BI2026	Kernel Based Pattern Recognition	3:0:0
14BI2027	Cheminformatics and QSAR	3:0:0
14BI2028	Cheminformatics and QSAR Lab	0:0:2
14BI2029	Network Biology Lab	0:0:2
14BI2030	R Programming Lab	0:0:2
14BI2031	Clinical Database Management	3:0:0
14BI2032	Health Care Informatics	3:0:0
14BI2033	Medical Coding and Transcription	3:0:0
14BI2034	Scientific Writing	3:0:0
14BI2035	Clinical Practices and Regulations	3:0:0
14BI2036	Drug Discovery and Clinical Trails	3:0:0
14BI2037	Medical Coding and Transcription Lab	0:0:2
14BI2038	Clinical Database Management lab	0:0:2
14BI3001	Tele Health Technology	3:0:0
14BI3002	Biocomputing and BIOMEMS Laboratory	0:0:2

14BI2001 ANALYTICAL BIOINFORMATICS

Credits: 3:0:0

Objective:

- To provide the necessary protocols about biological resources.
- To teach the tools used for biological sequential data analysis and phylogenetics.
- To understand the methods of analyzing and gene and promoter prediction.

Outcome:

- The students are able to understand the basics of Bioinformatics resources.
- They can carry out pair-wise, multiple and phylogenetic alignment.
- They have learned the gene and promoter prediction concepts.

Description:

Major Bioinformatics Resources - NCBI, EBI, ExPASy, RCSB - Open access bibliographic resources - Nucleic acid and Protein sequence databases - High throughput genomic sequence and genome repositories - Structural Database - Gene Expression database - Derived Databases Protein-Protein interaction database - Pairwise Sequence alignment - Scoring matrices - Local and global alignment, Dynamic programming, Needleman-Wunch algorithm, Smith-Waterman algorithm - Multiple sequence alignment - CLUSTALW, PILEUP - FASTA and BLAST - Protein motifs and domain prediction - Molecular Phylogenetics - maximum parsimony method, distance methods, the maximum likelihood approach - Gene and promoter prediction - Gene prediction in prokaryotic genomes and in eukaryotes, promoter prediction in E.coli, and in eukaryotes.

Reference Books:-

1. D.W. Mount. Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbour Laboratory Press, New York, 2001.
2. Andreas D. Baxevanis, B. F. Francis Ouellette, Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 3rd Edition, Wiley and Sons, 2004
3. S.C. Rastogi and N. Mendiratla and P.Rastogi. Bioinformatics methods and applications- Genomics, Proteomics and Drug Discovery. Prentice Hall India, 2004
4. A.M. Lesk. Introduction to Bioinformatics. Oxford University Press India, 2005.
5. Richard Durbin , Sean R. Eddy, Anders Krogh, Graeme Mitchison, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, 2002

14BI2002 INSTRUMENTAL METHODS OF ANALYSIS

Credits: 3:0:0

Objectives:

- To develop skills of students in instrumentation and biological techniques.
- To study the definitions, preparations of buffering systems and its application,
- To explain the principles and applications of the important instruments used in biology.

Outcomes:

- Students are exposed to the principles of spectroscopy, Electrophoresis & Chromatography and their biotechniques.
- The students learn the principles of buffering systems, its preparation and application.
- They learn the principles and working of instruments and are familiar with techniques to analyze biological samples

Description:

Buffers preparation and pH measurement, calibration of instruments, derivation of Henderson-Hasselbalch equation and its application, Beer - Lambert's law and spectroscopic techniques, colorimetry, flourimetry, centrifugation, Chromatography techniques and types of electrophoresis, ion-exchange, affinity, gel filtration, GC and HPLC,

radioactive isotopes- its measurements and thermal analysis techniques and its applications, RIA, GM counter, Scintillation counter and Autoradiography, thermo analytical techniques: DTA, DSC.

Reference Books:

1. Willard and Merrit, "Instrumental Methods and Analysis", CBS Publishers & Distributors, 6th edition, 2002.
2. Skoog.D, "Instrumental Methods of Analysis", Saunders College Pub., 2000.
3. Ewing GW, "Instrumental methods of Chemical Analysis", McGraw Hill Book Company, 2000.
4. Upadhyay, Upadhyay & Nath, Biophysical Chemistry: Principles and Techniques, Himalya publications, 2012

14BI2003 MOLECULAR BIOLOGY AND GENETIC ENGINEERING

Credits: 3:0:0

Pre-requisite: 14BT2059 Cell Biology and Microbiology

Objective:

- To understand the basics of Molecular Biology and Genetic engineering.
- To understand the fundamental concepts of molecular genetics
- This is a pre-requisite for course 14BI2005-Genomics and Proteomics

Outcome:

- The students learn the latest developments in molecular biology
- The students are exposed to the techniques of molecular genetics
- They are trained in the principles of recombinant DNA technology

Description:

Molecular genetics, classical experiments on DNA, Replication and transcription, types of DNA replication, RNA splicing, Gene variants, Translation, Regulation of gene expression- lac and trp operons, Recombinant DNA technology, DNA cloning, techniques for screening libraries with clones, Northern, Southern and Western Blotting and PCR, applications of Recombinant DNA Technology such as Plant Cloning, Recombinant vaccines, GM organisms, Gene therapy.

Reference Books:

1. Primrose SB & Twyman, "Principles Of Gene Manipulation, An Introduction To Genetic Engineering ", Blackwell Science Publications, 2006.
2. Geoffrey M. Cooper, Robert E. Hausman, "Cell: A Molecular Approach, 5th Edition", ASM Press, 2009.
3. Dr. Desmond and S. T. Nicholl, "An Introduction to Genetic Engineering", 3rd Edition, Cambridge University Press, 2008.
4. T. A. Brown, Gene Cloning and DNA Analysis: An Introduction, 6th Edition, Wiley-Blackwell Publishers, 2010.

14BI2004 GENOMICS AND PROTEOMICS

Credits: 3:0:0

Pre-requisite: 14BT2059 Cell Biology and Microbiology

Objective:

- To develop skills of the students in the area of genomics and proteomics.
- To understand the various tools available for proteomics and their applications
- This is a pre-requisite for course 14BI2030-Functional Genomics Technologies

Outcome:

- Students are enabled to apply computational methods for gene and genome analysis
- Students are exposed to the high-throughput technologies available for proteome research
- Students understand the genome features of prokaryote & eukaryote

Description:

Overview to genomes, Changes and regulation of genome activity in prokaryotes and eukaryotes, Structure and organization of prokaryotic & eukaryotic genome, Mapping and sequencing, Mapping techniques, Types of markers, Sequencing method s, Assembly of contiguous DNA sequence, Tools for sequence assembly, Functional Genomics, Analytical Proteomics, Importance of 2D Electrophoresis in proteomics, protein sequence databases, Application of proteomics to medicine, proteomics, toxicology.

Reference Books:

1. T.A. Brown, Genomes, 3rd edition, Garland Science, 2006.
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.
4. Greg Gibson, Spencer V. Muse, A primer of genome science, Sinauer associates Inc. Publishers, 2002.

14BI2005 STRUCTURAL BIOLOGY AND BIOPHYSICAL TECHNIQUES

Credits: 3:0:0

Pre-requisite: 14BT2001Basics of Biochemistry
14BI2002 Instrumental Methods of Analysis

Objective:

- To introduce the strategy and tactics of Structural Biology
- To study the Biophysical Techniques for macromolecules
- This is a pre-requisite for course 14BI2012-Molecular modeling and CADD.

Outcome:

- The students understand the structures of biological macromolecules and their conformations
- The students learn the forces stabilizing the macromolecular structures.
- The students can apply the biophysical techniques for structure determination

Description:

Bonds and energetic of macromolecular interactions – Hierarchical organization of protein structure - Peptide bond, phi, psi and chi torsion angles, Ramachandran map – Primary, Secondary, Super secondary, Tertiary and Quaternary structure - Hydrophobicity of amino acids, Secondary structure prediction algorithms - Structure and Conformation of DNA and RNA - base pairing – Watson-Crick and Hoogsteen - types of double helices (A, B, Z), triple and quadruple stranded DNA structures, RNA secondary and tertiary structures - Structure and Conformation of Carbohydrates - monosaccharides, configurations and conformations - formations of polysaccharides and structural diversity due to the different types of linkages. Glyco-conjugates, glycolipids and glycoproteins - Architecture of biological membrane – Lipid bilayer – Micelles and Liposomes – Lamellar structure – Lipid packing – Lipid domains and rafts – Biophysical techniques for Bimolecular size, shape and structure determination: X-ray crystallography and NMR, electron microscopy, neutron scattering, light scattering, ultra centrifugation.

Reference Books:

1. Gu, J and Bourne, P.E., Structural Bioinformatics, 2nd Edition, Wiley, 2009.
2. Cantor R., and Schimmel P.R, "Biophysical Chemistry", Freeman and Co., New York, 2004.

3. Anders L., Lars L., Jure P., Goran L., Poul N., and Morten K., "Text Book on Structural Biology", World Scientific Publishing Co., Singapore, 2009.
4. Philip E. Bourne, Helge Weissig, Structural Bioinformatics (Methods of Biochemical Analysis), John and Wiley and sons, 2003

14BI2006 PERL AND PYTHON PROGRAMMING

Credits: 3:0:0

Objective:

- To focus on core PERL and PYTHON language concepts
- To explore their role in common domain such as the Web, graphical user interface, databases and Bioinformatics.
- To learn writing programs in PERL and PYTHON language.

Outcome:

- To learn the PERL and PYTHON programming language and apply for biological data.
- Students are able to write scripts to perform various administrative tasks.
- Students are able to combine the modern robustness of Java with scripting languages.

Description:

Scalar Data, Lists and arrays, Input and output, Hashes, Control Structures. Subroutines. Regular expressions, Modules and file test. Moving around the Directory tree, Globing, Directory Handles, Recursive directory listing, Manipulating Files and Directories, Removing files, Renaming files, Python Object Types, Numeric Types, Dynamic Typing Interlude, Strings, Lists and Dictionaries, Tuples, Files. Python Statements, Assignment, Expressions, Prints and control structures, The Documentation Interlude. Scopes,Iterations and Comprehensions. Module Coding Basics, Module Packages, Operator Overloading, Designing with Classes, Advanced Class

Reference Books:

1. Randal L. Schwartz, brian d foy, Tom Phoenix, "Learning Perl" O'Reilly Media, Inc., 2011
2. Brown, "Perl: The Complete Reference", Tata McGraw-Hill Education, 2001
3. Mark Lutz, "Learning Python" "O'Reilly Media, Inc.", 2013
4. Wesley Chun, "Core Python Programming" Pearson Education, 2006.

14BI2007 IMMUNOINFORMATICS

Credits: 3:1:0

Pre-requisite: 14BI2004 Genomics and Proteomics

Objective:

- To introduce Immunological foundations
- To explain Informational technology to study immune systems
- To focus on different immunological databases in relation to immune system

Outcome:

- The students understand the concepts of Immunology
- The students understand immunotechniques in antibody production
- The students can access immunoinformatics and its application in different immune databases

Description:

Types of Immunity, Cells and organs of the immune system, Antigens – epitopes, antigenicity, factors influencing antigenicity, Data bases in immunology. Structure and types of Immunoglobulins, Monoclonal antibodies, Cytokines, Complement system. Antigen-antibody interactions precipitation, agglutination, Radio Immuno Assay, ELISA, Western blotting, Immunoprecipitation, Immunofluorescence, Flow cytometer for separation of immune

cells, Major Histocompatiblity Complex (MHC), Antigen processing and presentation. T cell and B cell activation, Immunoinformatics, Prediction of epitopes, Vaccine design, Reverse Vaccinology, Web based tools for vaccine design.

Reference Books:

1. Richard A. G and Thomas J. K., "Kuby Immunology", W.H.Freeman and Company, New Jersey, 4th edition, 2000.
2. K. Chakravarthy, "Immunology and Immunotechnology", Oxford University Press, New Delhi, 2006.
3. Darren R.F., "Immunoinformatics: Predictive Immunogenicity *insilico*", Humana Press, New Jersey, 2007.
4. Ole Lund, "Immunological Bioinformatics", MIT Press, USA, 2005.

14BI2008 MOLECULAR MODELING AND CADD

Credits: 3:0:0

Objective:

- To teach the principles of molecular modeling techniques
- To study Molecular mechanics, Monte-Carlo and Molecular dynamics simulations
- To understand the CADD concepts through target structure prediction and drug-receptor interactions.

Outcome:

- Students are equipped to understand the principles of Molecular modeling
- Students are enabled to perform molecular simulations
- Students can demonstrate the Computer Aided Drug Design methods

Description:

Introduction to Molecular Modeling - different types of computer representations of molecules- Coordinate systems - Potential energy surfaces - Visualization of structures using Rasmol, SPDBV, CHIME, VMD – Force field models - Bond stretching, Angle bending, Torsional terms, Non-bonded interactions - Electrostatic interactions, Van der Waals interactions - Hydrogen bonding in molecular mechanics – Non-derivative and derivative energy minimization: Steepest Descent, Conjugate gradient and Newton-Raphson minimization methods - Molecular dynamics simulation methods – continuous potentials, constant temperature and pressure - Metropolis method - Monte Carlo simulation of molecules - Homology Modeling/Comparative modeling, fold recognition, threading and ab-initio structure prediction Methods - Structure analysis and validation: Pdbsum, Whatcheck, Procheck,Verify3D – CASP – Computer aided drug design and Drug discovery - Target identification, validation and lead optimization - SMILES - Molecular docking methods and scores - Structure-based De Novo Ligand design - QSARs and QSPRs, Pharmacophore mapping - *In silico* prediction of ADMET - Chemoinformatics

Reference Books:

1. Leach A.R, "Molecular Modelling Principles and Application", Pearson – Prentice Hall, New Delhi, 2nd Edition 2001.
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.
4. Andrew R. Leach, Valerie J. Gillet Cluwer, Introduction to Chemoinformatics, Academic Publisher, Netherlands, 2003

14BI2009 BIOETHICS, IPR AND BIOSAFETY

Credits: 3:0:0

Objective:

- To Evaluate basic terminology, principles and methods of Bioethics
- To understand ethical principles for discussion and analysis of clinical cases
- To Review ethical issues and policies addressed by clinical ethics committees

Outcome:

- Students learn the concepts of ethical and environmental issues related to life sciences
- They can identify ethical issues when they arise in the context of healthcare, Biotechnology and Bioinformatics.
- They can differentiate between ethical questions and non-moral questions

Description:

Engineering ethics- Senses of Engineering Ethics- variety of moral issues - types of inquiry - moral dilemmas - moral autonomy, Environmental aspects of Biotech applications- Use of genetically modified organisms and their release in environment Special procedures for r-DNA based product production, Intellectual property rights- TRIPS, International conventions patents and methods application of patents, Global issues, Legal and socioeconomic impacts of Biotechnology

Reference Books:

1. Shaleesha AS., "Bioethics", Wisdom Educational service publications, Chennai, Edition 1, 2008
2. Jeyakumar V, "Professional ethics and Human values", Anuradha Publications, Chennai, 2006
3. Lewis Vaughn, "Bioethics: Principles, Issues, and Cases", Oxford University Press, Edition 1, 2009
4. Thomas A. Shannon and Nicholas J. Kockler, " An Introduction to Bioethics", Paulist Pr, Edition 4, 2009

14BI2010 COMPUTATIONAL SYSTEMS BIOLOGY

Credits: 3:0:0

Objective:

- To introduce the student to the systems approach for biological application
- To explain the metabolic pathways using theoretical and Modeling techniques
- This is a pre-requisite for course 14BI2026-Network Biology, 14BI2031-Pathway modeling and Simulation

Outcome:

- Students are equipped in modeling techniques for biological pathways
- Students can identify important target proteins and pathways for any disease.
- Students can carry out network analysis for large data

Description:

Mathematics to networks, measures and large scale- networks as graphs- centrality parameters, power law, System-level Understanding of Biological Systems -Genetic Networks, Experimental techniques for System Biology, Methods for Protein-Protein interaction network, Metabolic and Regulatory Network, Theoretical and Modeling techniques, SBML models and MATHSBML, Cell Designer, Systematic detection of biological networks, Storing, searching and Dissecting experimental proteomic data.method and software platform for System biology

Reference Books:

1. Sang dun Choi, Introduction to Systems Biology, Human Press, 2007
2. Hiroaki Kitano (Editor), Foundations of Systems Biology, MIT Press, 2001
3. Kindle Edition, Networks: An Introduction, Mark Newman, 2005
4. Uri Alon, An Introduction to Systems Biology: Design Principles of Biological Circuits (Chapman & Hall/CRC Mathematical & Computational Biology), Kindle Edition, 2011

14BI2011 ANALYTICAL BIOCHEMISTRY LAB

Credits: 0:0:2

Co-Requisite: 14BT2001 Basics of Biochemistry

Objective:

- To demonstrate practical knowledge on the chemical basis of carbohydrates
- To teach identification and quantification of proteins and aminoacids.
- To analyze the biochemical parameters in a given sample

Outcome:

- Students have learned the estimation techniques in Biochemistry
- Students are enabled to classify different biochemical components into various categories.
- Students have gained training in biochemical parameters and their inference.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2012 INSTRUMENTAL METHODS OF ANALYSIS LAB

Credits: 0:0:2

Co-Requisite: 14BI2002 Instrumental Methods of Analysis

Objective:

- To impart technical knowledge about the principle and working of biochemical instruments
- To train in the applications of different equipments related to biological experiments.
- To do experiments related to the separation techniques of plant and food samples

Outcome:

- The students gain the basic hands on training in media preparation and calculation
- They are trained in using different equipments
- They are able to perform purification and separation from plant and food samples

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2013 ANALYTICAL BIOINFORMATICS LAB

Credit: 0:0:2

Co-Requisite: 14BI2001 Analytical Bioinformatics

Objective:

- To provide the practical protocols about biological resources
- To gain hands-on experience on the tools used for biological sequential data analysis
- To execute the methods of analyzing genetic and protein information.

Outcome:

- Students are enabled to practically carry out the protocols about Bioinformatics resources.
- Students have gained hands-on experience on pair-wise, multiple sequence alignment along with molecular phylogenetics
- Students are practically trained in gene and promoter prediction.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2014 MOLECULAR BIOLOGY AND GENETIC ENGINEERING LAB

Credits: 0:0:2

Co-Requisite: 14BI2003 Molecular Biology and Genetic Engineering

Objective:

- To learn various practical techniques in Molecular Biology and Genetic Engineering.
- To understand the practical concepts of Genetics and recombinant DNA technology.
- To introduce practical techniques for Genetic Engineering

Outcome:

- Students acquire skill in conducting experiments on Molecular Biology and Genetic Engineering
- Students are able to understand some practical methods of molecular biology
- Students acquire practical knowledge about the methods of DNA isolation.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2015 PERL AND PYTHON PROGRAMMING LAB

Credits: 0:0:2

Co-Requisite: 14BI2006 Perl and Python Programming

Objective:

- To focus on core PERL and PYTHON language applications in databases and Bioinformatics
- To use scalars, arrays and associative arrays
- To demonstrate how to write and properly use regular expressions

Outcome:

- Students learn the programming language and apply it well in biological applications
- Students understand the advantages of using Perl and Python for a scripting tool
- Students can demonstrate the proper use of Perl syntax, including control structures and expressions

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2016 MOLECULAR MODELING AND CADD LAB

Credits: 0:0:2

Co-Requisite: 14BI2008 Molecular Modeling and CADD

Objective:

- To train in molecular modeling of biological molecules
- To perform exercises related to molecular mechanics and molecular dynamics simulation exercises.
- To carry out computer aided drug design through target structure prediction and drug-receptor interactions.

Outcome:

- Students are practically trained to carry out Molecular modeling
- They can perform comparative modeling procedures.

- They can execute Computer Aided Drug Design methods.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2017 COMPUTATIONAL SYSTEMS BIOLOGY LAB

Credits: 0:0:2

Co-Requisite: 14BI2010 Computational Systems Biology

Objective:

- To impart the knowledge in modeling of genomics, proteomics
- To perform the metabolic pathways for biological process
- To train in the use of different software on computational modeling

Outcome:

- The students are enabled to identify important target proteins
- Students are able to analyze pathways for any disease using the databases and software
- Students are able to execute different plug-ins in network analysis

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2018 NETWORK BIOLOGY

Credits: 3:0:0

Objective:

- Students will be introduced to different computational approaches to understand large biological data using network biology
- Students will understand interactive networks and models
- Students will learn Omics data analysis

Outcome:

- Students have learned transcriptomics data interpretation
- Students can carry out the application of protein interaction networks
- Students are able to evaluate the centrality properties

Description:

Computational approaches - Data analysis - Experimental approaches - Gene isoforms - Gene sequences - National Resource for Network Biology, Complex Diseases- Interaction networks - Metabolite concentrations – Models of complex networks- statistical testing of network properties- Network clustering- Next-generation sequencing - Protein complexes - Quantitative 'omic' datasets - mRNA transcripts- Quantitative modeling and analysis- signal transduction and gene regulation networks- Phylogenetic networks.

Reference Books:

1. Network Biology: Methods and Applications, Cagney, Gerard; Emili, Andrew, A product of Humana Press Vol. 781, 2011
2. Analysis of Biological Networks, Björn H. Junker, Falk Schreiber, John Wiley and Sons, 2011
3. Alpan Raval, Animesh Ray, Introduction to Biological Networks, Chapman and Hall/CRC publisher, 2013
4. Networks: An Introduction, Mark Newman, Kindle Edition, 2005

14BI2019 R PROGRAMMING

Credits: 3:0:0

Objective:

- To express fundamental programming constructs such as input and output, R function, loops, Graphics and OOP in R.
- To teach programs for Packages and Data Technologies in R
- To understand the basic object types and data structures in graphing and parallel processing

Outcome:

- Students are able to write, compile, and run R programs, analyze the R function, OOP and mapping using R environment.
- They are able to create R programs that make use of Packages and Data Technologies
- They are able to analyze clinical data using R programming.

Description:

Introduction to Data structures-Managing R session, Language basics, Subscripting and sub setting- R functions: Vectorized, Replacement functions, Writing functions, Flow control, Exception handling, Evaluation, Lexical scope and graphics-object-oriented programming in r-working with character data- packages and data technologies, Simple Linear Regression, Multiple Regression, Curvilinear Regression, Plotting Linear Models and Curve Fitting, Adding Elements to Existing Plots, Matrix Plots Multiple Series on One Graph, Multiple Plots in One Window, Exporting Graphs

Reference Books:

1. Robert Gentleman, "R programming for bioinformatics" Taylor and Francis Group, USA, 1st Edition, 2009
2. Sunil K. Mathur, " Statistical bioinformatics with R" Academic Press Elsevier, California,1st Edition, 2010
3. Mark Gardener, "Beginning R: The Statistical Programming Language", John Wiley & Sons, 2012
4. Norman Matloff, Norman S. Matloff, "The Art of R Programming: A Tour of Statistical Software Design", No Starch Press, 2011

14BI2020 NEXT GENERATION SEQUENCING

Credits: 3:0:0

Objective:

- To explain the history and development of NGS technologies
- To understand the interpretation of NGS data analysis
- To analyze computational genomics using advanced statistical methods for solving bioinformatics problems.

Outcome:

- Students are able to understand the existing methodology for the analysis of DNA sequencing, massively parallel sequencing,
- Students are able to know the current challenges and open issues in computational genomics
- Students are able to obtain skills in developing novel statistical approaches to study NGS data

Description:

DNA sequencing, Visualization of Next Generation Sequencing Data, Genome assembly, Short Sequence reads- New challenges by short sequences; Overlap-layout-consensus, ChIP-Seq- DNA binding proteins and histone modifications, Genome annotation, Sequence variants- Amplifications, large deletions, rearrangements; overexpression by multiple copies (e.g. MYC), activating and inactivating gene fusions, loss of heterozygosity, copy number profiles, RNA sequencing with Next Generation Sequence, Metagenomics, High Performance Computing in Next Generation Sequencing data.

Reference Books:

1. Next-Generation DNA Sequencing Informatics [Kindle Edition] by Stuart Brown, Cold Spring Harbor Laboratory Press Newyork, 2013.
2. Tag-based Next Generation Sequencing by Matthias Harbers and Guenter Kahl (Wiley Blackwell Germany 2012
3. Wong, Lee-Jun C., Next Generation Sequencing- Translation to Clinical Diagnostics, Springer, 2013

14BI2021 PHARMACOGENOMICS

Credits: 3:0:0

Objective:

- To introduce the scientific knowledge of drugs that reacts with the biomolecules
- To understand the novel concepts in Pharmacogenomics
- To understand the novel drug discovery process

Outcome:

- Students have an understanding of the principles and applications of human genomics
- Students have an understanding the concepts in Pharmacogenomics
- Students have an understanding of the concepts in drug therapy optimization & patient care

Description:

The Human Genome structure and mechanism, Turning SNPs into useful markers of drug response, Association studies in Pharmacogenomics- pharmacokinetics and pharmacodynamics, pharmacogenetics in drug discovery, cells as targets for hydroxy urea, natural alkalides, terpenoids, flavoinides, pharmacogenomics for the treatment of neurological, autoimmuine, physiological diseases, pharmacogenomics of alcoholism, Genomics Applications that facilitate the understanding of Drug Action and Toxicity, Human P-Glycoprotein, Drug Transporters

Reference Books:

1. "Pharmacogenomics: The Search for Individualized Therapies,"Julio Licinio & Ma-Li Wong (Eds.), 2002.
2. Wu, X., Zhao, H., Suk, R., Christiani, D.C. Genetic susceptibility to tobacco-related cancer. Oncogene 23 (38), 6500-6523, 2004
3. Evans, W.E., Relling, M.V. Moving towards individualized medicine with pharmacogenomics. Nature 429 (6990), 464-8, 2004
4. Ingelman-Sundberg, M. Human drug metabolising cytochrome P450 enzymes: properties and polymorphisms. Archives of Pharmacology 369, 89-104, 2004
5. Ruano, G.Quo vadis personalized medicine, Personalized Medicine (1), 1-7, 2004
6. Lee, W., et al. Cancer Pharmacogenomics: Powerful Tools in Cancer Chemotherapy and Drug Development. Oncologist 10 (2), 104-111, 2005

14BI2022 FUNCTIONAL GENOMICS TECHNOLOGIES

Credits: 3:0:0

Objective:

- To provide an introduction to functional genomics
- To emphasize applications of genomics technologies, data analysis and experimental design
- To learn about the cutting edge technologies such as advanced array technologies

Outcome:

- Students learn the application of High throughput data for genome-wide analysis
- Students acquire an understanding of the emerging technologies in functional genomics.
- Students are able to design experiments, interpret and analyze biological data.

Description:
Historical Perspective of Genomics, Challenges of studying Functional Genomics, Computational Genome annotation and Functional prediction of genes, Functional cell microarrays, the analysis of non-coding sequence data (identification of transcription factor binding sites), single nucleotide polymorphisms, methods for SNP identification, High through put technologies, inference of biological networks, and integrative Bioinformatics approaches Functional genomics analysis of model organisms and bacterial pathogens

Reference Books:

1. Microbial Functional Genomics, Jizhong Zhou, Dorothea K. Thompson, Ying Xu, James M. Tiedje, 2004, John Wiley & Sons, Inc.
2. Functional Genomics (Methods in Molecular Biology), Michael J. Brownstein , Arkady Khodursky, 2003, Humana Press
3. Functional Genomics: Methods and Protocols (Methods in Molecular Biology), Michael Kaufmann , Claudia Klinger, 2011, 3rd Edition, Humana Press
4. Functional Genomics: A Practical Approach (Practical Approach Series), Stephen Hunt, Frederick Livesey**,** 2000, OUP Oxford

14BI2023 PATHWAY MODELING AND SIMULATION

Credits: 3:0:0

Objective:
- To express fundamental constructs in relation to pathway modelling
- To explain the simulation techniques involved in pathway identification
- To learn the process of identification of targets and small molecules

Outcome:
- Students are able to apply the programming skills in pathway modelling and simulations
- They can learn to stand alone tools for modelling biological pathways
- They can do the whole cell simulations using varied tools

Description:
Intercellular events: Transcription, Translation and Regulation, Signaling pathways and Proteins, Metabolism and Genes, Pathway databases, Modeling and simulation in signal transduction pathways, COPASI—a Complex Pathway Simulator, Software pathways display, file formats for pathways, pathway simulation software, cell illustrator, Modeling biological systems, pathway modeling and simulations, genetic networks, abstract relational biology, metabolic-replication systems, Neuron models.

Reference Books:

1. Foundations of Systems Biology: Using Cell Illustrator and Pathway Databases, Masao Nagasaki, Ayumu Saito, Atsushi Doi, Hiroshi Matsuno, Satoru Miyano, Springer, 2009
2. Foundations of Systems Biology, Hiroaki Kitano (Editor), MIT Press, 2001
3. Networks: An Introduction, Mark Newman, Kindle Edition, 2005
4. Dokholyan, Nikolay, Computational Modeling of Biological Systems: From Molecules to Pathways, Springer, 2012

14BI2024 SYNTHETIC BIOLOGY

Credits: 3:0:0

Objectives:
- To introduce Synthetic biology and its natural scientific and engineering basics
- To understand the cellular, molecular biology, biophysical, dynamical and engineering of synthetic systems
- To understand the design and operation of natural and synthetic circuits to design new biology based systems.

Outcomes:

- The students are enabled to design simple cellular circuitry to meet engineering specification.
- They are enabled to design experiments to characterize and diagnose operation of natural and synthetic bimolecular network
- They can apply the knowledge in scientific, safety and ethical issues of synthetic biology.

Description:

To introduce the basics of Synthetic Biology, including quantitative cellular network characterization and modelling, to introduce the principles of discovery and genetic factoring of useful cellular activities into reusable functions for design, realistic and biological model design and simulations, Theoretical biocomponent complex model, inculcate the principles of bimolecular system design and diagnosis of designed systems, and illustrate cutting edge applications in Synthetic Biology

Reference Books:

1. H. Lodish, ed., Molecular Cell Biology, 4th Edition, New York: Scientific American Books, 2000.
2. Lewin, Genes VII, Oxford University Press, 2000.
3. G. G. Hammes, Thermodynamics and Kinetics for the Biological Sciences, John Wiley & Sons, New York, 2000.
4. V. Bloomfield, D. Crothers and I. Tinoco, Jr, Nucleic Acids, University Science Books, Sausalito, California, 2000.
5. J. Savage, Models of Computation: Exploring the Power of Computing, Addison Wesley Longman, Inc., Berkeley,California, 2002.

14BI2025 MICROARRAY TECHNOLOGY AND STATISTICAL ANALYSIS

Credits: 3:0:0

Objective:

- To explain how microarray technology works, including the various types
- To understand how data is retrieved in different formats produced by microarrays
- To understand biological data normalization

Outcome:

- Students can demonstrate the working of microarray by different technologies
- Students can carry out different algorithms for normalization
- Students are able to do different statistical analysis of normalized and preprocessed data

Description:

Introduction to microarrays, Genes and Genomes, Microarray surfaces, Targets and Probes, Microarray databases, LIMS, MIPS, MGED, microarray experiments and image analysis, image scanning, image processing: Microarray Data cleaning and Preprocessing- data transformation, Missing value Estimation, Data Normalization- Global normalization, Proximity measurement for gene expression data - Euclidean distance, Correlation Coefficient, Partition Based approaches - statistics for the analysis of differentially expressed genes- T- tests, ANOVAs, gene based analysis.

Reference Books:

1. Mark Schena, Microarray Analysis, John Wiley and Sons ltd, America, 2003
2. Aidong Zhang, "Advanced analysis of Gene expression microarray data", World Scientific Publishing House, New Delhi, 2006.
3. Dov Stekel, "Microarray Bioinformatics" Cambridge University Press, UK, 2005.
4. Müller, Uwe R.; Nicolau, Miguel, Microarray Technology and Its Applications, Springer, 2005,

14BI2026 KERNEL BASED PATTERN RECOGNITION

Credits: 3:0:0

Objective:

- To introduce pattern recognition problems using support vector machines.
- To understand novel kernel fusion algorithms and applications in supervised and unsupervised learning
- To apply support vector machines in literature mining.

Outcome:

- The students are able to apply fusion and pattern recognition methods.
- They are able to understand the pattern recognition algorithms in to identify disease relevant genes
- They are able to implement kernel based software

Description:

History of Multi-source Learning and Data Fusion and pattern recognition, Rayleigh Quotient – Optimization, Type Problems in Machine Learning, multiple kernel learning (mkl) and support vector machines (svm), text mining, Computational Gene Prioritization, Clustering by Heterogeneous Data Sources, Single View Gene Prioritization, Data Fusion for Gene Prioritization, optimized data fusion, 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.

Reference Books:

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.
2. Guihai Chen, Yi Pan, Minyi Guo, Jian Lu, "Parallel and Distributed Processing and Application ISPA 2005", Springer, Heidelberg, 1st Edition, 2005.
3. Patrick S. P. Wang, "Pattern Recognition, Machine Intelligence and Biometrics", Springer, 2012
4. John Shawe-Taylor, Nello Cristianini, "Kernel Methods for Pattern Analysis", Cambridge University Press, 2004

14BI2027 CHEMINFORMATICS AND QSAR

Credit: 3: 0: 0

Objective:

- To introduce different methods of Cheminformatics in modern drug discovery
- To provide an overview of computer aided drug design
- To acquire an understanding of Quantitative Structure Activity Relationship

Outcome:

Students learn how to retrieve specific information from the chemical literature.

- Students acquire an overview of computational chemistry and its manifestations
- Student are exposed to the applications in QSAR and Drug Design.

Description:

Scope of Cheminformatics, Nomenclature; Different types of Notations; SMILES coding; Matrix Representations; Libraries and toolkits; Reaction classification, 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-Structure Based Virtual Screening- Protein Ligand Docking, Scoring Functions for Protein Ligand docking, Practical aspects of structure based Virtual Screening; Prediction of ADMET Properties-Quantitative Structure-Property Relations; Descriptor Analysis; Computer Assisted Structure elucidations; Target Identification and Validation; Lead Finding and Optimization; Design of Combinatorial Libraries, 1D and 2D Quantitative Structure Activity Relationship (QSAR), multi dimensional QSAR

Reference Books:

1. Introduction to Chemoinformatics by Andrew R. Leach, Valerie J. Gillet Cluwer Academic Publishe, Netherlands, 2003
2. Combinatorial Library Methods and Protocols edited by Lisa B. English. Humana Press Inc, Volume:201, 2002
3. Introduction to Computational Chemistry by Frank Jensen Wiley Publisher, Second Edition, 2006
4. R.K.Prasad, Quantum chemistry , Halsted Press, 2002

14BI2028 CHEMINFORMATICS AND QSAR LAB

Credits: 0:0:2

Co-Requisite: 14BI2027 Cheminformatics and QSAR

Objective:

- To introduce different practical methods of Cheminformatics
- To emphasis on the applications of modern drug discovery
- To teach QSAR and related exercises

Outcome:

- Students acquire hands on experience through Cheminformatics
- They have learned the current practical applications of QSAR
- They have gained ability to do Drug Design protocols.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2029 NETWORK BIOLOGY LAB

Credits: 0:0:2

Co-Requisite: 14BI2018 Network Biology

Objective:

- To provide practical exercises related to biological networks
- To learn hands on skills on biological systems and their subunits
- To apply network based approach in biological context.

Outcome:

- The students gain practical skills related to biological networks
- They have learned social and ecological network data analysis
- They are able to apply network biology algorithms in software applications

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2030 R PROGRAMMING LAB

Credits: 0:0:2

Co-Requisite: 14BI2019 R Programming

Objective:

- To get an introduction to the R programming language
- To have hands-on R programming skills.

- To demonstrate R programming applications

Outcome:
- Students understand the basic R Programming
- They have gained ability to apply R language in today's scientific context
- They are trained to execute R programming in biological data.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI2031 CLINICAL DATABASE MANAGEMENT

Credits: 3:0:0

Objective:
- To teach important concepts related to clinical data management.
- To demonstrate the collection, storage, migrating and archiving of clinical data
- To know managing and creating report of clinical data

Outcome:
- Students understand the role of clinical data management.
- They are able to analyze clinical data.
- They can design database consideration and implementation

Description:
The data management plan – Using data management plans – CRF design consideration – Data cleaning issues and Data processing issues - Database design consideration – Making design decisions – Operating procedures for database design – Dealing with problem data – modifying data – Quality control through database audits - Cleaning data – Identifying and managing discrepancies – Quality control and assurance – Managing laboratory data – Storing lab data Creating report and transferring data – Data transfers - Clinical data management systems – Electronic data capture systems – System Validation - Migrating and archiving data.

Reference Books:

1. Susanne Prokscha, Practical Guide to Clinical Data Management, Second Edition, CRC press book, 2006.
2. Eleanor McFadden, Management of Data in Clinical Trials, Second edition, John wiley and sons, 2007.
3. Shien -chung chow, Jen-pei Lu, Design Analysis of Clinical Trials, John wiley and sons, 2008.
4. Richard K, Sheila A. Varley, Colin F.Webb, Clinical Data Management, Wiley Publications, 2005.

14BI2032 HEALTH CARE INFORMATICS

Credits: 3:0:0

Objective:
- To introduce students to the concepts and practices of health informatics
- To enable the students to understand patient- physician interaction
- To enable the students to understand the patient profile documentation

Outcome:
- Students understand the issues in health practices.
- Students gain insight in planning and building healthcare information systems
- Students learn software design and human-computer interaction issues.

Description:
Basic concepts in health informatics and its history, Definitions, Sub disciplines and professional organizations and activities, Major health informatics applications including electronic medical records (EHR) and computerized physician order entry (CPOE), good clinical practices (gcp)**,**
information systems design and engineering, new opportunities and emerging trends**:** Information technologies in healthcare; wireless and handheld devices, social computing paradigms, and eHealth applications, web-based tools.

Reference Books:

1. Taylor Paul, "From Patient Data to Medical Knowledge: The Principles and Practice of Health Informatics", Blackwell Scientific Publishing, UK, 2006.
2. Shortliffe and Cimino, "Biomedical informatics: computer applications in health care and biomedicine", Springer, NewYork, 3rd edition, 2006
3. Frank M. S. and Jeremy C. Wyatt, "ABC of health informatics", Blackwell publishing, Massachusetts, USA, 2006.
4. Perry, S., Hockenberry, M., Lowdermilk, D., & Wilson, D. . Maternal child nursing care (4th ed.), 2010.
5. Silvestri, L.A. . Saunders comprenhensive review for the NCLEX-RN examination (5th ed.). St. Louis, MO: Saunders, 2011.
6. Townsend, M.C. Essentials of psychiatric mental health nursing: Concepts of care in evidence-based practice (5th ed.). Philadelphia: FA Davis, 2011

14BI2033 MEDICAL CODING AND TRANSCRIPTION

Credits: 3:0:0

Objective:
- To understand medical coding in health sector
- To understand the guidelines for specific transcription mechanics and techniques
- To be trained for a minimum entry level medical coding positions normally available in medical offices, hospitals and insurance companies

Outcome:
- Students understand the basic systems and processes in billing, reimbursement and insurance coverage.
- Students are able to gain knowledge from the medical information system.
- Student are able to analyze medical records (charts) and codes for indexing diagnosis

Description:
Medical coding history, Diagnosis coding, Procedure coding, Codes used for reimbursement, Solving health care coding problems, Coding as a career. Introduction to medical transcription, medical transcription transcribing tools, telecommunication tools in medical transcription, Medical transcription formats, medical transcription mechanics, Medical Transcription skills, Consultation Reports, History and Physical Examination Reports, Special Procedures Reports, Operative Reports, SECTION VH Discharge Summary Reports, Challenge Reports

Reference Books:

1. Donna Avila-Weil, Rhonda Regan, "Independent Medical Coding: The Comprehensive Guidebook for Career Success as a Medical Coder", Rayve Productions, 2007.
2. Patricia Aalseth, "Medical Coding: What it is and How it Works", Jones & Bartlett Learning, 2005.
3. Lois Burns, Florence Maloney, "Medical Transcription & Terminology: An Integrated Approach", Cengage Learning, 2003
4. Sandra Johnson, Robin Linker, "Understanding Medical Coding: A Comprehensive Guide", Cengage Learning, 2012

14BI2034 SCIENTIFIC WRITING

Credits: 3:0:0

Objective:

- To understand the guidelines for style, grammar, specific writing and skills of scientific writing.
- To understand software tools relying on Natural Language Processing
- To focus on their research and still get published in top journals.

Outcome:

- Students understand the six qualities of unique writing techniques, i.e. fluid, organized, clear, concise, convincing and interesting.
- They acquire knowledge about different methods of publication
- They are able to follow various conventions of writing style

Description:

The reading Toolkit, Sustain Attention to ensure continuous reading, Reduce reading time, Keep the reader motivated, bridge the knowledge gap, set the reader's expectations, set progression tracks for fluid reading, detect sentence fluidity problems, control reading energy consumption, paper structure and purpose, Abstract, headings – subheadings, Introduction, visuals, conclusions, Additional resources, Maximizing Chances of Publication, Essential Steps Before Writing a Paper, Drafting Papers, Complex Studies, Linguistic Points, Covering Letters and Referees Objections.

Reference Books:

1. Jean-Luc Lebrun, "Scientific Writing 2.0: A Reader and Writers Guide", World Scientific, 2011.
2. David Lindsay, "Scientific Writing", Csiro Publishing, 2011.
3. Jennifer Ouellette, "The Best Science Writing Online 2012", Macmillan, 2012
4. John Blackwell, Jan Martin, "A Scientific Approach to Scientific Writing", Springer, 2011

14BI2035 CLINICAL PRACTICES AND REGULATIONS

Credits: 3:0:0

Objectives:

- To emphasize on the delivery of safe and evidence based healthcare for clients
- To focus on the evaluation of healthcare outcomes in individuals and groups with varied levels of acuity across the lifespan.
- To lay emphasis on complicated disease, injury and various degrees of disability

Outcome:

- The student is able to implement evidence-based collaborative interventions in the care of clients with complicated illnesses.
- They are able to apply legal and ethical principles in the care of clients with complicated disease, injury, and disability.
- The student has knowledge in drug safety and regulations

Description:

Basic epidemiology and observational methods, interventional and randomized controlled trials, and Clinical epidemiology and evidence-based medicine. Concepts of association and outcome, standard epidemiological concepts of incidence and prevalence, define and describe relative risk, absolute risk, attributable risk and the various methods for calculating those quantities in different observational research designs. Methods for reducing bias and confounding. Interventional trials, including the four phases of drug trials, the importance and effects of randomization, analysis and interpretation of controlled trials.

Reference books:

1. Designing Clinical Research: An Epidemiologic Approach, Third Edition. SB Hulley, SR Cummings, WS Browner, D Grady, and TB Newman. 2007
2. Clinical Trials: A Methodologic Perspective.S Piantadosi. Wiley Interscience, 2001
3. Clinical Trials: Design, Conduct and Analysis (Monogra phs in Epidemiology and Biostatistics Vol 8. CL Meinert. Oxford University Press, 2000
4. Seidel, HM, et al. Mosby's Guide to Physical Examination. Sixth Edition. Elsevier Science, St. Louis, 2006

14BI2036 DRUG DISCOVERY AND CLINICAL TRAILS

Credits: 3:0:0

Objective:

- To provide a systematic application of information science and technology to support patient care
- To lay emphasis on the use of information systems/technology to evaluate health care systems for quality improvement
- To provide leadership skills within health care systems and/or academic settings.

Outcome:

- The students are able to identify terminology and concepts in drug discovery informatics.
- They are able to demonstrate informatics skills in complex decision making in clinical trails
- They are able to evaluate technical and scientific health care information

Description:

Terminology, concepts, technology, and systems used in drug discovery, Pharmacodynamics and pharmacokinetics, Phamacology and Toxicology. Present and future role of technology in revolutionizing/transforming advanced clinical trials. Design clinical trials and therapeutic trails. Experimental methodology and operational execution in clinical trials. Use of health care technologies in clinical decision making, quality improvement, patient education, and practice management- Analysis of evolving issues in the field of drug discovery informatics, Legal and ethical implications of health care technology- sample size estimation and safety assessment

Reference Books:

1. J. Rick Turner, New Drug Development: An Introduction to Clinical Trials, Springer, 2010
2. SK Gupta, Drug Discovery and Clinical Research, Jaypee digital. Pub, 2011
3. Epidemiology, Fourth Edition. L Gordis, 2008
4. Fundamentals of Clinical Trials, 3rd edition. Friedman, Furberg ad Dements. Spring Publisher, 2000

14BI2037 MEDICAL CODING AND TRANSCRIPTION LAB

Credits: 0:0:2

Co-Requisite: 14BI2033 Medical Coding and Transcription

Objectives:

- To resolve diagnostic questions and medical codes
- To learn referring to comprehensive code books such as the International Classification of Diseases (ICD)
- To teach how to convert voice-recorded reports as dictated by physicians or other healthcare professionals, into text format.

Outcomes:

- Students have learned medical terminology and codes
- They are trained in medical insurance processing and coding
- They have gained ability to manage the flow of medical records.

14BI2038 CLINICAL DATABASE MANAGEMENT LAB

Credits: 0:0:2

Co-Requisite: 14BI2031 Clinical Database Management

Objective:

- To teach important practical exercises related to clinical data management plan
- To learn clinical data retrieval process
- To teach clinical data analysis exercises

Outcome:

- Students understand the role of clinical data management in clinical trials
- They gain experience in clinical data retrieval process
- They gain ability to design and analyze database consideration

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.

14BI3001 TELE HEALTH TECHNOLOGY

Credits: 3:0:0

Course Objective:

- To learn about the current scenario in medical informatics.
- To study the tools used in medical information systems.
- To understand real time applications of medical informatics used in biomedical field.

Course Outcome:

- Demonstrate how medical information is interpreted, stored and used.
- Use Internet and on – line database resources to find relevant information .
- Be aware of Applications of computer assisted medical informatics

Introduction to Medical informatics, Historical highlights, standards, Medical data formats, PACS, DICOM standards and Quality improvement, Computer based medical information retrieval, Databases, web based search engines, Online databases, Electronic publishing, Electronic journals, Hospital information system, Computer assisted medical decision making, medical education, Telemedicine, tele health monitoring.

References

1. Mohan Bansal, “Medical Informatics –A Primer”, Tata McGraw Hill publishing company limited 2003.
2. Lele R.D. "Computers in Medicine", Tata McGraw Hill Publishing company limited, second reprint 2008.
3. Robert Hoyt, Melanie Sutton, Ann Yoshihashi, “Medical Informatics: Practical Guide for the Healthcare Professional”, 2007,.
4. Edward Hance Shortliffe, James J. Cimino, “Biomedical informatics: Computer applications in health care and biomedicine, Springer, 2006.
5. Joseph D Bronzino, “Biomedical engineering handbook”, Vol 2, CRC press, USA, 2000.

14BI3002 BIOCOMPUTING AND BIOMEMS LABORATORY

Credits: 0:0:2

Course Objective:

- To strengthen the knowledge of Virtual Instrumentation, Data Acquisition and control
- To understand the concept of signal and image analysis using evolutionary computing techniques
- To introduce the concept of MEMS sensor design and analysis

Course Outcome:

- Design the Virtual instruments and innovate in new methods of diagnosis, configure instruments and develop a work bench to analyze biosignals.
- Apply the knowledge on biomedical signal analysis and know to choose the one for a right application.
- Design the MEMS sensor and analyze using software tools.

The faculty conducting the laboratory will prepare a list of 12 experiments and get the approval of HoD/Director and notify it at the beginning of each semester.