**V SEMESTER**

| S.No | SUBJECT NAME | L | P | M |
|---|---|---|---|---|
| | **THEORY** | | | |
| 01 | Proteomics | 4 | 0 | 100 |
| 02 | Genomics | 4 | 0 | 100 |
| 03 | Computational Biology | 4 | 0 | 100 |
| 04 | Biophysics | 4 | 0 | 100 |
| 05 | Molecular evolution and phylogeny | 4 | 0 | 100 |
| 06 | Perl for Bioinformatics | 4 | 0 | 100 |
| | **PRACTICALS** | | | |
| 01 | Perl Lab | 0 | 3 | 100 |
| 02 | GCG Lab | 0 | 3 | 100 |

## BIOPHYSICS

**Objectives:**

The concept of biophysical properties of biological macromolecules is made to understand the idea about the energetic and the kinetics of these macromolecules are explained along with the techniques involved in their structural assessment.

**Unit I** **7 hours**

**Classical Mechanics:**

Introduction to Mechanics – Types - La Grange Equations and Hamilton's Equations, Quantum Mechanics: Schrodinger Wave Equations, Uncertainty Principle.Quantum Chemistry, Molecular Orbital. Macromolecular Structure and Dynamics.Biological Macromolecules configuration and conformation. Molecular interactions in macromolecular structure

**Unit II** **9 hours**

**Bioenergetics Principles:**

Concept of energy, Thermodynamics principles. Free energy, standard free energy - additive nature, calculation of $\Delta G°$. Standard free energy of formation, Spontaneity, exergonic and endergonic reactions, enthalpy, entropy, Heat of reversible process, equilibrium constant. Conventions in Biochemical energetics, Standard free energy changes for representative chemical reactions. ATP as the Universal currency for free energy in biological systems, Simulating macromolecular structure - energy minimization, molecular dynamics entropy, hydration and hydrophobic effects, free energy method.

**Unit III** **8 hours**

**Kinetics of Biological systems:**

Molecular structure of biological system-Biological polymer, membrane and energy. Transport processes, excitable membranes and control of the movement, nerves signal and memory.

**Unit IV** **11hours**

**Kinetics of Biomolecular Interactions:**

Ramachandran Plot - Biochemical kinetics studies, biomolecular reactions, simple biomolecular intermediates, Steady state kinetics, Catalytic efficiency. Physical interaction and determining the properties of biomolecules. Calculation of kinetic rate constants, High kinetic resolution of protein folding events, Kinetic molecules of slow reaction, Resolution of protein structure in solution, High standard resolution of transient protein conformations.

**Unit V** **10 hours**

**X-ray Crystallography:**

Structures at atomic resolution, Crystals - growing crystals, condition for macromolecular crystallization, Theory of XRD - Bragg's law, von Laue condition for diffraction, Determination of crystal morphology. Solving macromolecular structures by XRD. Fibre diffraction - fibre unit cell - diffraction of continuous and discontinuous helices.

**Prescribed Books:**

1. Colin, Banwell and Elaine, "Fundamentals of molecular spectroscopy", Tata McGraw-Hill.
2. Daniel .M.Basic "Biophysics for Biologist".
3. James E.House, "Fundamentals of Quantum Chemistry", Second Edition Academic Press.
4. N.Gautam & Vasanta Pattabi "Biophysics", Narosa Publication.
5. P.K .Srivastava, "Elementary Biophysics -An Introduction", Narosa publication Press.
6. Rodney & Cotteril, "Biophysics-An Introduction", Wiley publication.

**Reference Books:**

1. Bergethon Simons, "Biophyscial Chemistry", Springer.
2. Contor and Schimmel, "Biophysical chemistry Volume I, II & III", W.H - Freeman & co.
3. David Blow, "Welfare of crystallography for Biologist", Oxford Press.
4. Giacovazzo "Fundamentals of crystallography", Oxford publication.
5. Hammond "The basic of crystallography and diffraction", Oxford press.
6. Manfred Schliwa, "Molecular motors", Wiley-VCH.

**Reference Websites:**

1. http://en.wikipedia.org/wiki/Biophysics.
2. http://en.wikipedia.org/wiki/X-ray_crystallography.
3. http://en.wikipedia.org/wiki/Systems_biology.

## COMPUTATIONAL BIOLOGY

**Aim and Objective:**

To have an overview of Computational Biology,the methods of sequence analysis, and to predict the structure of RNA and Genome analysis. The students are benefited in step wise approach to analysis the macromolecules like proteins and nucleic acids. The basics of Computational Biology is clearly understood.

**UNIT I: Overview of Computational Biology: 9 hours**

Fundametals of proteins and nucliec acids. Sequence analysis, Motif finding, an overview of energy fields including expression profilling, quantitative image analysis, Strings, Graphics and Algorithms.

**UNIT II: SEQUENCE ALIGNMENT: 9 hours**

Heuristic approach, Database search methods and tools, scoring matrices and affine Gap costs, Deteailed method of derivation of PAM and BLOSUM matrices, Diffrence between distance and similarity matrix, Assessing the significance of sequence alignment.

**UNIT III: MULTIPLE SEQUENCE ALIGNMENT: 9 hours**

MSA- various approaches for MSA Progressive and iterative), Significance on MSA, Profile analysis, Block analysis, Pattern searching, Motif analysis, Statistical method for aiding alignment - Expectation Maxization, MEME, Gibbs sampling, Markov chain approaches, Bali Base - Scoring of MSA, PSI/PHI - Blast.

**UNIT IV:**

**RNA secondary structure and Gene Prediction: 9 hours**

RNA secondary structure prediction methods, and it's limitations mfold method of Zuker, RNA fold program, tertiary structures on rRNA, Applications of RNA structure modelling.

Gene Prediction methods, neral networks, pattern Discrimination methods, signal sites prediction (promoter,slice, UTR, CpG- islands), Evaluation of genepredictions methods, Fragment assembly of DNA, DNA Cumputing.

**UNIT V: GENOME ANALYSIS: 9 hours**

Genome databases, gene density, gene ontology, gene Order ( synteny)(, plasicity zone, gene network, tandem repeats, transposable elements, psedogenes, gene clusters, segmental duplication, Non-coding conservation. Comparative genomics, imprtance on full genome Alignments, Cocepts and application of Suffix tree in comrative genomics, Algorithms for BLAST2, Mege Blast, MUMMER.

**Prescibed Books:**

1. Introduction to Bioinformatics-A.Lesk 2002, Oxford University Press.

2. Fundamental concepts of Bioinformatics by D.E.Krane AND M.L. Raymer ,Pearson Education 2003,ISBN 81-297-004-1.
3. Introduction to Computational Biology, M.Waterman, Chapman and Hall.
4. Bioinformatics by David W. Mount,Cold Spring Harbor Laborator Press,2001,ISBN,0-87969-608-7.
5. Current protocols in Bioinformatics,Edited by A.D.Baxevanis et.al., Wiley Publishers 2005.

Reference Books:

1.Introduction to Computational Biology BY Joao Carlos Setubal, Joao Meidanis, Jooao Carlos Setubal.
2.Computational Molecular Biology by P.A.Pevzner, Prentice Hall of India Ltd,2004 ISBN 81-203-2550-8.
3.DNA and Protein Sequence Analysis, M.Bishop and C.Rawlings Eds.,IRL Press.
4.Computational Methods in Molecular Biology, S.Salzberg, D.Searls and S.Kasif eds.,Elsevier.

**Web site Adressess:**

1. **http://www.genome.gov/Course2003/.**
2. **http://compbio.ornl.gov/.**
3. **http://www.bioinfo.rpi.edu/~zukerm/Bio-5495/RNAfold-html/.**
4. **http://en.wikipedia.org/wiki/Sequence_alignment_software.**
5. **http://www.geneious.com/.**

## GENOMICS

**45 hours**

**Objectives:**

To equip the students with the basic knowledge in Genomics and make them understand the various techniques involved in the analysis of genomics and make them apply the knowledge gained in industries and diagnosis.

**Unit I** **5 hours**

**Gene & Genomics:**

Definition, Principles of Gene expression, sequencing whole genome, Genome sequence to annotation, genome acquisition, analysis and genomic variations.

**Unit II** **7 hours**

**Organization & function of Eukaryotic genomes:**

Mitochondrion & Chloroplast genomes – Methods for whole genome sequence – DNA chip technology & Microarray, Subtractive DNA library screening, differential display & representational difference analysis, SAGE.

**Unit III** **10 hours**

**Mapping & Sequencing of Genome:**

Mapping strategies – Genetic linkage maps – physical maps – low and high resolution physical mapping – Chromosome map, cDNA map, STS maps, Cytogenetic mapping techniques.

**Unit IV** **11 hours**

**Genome:**

Human Genome – Organization of Human Genome – HGP and its applications, Genome of Fungil, Bacteria and Crop - Genomics in agriculture – Computational Genomics – Genome database management, Databases: PEDANT, COG, KEGG, MBGD, WIT.

**Unit V** **12 hours**

**Applications of Genomics:**

Genomics in biopharmaceutical industry, Genomics in molecular diagnosis, Comparative genomics: Methods of comparison – Comparison at Nucleotide level, Breakpoints level, Gene cluster level, Ontological comparison, Phylogenetic comparison, Example for Comparative Genomics.

**Prescribed Books:**


1. Dawson, "Gene Technology", BIOS publications.
2. Hunt & Livesey, "Functional Genomics", Oxford University Press.
3. S.B. Primrose & R M Twyman, "Principles of genome analysis & Genomics", Blackwell publishing.
4. S.B.Primrose & R.M.Twyman, "Genomics: Applications in Human".
5. T.Brown, "Genomes", Wiley Bios.


**Reference Books:**

1. Mannhold Kubinyi, “Bioinformatics from Genomics to Drugs”, Wiley – VCH.
2. Peusner, “Bioinformatics and Functional Genomics”, Wiley – Liss.

**Reference Websites:**

1. http://www.answers.com/topic/genomics?cat=health
2. http://www.cdc.gov/genomics/sitemap.htm
3. http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml

## PROTEOMICS

**Aim and Objective:**

**Students would gain wide knowledge from the basics of proteome ,protein Engineering, structure prediction ,tools used in the study of proteomics and its application thoroughly. It gives them a strong background about proteomics for further research work.**

**UNIT I: INTRODUCTION TO PROTEOMICS AND PROTEOME 9 hours**

Proteomics and the new biology, proteome and genome , protein evaluation, Life and death of a protein, Protein as modular structure, functional protein families, deducing Proteome from Genome gene expression codon bias and protein levels

**UNTI II: PROTEIN ENGINEERING AND FOLDING:- (PREDICTION AND DESIGN) 9 hours**

Protein folding patterns thermodynamics of protein folding, Integration and pattern, control of protein function, protein turnover, effect of denaturants on rates of protein folding and unfolding chevron plots, molten globule, folding funnels, protein misfolding.

**UNIT III: PROTEIN STRUCTURE PREDICTION AND DESIGN 9 hours**

Prediction of protein structure, CSAP, Homology modeling Threading, Prediction of novel folds[Conformational energy calculation, and molecular dynamics], Rosetta-Linus , Prediction of Protein function, Protein design, Protein-Partner.

**UNIT IV : TOOLS FOR PRETEOMICS 9 hours**

Overview of analytical proteomics, Analytical proteins and peptide separation, protein digestion Techniques, Mass Spectrometer for protein and peptide analysis, protein identification by peptide mass finger printing, peptide analysis by tandem MS, Protein identification and Tandem MS data. SALSA - Phage antibodies as tools for proteomics.

**UNIT V: APPLICATIONS OF PROTEOMICS:- 9 hours**

Mining proteomes, protein expression profiling, identifying protein-protein interaction and protein complexes, mapping protein modification, new directions in proteomics, proteomics as tool for plant genetics and breeding.

**Prescibed Books:**

1. S.R Pennington, M.J.dunn, "Proteomcs- form protein sequence to Function", viva Books PVT LTD, 2002 First edtion.
2. Introduction to protein science-"Architecture, Function and Genomics, Arthur

M.Lesk, Oxford University press 2004.
3. Introduction to Proteomics -Tool for new biology Daniel Liebler, Humna Press,2006

**Reference Books:**

1.. An introduction to protein Information - by Karl Heig Zimmermann Springer International edtion,2007.
2.Genomics and Proteomics - functional and computational Aspects- Sandor Suhai, International edtion,2005.

**Website Adressess:**

1. **http://en.wikibooks.org/wiki/Proteomics/Introduction_to_Proteomics**
2. **http://cmgm.stanford.edu/WWW/www_predict.html.**
3. **http://www.proteindesign.com/.**
4. **http://bfgp.oxfordjournals.org/cgi/reprint/2/3/185.pdf.**

## MOLECULAR EVOLUTION AND PHYLOGENY

**45 hour**

**Objectives:**

To make the students understand the concept of molecular evolution and the driving forces involved, the role of mutations in sequence analysis and their substitution patterns, and the phylogenetic analysis and its algorithmic approach used to make the evolutionary & phylogenic predictions more interesting.

**Unit I** **9 hours**

**Molecular Evolution:**

Introduction to molecular evolution, Archaeology of the genome- Fundamentals of Population Genetics The nature of molecular evolution, driving forces in evolution, evolutionary changes in nucleotide sequences, dynamics of gene & population.Evolution of gene duplication & domain suffelling.

**Unit II** **9 hours**

**Evolutionary Analysis:**

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

**Unit III** **9 hours**

**Molecular Phylogenetics:**

Molecular phylogenetics, Terminology of phylogenetic trees, trees and distances, molecular phylogenetic archaeology, molecular phylogenetic examples, the universal phylogeny

**Unit IV** **9 hours**

**Phylogeny Algorithms:**

Measuring genetic change, sequence alignment and homology- Genetic distance- Measuring evolutionary change on trees, Kinds of data, Methods of reconstruction- Distance matrix methods, Maximum parsimony methods, Maximum likelihood methods- Analysis of true tree- Problems associated with phylogenetic reconstruction

**Unit V** **9 hours**

**Evolutionary Tree:**

Tree evolution – Phylogenetic software – PHYLIP, PAPU,PUZZLE, MACCLADE, MOLPHY, Internet-Accessible Phylogenetic analysis software – Applications of molecular Phylogenetic – Gene trees and Species trees, age and rates of diversification phylogeny in molecular epidemiology, host parasite co-speciation.

**Prescribed Books:**

1. David.E.Clark, "Evolutionary Algorithms in Molecular Design", Wekey Publications.
2. Higgs & Attwood, "Bioinformatics & Molecular Evolution", Backwell Publications.
3. Ryan Gregory, "The Evolution of the Genome", Elsevier Publiction.
4. Fundamentals of Molecular evolution, Dan Graur and Wen-Hsiung Li., II eds. Sinauer Associates, INC., 2000.

**Reference Books:**

1 Laura.F, Land webur, "Evolution as Computation", Springer.
2 Molecular evolution, "A phylogenetic approach", Roderic D. M. Page, Edward.C. Holmes, Blackwell Science Inc; (October 1998).
3 Wen – H suing Li, "Molecular Evolution", Sinauer Associates, Inc.

**Reference Websites:**

1 http://en.wikipedia.org/wiki/Molecular_evolution
2 http://biomed.brown.edu/Courses/BIO48/12.Molecular.Evolution.HTML
3 http://en.wikipedia.org/wiki/Phylogenetics
4 http://www.ucmp.berkeley.edu/exhibit/introphylo.html

## PERL FOR BIOINFORMATICS

**Aim**

To know about the UNIX operating system and PERL language.

**Objectives**

To have the thorough knowledge about

1 UNIX operating system
2 UNIX commands, files and security
3 PERL installation and fundamentals
4 Applications of PERL in biology

**UNIT I**

**Introduction to UNIX:-** **9**

UNIX. History and Principles, GNU Project and the GPL, Linux Origins & Benefits. Recommended Hardware Requirements. Linux File Hierarchy Concepts, Current Working Directory, Changing directories, Listing Directory Contents, the Home Directory, Absolute Path-names, Relative Path-names, File Names, Copying Files & Directories, Moving & Renaming Files & Directories, Removing & Creating Files, Creating & Removing Directories, Viewing an Entire Text File,

**UNIT II**

**UNIX Essentials:-** **9**

Bash Shell, Command Line Shortcuts, Command Line Expansion and Protecting from Expansion, Command Line History and Editing Tricks. Users, Groups and the root User. Security.

vi Editor: Starting vi; Cursor Movement; Entering & Leaving Insert Mode; Changing, Deleting, Yanking & Putting Text; Undoing Changes; Searching for Text; Saving & Exiting;

**UNIT III**

**Introduction to Perl** **9**

Perl Introduction – Installations – Perl components – Perl Parsing – Variables and Data Statements and Control Structures, Arrays, Hashes, Loops and File handles; Regular Expressions.

**UNIT IV**

**Features in Perl** **9**

Data manipulation – Errors and trapping – complex. Data Structures – System information. Networking – database systems – Interprocess communication

**UNIT V**

**Enhancement of Perl:-** **9**

Developing applications: Interface tools – advanced user interface – Developing for WWW – Perl – Applications in biology. Overview of BioPerl and its uses.

**Prescribed books**

1. PERL - the Complete Reference, Martin C. Brown, 2nd Edition – Tata McGraw Hill.
2. Exploring the UNIX system, Stephen.J.kochan,3rd edition, Sams techmedia publishers.
3. UNIX, kanethker,internet edition unleashed, techmedia publishers.

**Reference books:-**

1. Perl Black Book -Steven Holzner, Steven Holzner, Ph.D,Published 2001
2. Sams Teach Yourself Perl in 21 Days Laura Lemay, Richard Colburn, Rafe Colburn sams publishing
3. Programming Perl By Larry Wall, Tom Christiansen, Jon Orwant O'Reilly publication

**Reference websites:-**

**http://www.cs.cmu.edu/cgi-bin/perl-man**

**http://www.computerhope.com/unix/uperl.htm**

**http://www.math.utah.edu/docs/info/perl_11.html**

# PERL LAB

**Aim**

To know about the UNIX operating system and PERL language.

**Objectives**

To have the thorough knowledge about

1 UNIX operating system
2 UNIX commands, files and security
3 PERL installation and fundamental programming

**SYLLABUS**

**UNIX**

1. Installation of UNIX
2. UNIX filenames and file protections
3. UNIX commands for working with directories
4. Additional UNIX commands
5. UNIX vi Commands
6. Perl Installations

**PERL**

7. Program using Different operators of perl
8. Program to convert DNA to RNA
9. Program to Translate of RNA to Protein
10. Program to find palindrome sequence
11. Program to find the total length of the given sequence.
12. Program on UPGMA algorithm
13. Finding sequence patterns using PERL.
14. Program on Reverse transcription
15. String Comparison using PERL/Bio PERL
16. Program to calculate the total GC content
17. Program to check the privilege of file using file test operator.
18. Program for random number generation.
19. Program to find TATA box
20. Program to Determine frequency of Nucleotide
21. Program to read the FASTA sequence.

## GCG Lab

**Aim and Objectives:**

The GCG Lab is meant for the students usage of the commercial software been provided.The main heading given below has various modules to practice by the students.

(1) Comparison.
(2) DNA/RNA Secondary Structure.
(3) Evolution.
(4) Gene Finding and Pattern Recognition.
(5) Mapping.
(6) Protein Analysis