MANONMANIAM SUNDARANAR UNIVERSITY
TIRUNELVELI
UG COURSES – AFFILIATED COLLEGES
B.Sc. Bio Informatics
(Choice Based Credit System)
(with effect from the academic year 2016-2017 onwards)

Sem	Pt I/ II/ III/ IV	Sub No.	Subject status	Subject Title	Hrs/ week	Credits	Marks				
							Maximum			Passing minimum	
							Int.	Ext.	Tot.	Ext.	Tot.
V	I	33	Core - 7	Genetics & Evaluation	4	4	25	75	100	30	40
	II	34	Core - 8	Structural Biology	4	4	25	75	100	30	40
	III	35	Elective – 1 (Select any one)	A) Introduction to DBMS B) Introduction to Bimolecular Instrumentation	5	5	25	75	100	30	40
		36	Elective – 2 (Select any one)	A) Programming in Visual Basic B) Applications in Bioinformatics	5	5	25	75	100	30	40
		37	Practical - 5	Lab in Structural Biology, Molecular Modeling & drug design	3	-	50	50	100	20	40
		38	Practical - 6	Lab in Genetics and Genomics & Proteomics	3	-	50	50	100	20	40
		39	Practical - 7	Lab in Operating System and Web Programming	2	-	50	50	100	20	40
	IV	40	Skill Based subject (Common)	Personality Development/ Effective Communication/ Youth Leadership	4	4	25	75	100	30	40
					30	24					

Sem	Pt I/ II/ III/ IV	Sub No.	Subject status	Subject Title	Hrs/ week	Credits	Marks				
							Maximum			Passing minimum	
							Int.	Ext	Tot.	Ext.	Tot.
VI	I	41	Core - 9	Genomics & Proteomics	6	4	25	75	100	30	40
	II	42	Core - 10	Molecular Modeling & Drug Designing	6	4	25	75	100	30	40
	III	43	Core - 11	Operating System & Web Programming	5	4	25	75	100	30	40
		44	Elective – 3 (Select any one)	A).System Biology B).Open Source Bioinformatics	5	5	25	75	100	30	40
		45	Practical – 5	Lab in Structural Biology, Molecular Modeling & drug design	3	4	50	50	100	20	40
		46	Practical – 6	Lab in Genetics and Genomics & Proteomics	3	4	50	50	100	20	40
		47	Practical - 7	Lab in Operating System and Web Programming	2	4	50	50	100	20	40
				Subtotal	30	29					

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-V/Ppr.no.33/ Core-7

GENETICS AND EVOLUTION

UNIT – I

Mendelian principles : Dominance, segregation, independent assortment**.** Concept of gene : Allele, multiple alleles, pseudoallele, complementation tests. Codominance, incomplete dominance, gene interactions, pleiotropy, genomic imprinting, penetrance and expressivity, phenocopy, linkage and crossing over, sex linkage, sex limited and sex influenced characters.

UNIT – II

Chromosome: Aneuploidy, euploidy (haploidy and poly ploidy). Human chromosome: Sex chromosome – Barr bodies – Heterochromatinization – chromosomal – abnormalities.

Microbial genetics: DNA as the genetic material, Recombination in bacteria: Transformation, conjugation sexduction and Transduction. Recombination in bacteriophage – Mechanism of recombination, lytic and lysogenic cycles.

UNIT – III

Molecular genetics: Fine structure of gene – cistron, recon and muton - Gene expression and regulation in prokaryotes – Operon model – Lac and Trp Operon – Gene regulation in Eukaryotes – Britten and Davidson's model; histones and gene amplification. Gene mutations – spontaneous mutation: Base pair substitution, Frame shift mutation, and inducible mutations: Nitrous oxide, DMS, Acridine orange; suppressor mutations. Mutagens.

UNIT – IV

Origin of basic biological molecules; Abiotic synthesis of organic monomers and polymers; Concept of Oparin and Haldane; Experiement of Miller (1953); The first cell; Evolution of prokaryotes; Origin of eukaryotic cells; Evolution of unicellular eukaryotes; Anaerobic metabolism, photosynthesis and aerobic metabolism. Lamarckism; Darwinism; de Vries theory of mutation; Modern synthetic theory of evolution.

UNIT – V

Mimicry and animal colouration; Species concept; Isolating mechanisms; Population genetics – Populations, Gene pool, Gene frequency; Hardy-Weinberg Law; concepts and rate of change in gene frequency through natural selection, migration and random genetic drift; Adaptive radiation; Isolating mechanisms; Speciation; Allopatricity and Sympatricity; Convergent evolution; Sexual selection; Co-evolution

REFERNCES:

1. Friefelder. D. 1997. Microbial Genetics; Narosa Publishing, New Delhi.
2. Goodenough, U.1997. Genetics. Saunders Coelege Publishing International, NewYork.
3. Verma P .S. and Agarwal, V.K. 1997 – Genetics S.Chand & Co., New Delhi.
4. Kumar, H.D. 1998. Molecular Biology and Biotechnology. Vikas publishing House,New Delhi
5. Lewin, B. 2008. Gene XII . Wiley Eastern Ltd., New Delhi.
6. Verma, P.S. and V.K. Agarwal. 1997. Genetics. S.Chand & Co. New Delhi.
7. Strickberger, M.W. 2002 Genetics (3rd edition). Prentice Hall of India, New Delhi.
8. Arumugam, N. 1989. Organic Evolution –. Saras publication, Nagercoil.
9.Strickberger, M.W. 2000. Evolution. Jones and Bartlett Publishers.

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-V/Ppr.no.34/ Core - 8

STRUCTURAL BIOLOGY

UNIT-1

DNA and RNA: structure and types of base pairing – Watson-Crick and Hoogstein; types of double helices A, B, Z and their geometrical as well as structural features; structural and geometrical parameters of each form and their comparison; various types of interactions of DNA with proteins.

UNIT II

Proteins: Principles of protein structure; anatomy of proteins – Hierarchical organization of protein structure – Primary. Secondary, Super secondary, Tertiary and Quaternary structure; Hydrophobicity of amino acids, Pacing of protein structure, van der Waal and Solvent accessible surface, significance and applications of Ramachandran Map.

UNIT III

Carbohydrates: The various building blocks (monosaccharides), configurations and conformations of the building blocks; formations of polysaccharides and the different types of linkages. Glyco-conjugates: various types of glycolipids and glycoproteins

UNIT IV

Structure Prediction Strategies: Secondary structure prediction: Algorithms viz. Chou Fasman, GOR methods; analysis of results and measuring the accuracy of predictions using Q3, Segment overlap, Mathew's correlation coefficient, Identification/assignment of secondary structural elements.

UNIT V

Tertiary Structure prediction: Fundamentals of the methods for 3D structure prediction (sequence similarity/identity of target proteins of known structure, fundamental principles of protein folding etc.) Homology Modeling, fold recognition, threading approaches, and ab-initio structure prediction methods - protocols/algorithms. Prediction of protein structure: PHD and SI-PRED methods

REFERNCES:

1. Molecular Modeling Principles and Applications (2nd Ed.) by Andrew R. Leach, 2001, Prentice Hall, USA.
2. Principles of Protein Structure by G. E. Schulz, 2009, Springer
3. Lehninger Principles of Biochemistry by David L. Nelson and Michael M. Cox, 2005, W. H. Freeman

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-V/ Ppr.no.35(A)/ Elective –I (A)

INTRODUCTION TO DBMS

UNIT-I

Introduction - History of database systems - Applications of database systems - Database systems vs. file systems. - Data abstraction, Data models, Instances & schemes E-R Model: Entity and entity Sets, Relations and relationship sets, E-R diagrams, Data Model: Basic concepts, Hierarchical Data Model: Network, Relational and Object- Oriented Models) – RDBMS: Relational Database Management systems, distributed database processing

UNIT-II

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

UNIT III

Structured Query Language – Basic Structure, Set Operations, Aggregate Functions, Null Values, Nested Sub queries, Views, Integrity: Domain constraints, Joined Relations, Data- Definition Language

UNIT –IV

Telecommunications: introduction to telecommunications – computer networks – Communication systems – distributed systems

UNIT –V

New technologies in IT; E- Commerce – hypermedia – data warehouses and data marts – data mining – online analytical processing – Geographical information system.

REFERENCES:

1. Database System Concepts (6th Ed.) by Silberschatz, Henry F. Korth, S. Sudarshan, McGraw-Hill, 2010.
2. Computer Networks (3rd Ed.) by Tananbaum A.S., 1999, PHI.
3. Data Mining Concepts and Techniques – Jiawei Hen, Micheline Kambler, 2006, Academic Press Morgan kaufman Publishers.

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-V/Ppr.no.35(B)/ Elective –I (B)

INTRODUCTION TO BIOMOLECULAR INSTRUMENTATION

Unit I: Spectroscopy

Basic principles of spectroscopy; Nature of electromagnetic radiation; Interaction of light with matter; Absorption and emission of radiation; Electronic, vibrational and rotational spectroscopy of molecules; Principle, Methods and applications of UV - visible spectroscopy, IR spectroscopy, Raman spectroscopy, Fluorescence spectroscopy, Atomic absorption spectroscopy, Inductively coupled plasma atomic emission spectrophotometry, NMR spectroscopy, Nuclear quadrupole resonance spectroscopy, ESR spectroscopy, Mass spectroscopy, Photoacoustic spectroscopy.

Unit II: Electrophoresis

Electrophoresis: Principle; Electrophoretic mobility (EPM) estimation; Factors affecting EPM; Principle, Instrument design, Methods and applications of 2D electrophoresis and zone electrophoresis techniques (Paper, Agarose, Pulsed-field, PAGE, SDS-PAGE, Capillary).

Unit III: Chromatography and Microscopy

Chromatography: Basic concepts of adsorption and partition chromatography; Principle, Instrument design, Methods and applications of all types of adsorption and partition chromatography methods – Paper, Thin layer, Gas, HPLC and Ion chromatography.

Microscope: Principle, Instrumentation and Application of microscopy; Image formation; Magnification; Resolving power; Different types of Microscopy – Dark field, Phase contrast, Polarization, Fluorescence and Electron microscopy.

Unit IV: X-ray Crystallography

X-ray: Principle and applications, Unit cell, Crystal symmetry, Bravais lattices, Symmetry elements and operations, Point groups and space groups, Bragg's law, Diffraction, Atomic scattering factors, Structure factors, Fourier transformation, Amplitude and Phase, Protein crystallization, Electron density map.

Unit V: Microarray

Principle, Instrumentation and Application of DNA microarray and protein array; Sequence databases for microarrays; Image processing; Normalisation; Analysis of relationships between genes, tissues or treatments; Validation tools: GoMiner, qPCR, and TM4-MeV; Emerging applications of microarray and next generation sequencing.

REFERENCES:

1. Wilson K. and Walker J., Principles and Techniques of Biochemistry and Molecular Biology (6th Edition, Cambridge University Press, 2008).
2. Freifielder D., Physical Biochemistry, (2nd Edition, W.H. Freeman and Co., New York 1982).
3. Ghosal S. and Srivastav A.K., Fundamentals of Bioanalytical Techniques and Instrumentation, (PHI Learning Private Limited, New Delhi, 2009).
4. Wang, Junbai; Tan, Aik Choon; Tian, Tianhai (Eds.). Next Generation Microarray Bioinformatics (Methods and Protocols). Humana Press. 2012.
5. Dov Stekel, Microarray Bioinformatics. Cambridge University Press. 2003.

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-V/ Ppr.no.36 (A)/ Elective –II (A)

PROGRAMMING IN VISUAL BASIC

Unit-I

Visual Basic: Introduction to Client / Server technology- Introduction to Visual Basic features- Data types, Strings, Variant, Constant - Data Arrays -.

Unit – II

Looping and iterative statements:- Determinate Loops - Indeterminate Loops - Conditionals - Built-in Functions - Functions and Procedures.

Unit – III

Forms: Customizing a Form - Simple controls, Command buttons, text boxes, labels -Other Controls - rive list box, directory list box, file list box, combo box, check box, timer control - Image Controls - Writing Simple Programs - Creating Controls

Unit-IV

Introduction to data connectivity, different database connectivity approaches, simple connectivity program using data control.

Unit-V

VB Menu: Simple Menu creation, MDI forms

REFERNCES:

1. Visual Basic 6 from the Ground up, Gary Cornell - Tata McGraw Hill - 1999.
2. Visual Basic 6 (The Complete Reference), Noel Jerke - Tata McGraw Hill - 1999.
3. Using Visual Basic. Que Series. 2001.

APPLICATIONS IN BIOINFORMATICS

Unit I: Eukaryotic Genome applications

Sequencing of Complete Genomes – Characterization of Genomes using STS and EST Sequences – Sequence Tagged Sites are Landmarks in the Human Genome – Expressed Sequence Tags – Implementation of an EST Project – Identification of Unknown Genes – Discovery of Splice Variants – Genetic Causes for Individual Differences – Pharmacogenetics and Individual Medicine.

Unit II: Functional analysis of genomes

Identification of the Cellular Functions of Gene Products – Basic concepts of Transcriptomics, Proteomics, Metabolomics, Phenomics, Systems Biology.

Unit III: Medical and forensic applications of gene manipulation

Diagnosis and characterization of medical conditions – Treatment using rDNA technology – gene therapy – DNA profiling.

Unit IV: Transgenic plants and animals

Transgenic plants – need and scope – Ti plasmids as vectors for plant cells – Making transgenic plants – Putting the technology to work – Transgenic animals – importance of transgenic animals – Producing transgenic animals – Applications of transgenic animal technology.

Unit V: Patenting of Biological Materials

Product patents and its Importance to investors – Conditions for patenting – Patenting of Liveforms – Significance of Patents in India – Some example cases of patenting.

REFERENCES:

1. P.M. Selzer, R.J. Marhöfe and A. Rohwer, Applied Bioinformatics, Springer-Verlag, Heidelberg, 2008.
2. Desmond S. T. Nicholl, Introduction to Genetic Engineering, Cambridge Univ. Press, UK, 2002.
3. R.C. Dubey, A Textbook of Biotechnology, Rev. Edn., S.Chand & Company, New Delhi, 2006.

GENOMICS AND PROTEOMICS

UNIT 1

Genomics: Large scale genome sequencing strategies. Genome assembly and annotation. Genome databases of Plants, animals and pathogens. Metagenomics**:** Gene networks: basic concepts. Prediction of genes, promoters, splice sites, regulatory regions: basic principles, application of methods to prokaryotic and eukaryotic genomes and interpretation of results. Basic concepts on identification of disease genes.

UNIT II

Epigenetics: DNA microarray: database and basic tools, Gene Expression Omnibus (GEO), ArrayExpress, SAGE databases DNA microarray: understanding of microarray data, normalizing microarray data, detecting differential gene expression, correlation of gene expression data to biological process and computational analysis tools (especially clustering approaches)

UNIT III

Comparative genomics: Basic concepts and applications, whole genome alignments: understanding the significance; Artemis, BLAST2, MegaBlast algorithms, PipMaker, AVID, Vista, MUMmer, applications of suffix tree in comparative genomics, synteny and gene order comparisons Comparative genomics databases: COG, VOG.

UNIT IV

Functional genomics: Application of sequence based and structure-based approaches to assignment of gene functions – e.g. sequence comparison, structure analysis (especially active sites, binding sites) and comparison, pattern identification, etc. Use of various derived databases in function assignment, use of SNPs for identification of genetic traits. Gene/Protein function prediction.

UNIT V

Proteomics: Protein arrays: basic principles. Computational methods for identification of polypeptides from mass spectrometry. Protein arrays: bioinformatics-based tools for analysis of proteomics data (Tools available at ExPASy Proteomics server); databases (such as InterPro) and analysis tools. Protein-protein interactions: databases such as DIP, PPI server and tools for analysis of protein-protein interactions

REFERENCES:

1. Principles of Genome Analysis and Genomics (3rd Ed.) by Primrose, S.B. and Twyman, R.M., 2003, Blackwell Publishing Company, Oxford, UK.
2. Introduction to proteomics – Tools for the new biology (1st Ed.) by Liebler, D.C., 2002, Human Press Inc., New Jersey, USA.
3. Bioinformatics and Functional Genomics by Pevsner, J., 2003, John Wiley and Sons, New Jersey, USA.
4. Bioinformatics: Sequence and Genome Analysis by Mount, D., 2004, Cold Spring Harbor Laboratory Press, New York.

MOLECULAR MODELLING AND DRUG DESIGNING

Unit I: Molecular Modeling

Introduction to molecular modeling, Quantum chemistry, Schrödinger equation, Potential energy functions, Energy minimization, Local and global minima, Saddle point, Grid search, Various approximations; LCAO, HF, Semi-empirical calculations; Single point calculations, Full-geometry optimization methods, ZDO, MNDO, CNDO, NDDO, AM1, PM3, RM1, Conformational search, Z-matrix, Docking, Molecular modeling packages, Molecular Graphics.

Unit II: Chemical compounds structures

Representation of chemical compounds, Manipulations in 2D and 3D structures of chemical compounds, Representation of chemical reactions, Molecular descriptors, Calculations of physical and chemical data, Calculations of structural deciphers.

Unit III: Drug Development

Drugs, Development of drug, Source of drugs, Structural effects on drug action, Drug life cycle, Drug development time lines, Stages of drug discovery, Strategic issues in drug discovery, Emerging approaches to drug design and discovery, Drug metabolism, Drug design physicochemical properties: Hansch π; Hammett σ; Es, MR, Pharmacokinetic action of drug on human body, Prodrug design and applications.

Unit IV: Computer Aided Drug Design

Computer Aided Drug Design, Methods of computer aided drug design, Ligand design methods, Docking algorithms and programs, Drug design approaches, Strategy for target identification and validation, Lead compound identification and optimization, High throughput screening for lead discovery, Receptor theory, Receptor models and nomenclature.

Unit V: Virtual Screening and ADMET properties

Combinatorial Chemistry and Library Design, Virtual screening, Drug likeliness and Compound filters. ADMET (Absorption, Distribution, Metabolism, Excretion and toxicity) property prediction, Computer based tools for drug design.

REFERENCES:

1. Andrew R. Leach, Valerie J. Gillet, Introduction to Chemoinformatics, Springer, Netherlands, 2007.
2. Frank Jensen, Introduction to Computational Chemistry, Wiley, 1999.
3. S.P.Vyas and R.K.Khar, Targeted and Controlled Drug Discovery, CBS Publishers, 2012.
4. Johann Gasteiger and Thomas Engel, Cheminformatics, Wiley-VCH, 2003.
5. Thomas Lengauer (Ed.), Bioinformatics from Genome to Drug, Wiley-VCH, 2002.
6. Kerns, E.H.; Di, L. Drug-Like Properties: Concepts, Structure Design and Methods: from ADME to Toxicity Optimization, Academic Press, Oxford, 2008
7. Burger's Medicinal Chemistry and Drug Discovery, 5th Edition, Vol. 1. Principles and Practice, edited by M. E. Wolff, John Wiley & Sons: New York, 1995.
8. Principles of Medicinal Chemistry, 4th Edition, edited by W.O. Foye, T.L. Lemke, and D. A. Williams, Williams and Wilkins: Philadelphia, 1995.
9. Medicinal Chemistry: Principles and Practice, edited by F.D. King, Royal Society of Chemistry: Cambridge, 1994.
10. A Practical Guide to Combinatorial Chemistry, edited by A. W. Czarnik and S. H. DeWitt, American Chemical Society: Washington DC, 1997.

OPERATING SYSTEM AND WEB PROGRAMMING

UNIT – I

Introduction to operating systems – Unix/Linux basic commands – general purpose, file handling; Vi editor, basic commands – Shell programming

UNIT – II

Introduction to HTML – Elementary tags in HTML – List in HTML – Displaying text in lists – Using ordered lists – using unordered lists – Directory list. Definition lists –Combining list types graphics and image format – graphics and HTML documents. Images and hyperlink anchors – Image maps – Tables frames – Forms – Background graphics and color.

UNIT – III

Introduction to DHTML – Introduction to style sheets – setting the default style sheet language – Inline style information – External style sheets – Cascading style sheet.

UNIT - IV

Server side Programming - Introduction to PHP , PHP and HTML, essentials of PHP, Why Use PHP, Installation of Web Server,WAMP Configurations, Writing simple PHP program, embedding with HTML

UNIT - V

comments in PHP - Variables - Naming Conventions, Strings, String Concatenation, String functions, float functions, Arrays, Array – Key pair value, Array functions, is SET, UNSET, gettype(), settype(), control statements (if, switch), Loops, User Defined Functions (with argument, return values), global variable, default value, GET POST method - URL encoding, HTML Encoding, Cookies, Sessions, Include statement. File : read and write from the file.

REFERNCES:

1. Operating Systems; by Madnick S.E. and Donovan J.J; McGraw –Hill, 2001
2. HTML and Web designing by Kris Jama and Konrad king, publisher Tata McGraw-Hill Education, 2002
3. Faithe Wempen, HTML 5 Step by Step, Microsoft Press, PHI, 2012.
4. Jon Duckett , Beginning HTML , XHTML , CSS, and JavaScript, Wiley Publishing , 2010
5. Matt Doyle , Beginning PHP 5.3, Willey Publishing, 2010

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-VI/ Ppr.no.44(A)/ Elective -3(A)

SYSTEM BIOLOGY

Unit 1: Introduction to Systems Biology

Introduction to Systems Biology. Need for System Analysis in Biology. Basic Concepts in System Biology: Component vs System, Links and Functional States, Links to Networks, Hierarchical Organization in Biology.

Unit 2: Metabolic Networks and Models in System Biology

Basic Features of Metabolic Networks. Reconstruction Methods of Metabolic Networks. Models as Dynamical Systems. Parameter Problem. Meanings of Robustness.

Unit 3: Systems Biology Databases

KEGG (Kyoto Encyclopedia of Genes and Genomes). BRENDA (BRaunschweig ENzyme DAtabase). BioSilico. EMP (Embden-Meyerhof-Parnas). MetaCyc and AraCyc. SABIO-RK (System for the Analysis of Biochemical Pathways - Reaction Kinetics). BioModels.

Unit 4: Tools for System Biology

CellDesigner. Ali Baba. CellProfiler. JDesigner. Bio-SPICE (Biological Simulation Program for Intra and Inter Cellular Evaluation). SBML (Systems Biology Markup Language). SBGN (Systems Biology Graphical Notation). SBML-SAT (SBML based Sensitivity Analysis Tool).

Unit 5: Premises & Promises of Systems Biology

Premise of Systems Biology. Promise of Systems Biology. Challenges of Systems Biology. Applications of Systems Biology.

REFERENCES:

1. Bernhard O. Palsson (2006). *Systems Biology: Properties of Reconstructed Networks*. Cambridge University Press, New York.
2. Björn H. Junker, Falk Schreiber (2008). *Analysis of Biological Networks*. John Wiley & Sons, Inc., Hoboken, New Jersey.
3. Huma M. Lodhi, Stephen H. Muggleton. *Elements of Computational Systems Biology*. John Wiley & Sons, Inc., Hoboken, New Jersey.
4. M. Cánovas, J.L. Iborra and A. Manjón (2006). *Understanding and Exploiting Systems Biology in Biomedicine and Bioprocesses*. CajaMurcia Foundation, Spain.
5. http://www.systemsbiology.org
6. http://www.systems-biology.org

MSU/2016-17/UG-Colleges/Part-III (B.Sc. Bio Informatics)/Semester-VI/ Ppr.no.44(B)/

Elective -3(B)

OPEN SOURCE BIOINFORMATICS

Unit I: Introduction to Free and open-source software

Introduction to Free and open-source software (FOSS), Open Bioinformatics Foundation (O|B|F), Software license, Types of software, Types of software licenses, Software categories, Benefits and challenges, Bioinformatics Linux distributions (BioBrew, Bio-Linux, BioLand, Vlinux, Vigyaan, Bioknoppix, Dnalinux, and Quantian).

Unit II: Free and open-source software Tools I

.NET Bio, AMPHORA, Anduril, Armadillo workflow platform, AutoDock, Biochemical Algorithms Library (BALL), caCORE, caArray, LabKey Server, OpenClinica, PromKappa, MeV: Multi-Experiment Viewer, PathVisio, REDCRAFT

Unit III: Free and open-source software Tools II

EMBOSS, Gaggle, Galaxy, GenePattern, GeWorkbench, GMOD, GeneTalk, GenGIS, GenomeSpace, GENtle, Integrated Genome Browser, Argo Genome Browser, Integrative Genomics Viewer (IGV), IntAct, InterMine, Java Treeview.

Unit IV: Free and open-source software Tools III

SAM Tools, Staden Package, STAMP, Taverna workbench, TGAC Browser, T-REX WebServer, Unipro UGENE, Visomics, Genome Analysis Toolkit 1.0 (GATK 1.0).

Unit V: Bio Tools Projects

Bio4j, Bioclipse, Bioconductor, BioHaskell, BioJava, BioMOBY, BioPerl, BioPHP, Biopython, BioRails, BioRuby, BioSmalltalk, BioUno.

REFERENCES:

1. Edwards, David; Stajich, Jason; Hansen, David (Eds.), Bioinformatics: Tools and Applications, Springer, 2009.
2. World Wide Web

SEMESTER – V & VI

LAB IN STRUCTURAL BIOLOGY, MOLECULAR MODELING AND DRUG DESIGN

1. Homology modeling using Swiss-Model/MODELLER.
2. Protein structure and function predictions using I-TASSER/Phyre2.
3. Automatic fold recognition server for predicting the structure and/or function of your protein sequence.
4. *ab initio* protein folding and protein structure prediction using QUARK.
5. Protein side chain modeling using YASARA.
6. Protein ligand binding site prediction using COACH.
7. Search and download drug compounds using ZINC/ChEMBL/DrugBank.
8. Ligand binding site prediction using 3DLigandSite.
9. Docking using AutoDock/ZDOCK/PatchDock.
10. Protein-Ligand interaction plotting using LigPlot.

SEMESTER – V & VI
LAB IN GENETICS AND GENOMICS & PROTEOMICS

Wet Lab:

1. DNA isolation from bacteria
2. 16S rRNA gene amplification and sequencing
3. ITS gene amplification from eukaryotes.
4. Protein extraction from bacteria and quantification.
5. MALDI-TOF analysis of protein.
6. Protein analysis by 2-D-gel method.
7. Pedigree analysis.

Dry Lab:

1. Sequence Analysis Packages: EMBOSS, NCBI ToolKit, SMS
2. Database search engines: Entrez, SRS, DBGET
3. Pair wise alignment: a. Search tools against Databases: i. BLAST, ii. FASTA
4. Multiple sequence alignment: a. Clustal, b. Dialign, c. Multalign
5. Sequence patterns and profiles: a. generation of sequence profiles - PSI-BLAST
   b. derivation of and searching sequence patterns: MeMe, PRATT & PHI-BLAST
6. Protein motif and domain analysis:. MEME/MAST, eMotif, ProSite, Pfam
7. Phylogenetic analysis – MEGA, PAUP, PHYLIP
8. Genome annotation – Artemis.
9. Hypothetical Protein analysis
10. Genome Comparison

SEMESTER – V & VI

LAB IN OPERATING SYSTEM AND WEB PROGRAMMING

Operating System and HTML

1. Basic Unix Commands–Create and delete directories – View the contents of a directory – Renaming a directory – Changing directory.
2. Changing drives – Copying files – Copying a group of files – Renaming files – Deleting files – Viewing files –.
3. Usage of simple HTML commands, Graphics and image formats and hyperlinks
4. Use of tables, frames, forms, background graphics and color.
5. Simple Website creation using HTML
6. Simple DHTML and Cascading style sheet.

WEB and PHP PROGRAMMING

1. Creating forms using CGI
2. PHP program to demonstrate GET and POST method of passing the data between pages
3. PHP program to demonstrate Array , Key-pair values
4. Create a PHP page that uses Session and cookies.
5. File Handling in PHP