UNIVERSITY OF MUMBAI

Syllabus for the M.Sc.
Sem I, II, III, IV
Program: M.Sc.
Course: Bioinformatics

(Credit Based Semester and Grading System with effect from the academic year (2014-2015)
Introduction:

Last two decades have witnessed the emergence of Bioinformatics as a major thrust area in the global scientific scenario. It is the interface between the two most rapidly advancing fields of biological and computational sciences, Bioinformatics is a scientific discipline and asset of skills that has now become one of the most important information gathering, data mining, and knowledge building tools in recent current research and clinical applications.

Bioinformatics is an emerging field which has broad range of application to molecular biology, pharmacology, biotechnology, forensic science, drug designing, and various other disciplines.

Completion of the human genome project and explosion of genomic information from high throughput technique has created an unprecedented, but largely unmet, need for professionals to analyze data scientifically in order to extract the biological knowledge hidden in them for the general benefit of mankind with a working knowledge of the biological sciences and computational methods.

We can expect a comparable demand in hospital and other clinical settings as the impact of new technologies diffuses into clinical research and medical practice. The change has been so rapid that educational front have been caught unprepared, few offer suitable courses and virtually none offer a well integrated curriculum that meets the needs.

This M.Sc. Program in Bioinformatics is designed to address these needs through interdisciplinary training that bridges gap and meets the demand of pharmaceutical industry and strengthens research collaboration.

The proposed programme for Masters in Bioinformatics is a two year programme to meet the need of trained professionals.

Objectives Of The Course:

- Develop trained manpower in the field of Bioinformatics with specific emphasis for fulfilling expectations of Indian Pharma and Biotech industry.
- To develop skills needed to collect, understand, analyze and manage data generated through high throughput technology.
- Explain how the boundaries of knowledge in this professional discipline are advanced through research and enable students to conduct research through two targeted research projects.
- To give exposure to the students in national and international work.
Eligibility:

Bachelor degree from a recognized university in any of the following disciplines:
- Science (Biochemistry, Biology, Botany, Biotechnology, Chemistry, Environmental Science, Life Sciences, Physics, Mathematics, Microbiology, Statistics or Zoology)
- Agriculture
- Medicine
- Pharmacy
- Veterinary Science
- Computer Science

Staffing Pattern For The Course:

- Instrument technician - 01
- Technical assistance - 02
- Lecturer - 03 (Full Time)
- Lecturer - 01 (Part Time)
- Remaining workload will be shared with visiting faculty.

Faculty:

Post graduate or PhD degree in the subject of Bioinformatics, Computers, Microbiology, Biochemistry, Biotechnology, Life Science, Molecular Biology, Botany, Zoology, and Statistics, Mathematics with B+ grade and NET / SET.

Visiting Faculty From Industry & Research Institutes:

The visiting Faculty will be from a post equivalent to that of Senior Lecturer level with PhD and not less than 5 years of research experience or with experience in industry not below Assistant Manager Level.
SYLLABUS IN BRIEF

Distribution of Credits -

<table>
<thead>
<tr>
<th>Course</th>
<th>Code</th>
<th>Lectures</th>
<th>Credits</th>
<th>Code</th>
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*Lectures allotment includes periods for seminar & presentations.*

*Units equally distributed between two terms.*
Syllabus for M.Sc. Bioinformatics

Semester - II

<table>
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<tr>
<th>Paper</th>
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Semester - III

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### Semester IV

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**TOTAL CREDITS** 24

*Lectures allotment includes periods for seminar & presentations.*

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## Modular Distribution of Topics

<table>
<thead>
<tr>
<th>First Semester</th>
<th>Second Semester</th>
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<tbody>
<tr>
<td>101.1 Structure of Major Biomolecules</td>
<td>201.1 Concept of central dogma of life</td>
</tr>
<tr>
<td>101.2 Cell biology and Genetics</td>
<td>201.2 Genomics organization</td>
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<tr>
<td>101.3 Metabolism</td>
<td>201.3 Cell–Cell communication and Signal transduction</td>
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<td>101.4 Protein chemistry</td>
<td>201.4 Applied genomics</td>
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<tr>
<td><strong>(PSBI102: Sequence analysis and taxonomy)</strong></td>
<td><strong>(PSBI202: Sequence analysis and taxonomy)</strong></td>
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<tr>
<td>102.1 Sequence and Structure Databases</td>
<td>202.1 Heuristic Methods of Sequence alignment</td>
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<tr>
<td>102.2 Composite Databases</td>
<td>202.2 Multiple Sequence Alignments</td>
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<tr>
<td>102.3 Pair wise sequence alignment</td>
<td>202.3 Taxonomy and Phylogeny</td>
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<tr>
<td>102.4 Dynamic programming Algorithm</td>
<td>202.4 Data mining</td>
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<tr>
<td><strong>(PSBI103: Biostatistics)</strong></td>
<td><strong>(PSBI203: Immunology And Bioinformatics)</strong></td>
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<tr>
<td>103.1 Basics of Mathematics</td>
<td>203.1 Introduction to Immune systems</td>
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<tr>
<td>103.2 Statistical Measures</td>
<td>203.2 Receptors and MHC</td>
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<td>103.3 Bivariate Distribution</td>
<td>203.3 Immunoinformatics and vaccinology</td>
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<tr>
<td>103.4 An Introduction to Statistical inference</td>
<td>203.4 Patinformatics</td>
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<tr>
<td><strong>(PSBI104: Programming language and databases)</strong></td>
<td><strong>(PSBI204: Programming language and databases)</strong></td>
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<tr>
<td>104.1 Fundamentals of Computing and Database systems</td>
<td>204.1 SQL</td>
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<tr>
<td>104.2 Introduction to C</td>
<td>204.2 Introduction To Linux</td>
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<tr>
<td>104.3 Introduction to C++</td>
<td>204.3 HTML &amp; XML</td>
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<tr>
<td>104.4 RDBMS</td>
<td>204.4 Advanced C++</td>
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# Syllabus for M.Sc. Bioinformatics

## MODULAR DISTRIBUTION OF TOPICS

<table>
<thead>
<tr>
<th>THIRD SEMESTER</th>
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<tbody>
<tr>
<td>(PSBI301: Molecular modeling and drug designing)</td>
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<tr>
<td>301.1 Introduction to Molecular Modelling</td>
<td>401.1 Drug Delivery systems</td>
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<td>301.2 Cheminformatics</td>
<td>401.2 Orphan receptors &amp; reverse pharmacology</td>
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<td>301.3 Combinatorial Chemistry</td>
<td>401.3 QSAR</td>
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<td>301.4 Drug Designing</td>
<td>401.4 Molecular modeling &amp; drug designing softwares</td>
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<tr>
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<tr>
<td>302.1 Tools to study Structure of molecules</td>
<td>402.1 Global profiling technologies</td>
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<tr>
<td>302.2 Techniques for separation</td>
<td>402.2 Genomics</td>
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<td>302.3 Detection of known molecules</td>
<td>402.3 Applied Genomics</td>
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<tr>
<td>302.4 Sequencing of Nucleic acids and proteins</td>
<td>402.4 Functional proteomics</td>
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<th>(PSBI303: Applications of bioinformatics)</th>
<th>(PSBI403: Applications of bioinformatics)</th>
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<tr>
<td>303.1 Secondary Structure Prediction of Protein</td>
<td>403.1 Machine Learning Techniques</td>
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<td>303.2 Tertiary Structure Prediction of Protein</td>
<td>403.2 Algorithms and techniques for Microarray analysis</td>
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<td>303.3 Bioinformatics Perspectives on Human Diseases</td>
<td>403.3 Medical Informatics</td>
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<tr>
<td>303.4 Markov and Hidden Markov Models</td>
<td>403.4 Bioinformatics &amp; systems biology</td>
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<tr>
<td>304.1 Introduction to OOPs concept and JAVA</td>
<td>404.1 Introduction to Perl and data types</td>
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<td>304.2</td>
<td>Core JAVA</td>
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<td>304.4</td>
<td>BioJava</td>
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PSBI101 FUNDAMENTALS OF BIOLOGY

101.1 Cell Biology (15)
- Cell Membranes- fluid mosaic model and its functions. Membrane transport, Na-K Pump
- Structure, various models, its function. Cellular transport
- Structure and Function of cells and intracellular organelles (of both prokaryotes and eukaryotes)
- Organelles bounded by double membrane, viz. nucleus, mitochondria, chloroplast etc., endo symbiont theory
- Organelles bounded by single membrane viz. peroxisomes, lysosome, endoplasmic reticulum, Golgi apparatus, vacuoles etc.
- Cytoskeleton- Introduction to microfilaments, microtubules, and intermediate filaments, Nucleation
- Mechanism of cell division including (mitosis and meiosis) and concept of motors

101.2 Structure of Major Biomolecules (15)
- Carbohydrates: Structure and Classification, Glycosaminoglycans, Proteoglycans and Glycoproteins
- Lipids: Structure and Classification, Acylglycerols; Phospholipids, Sphingolipids, Cholesterol and Membranes; Isopienoids, Icosanoids and their biological importance
- Nucleic Acids: RNAand DNA; Different Structural Forms of DNA; Different Types of RNA.

101.3 Metabolism (15)
- Glycolysis, Feeder Pathways for Glycolysis, its regulatory mechanisms, Citric acid cycle and its regulations.
- Oxidative phosphorylation and electron transport chain.
- Digestion, Mobilization, and transport of fats.
- Oxidation of Fatty Acids, Ketone Bodies Biosynthesis of Fatty Acids, Membrane Phospholipids
- Overview of Nitrogen Metabolism, biosynthesis and Degradation of Amino Acids

101.4 Protein Chemistry (15)
- Amino Acids and Peptides; Primary, Secondary, Tertiary and Quaternary Structure.
- Various types of interactions –hydrophobic, hydrogen bonds, entropy, enthalpy etc.
- Protein Folding, Chaperones.
- Anfinsen experiment.
- Allosteric Proteins
PSBI102 SEQUENCE ANALYSIS AND TAXONOMY

102.1 Sequence and Structure Databases (15)
- Major Bioinformatics resources NCBI, EXPASY, EBI
- Literature database eg. PUBMED
- Nucleic acid: GENBANK, EMBL, DDBJ
- Protein structure: domains, motifs
- Protein sequence databases: PIR, SWISSPROT, TrEMBL
- Protein structure databases: NDB, PDB, CCSD.
- Genome Database at NCBI, EBI, TIGR, SANGER
  - Viral genomes
  - Archeal and Bacterial Genomes
  - Eukaryotic genomes with special reference to model organisms (yeast, Drosophila, C.elegans, Rat, Mouse) Human, Plants such as Arabidopsis thaliana, Rice, etc.
  - Repositories for high throughput genomic sequences: EST, STS, GSS

102.2 Composite Databases (15)
- Concepts of derived databases with examples
- History, content and applications of the following databases: Prosite, PRODOM, Pfam, PRINTS, DSSP, INTERPRO, Catalytic site atlas (EBI) etc. with examples

102.3 Pairwise Sequence alignment (15)
- Various file formats for bio-molecular sequences
- Basic Concepts of sequences similarity, Identity and homology
- Definition of homologues, orthologues, Paralogues
- DOT Matrix analysis
- Scoring matrices: Basic concepts of scoring matrix, PAM and BLOSUM series and principles based on which these matrices are derived. Difference between distance & similarity

102.4 Dynamic Programming Algorithm (15)
- Concepts of sequence alignments
- Needleman & Wunch, Smith & Waterman algorithms for Pairwise alignment
- Use of pairwise alignments for analysis of Nucleic acid and Protein
- Sequences and interpretation of results
- Advance sequence analysis methods: QTL, CNP, LOH
**PSBI103 Biostatistics**

103.1 Basics of Mathematics

- Limits, Complete and Partial Differentials of Function, Integration: Definite and Non definite, Logarithms, Ordinary differential equations (first order), Partial differential equations -example from biology, Additions and Subtraction, Dot product and cross product of vectors, Scalar triple product
- Matrix algebra and Eigen Vectors – Addition, Subtraction, Multiplication, transpose inverse and conjugate of matrix, Poisson and Extreme value Distribution
- Fourier Series, Fourier Transform, Laplace Transform

103.2 Statistical Measures (15)

- Mean, mode, median, Variance, standard deviation, coefficient of variation, Raw and Central Moments upto fourth order, measures of skewness and kurtosis
- Introduction to theory of Probability, Conditional Probability, Bayesian Rules,
- Random variable, Distributions of random variables, Binomial, Poisson, Geometric,Normal distribution, Central Limit Theorem. Normal approximation to Binomial and Poisson distributions

103.3 Bivariate Distribution (15)

- Discrete and Continuous. Marginal distributions.
- Conditional distributions independence
- **Linear Regression:**
  - Fitting of a straight line by Least Squares
  - Fitting of curves reducible to linear forms by transformation. Concept of Linear Regression Model with more than one explanatory variables Formulae of (Ordinary Least Square) OLS estimators of regression coefficients and their variances

103.4 An Introduction to statistical inference (15)

- Hypothesis testing: Simple and composite hypotheses ,Null and alternative hypotheses critical region Type I and Type II errors Level of significance p- value, power of a test
- Test of significance viz. Z test, t test, pair t test, chi2tests
- Non parametric tests: Single sample tests—Run test, sign test
- Two sample tests- Run test, sign test median test, , Kruscal-Wallis test
PSBI104 PROGRAMMING LANGUAGE & DATABASES

104.1 Fundamentals of Computing and introduction to Database systems (15)
- Overview and functions of a Computer System
- Memory: Register, buffer, RAM, PROM, EPROM, EEPROM
- Overview of various computer threats viz. Trojan horses, viruses etc.
- Operating systems concepts (Windows, Unix, Linux)
- Software Development Life cycle (SDLC)
- Concepts of various types of Databases
- Data models
- Instances & Schemes
- E – R Model:
  - Entity and entity sets
  - Relations and relationship sets
  - E – R Diagram
  - Reducing E- R diagram to tables
- Network Data model: Basic concepts
- Big data storage: Cloud computing

104.2 Introduction to C (15)
- Introduction to software programming
- Data types in C, int, float char etc
- Control statements, if, else, else if, loops like for, while, do while, Switch, break, Continue etc.
- Arrays (single and double), Sorting and searching method in array (linear & Binary)
- Functions (call by value, call by reference)
- Pointers (pointer to functions, pointer to array, pointer to structure)
- Structure in C and string manipulations
- Basic Input output and File handling etc.

104.3 Introduction to C++ (i) (15)
- Input and Output :cin, cout, escape sequences, include directives and Namespaces, indenting and comments, operator precedence
- Functions
- Function prototypes, built in functions and user defined functions, function overloading, call by reference, call by value, const member functions, inline and recursive functions, math library functions
- Derived data types
- Structure in C++ and string manipulations
- Basic Input output and File handling etc.

104.4 RDBMS (15)
Syllabus for M.Sc. Bioinformatics

- Relational database design; Oracle objects - Tables, Views, Indexes, Sequences; Synonyms, Snapshots
- Databases – table space, Data file, Blocks, Extents, Segments
- Oracle Background Processes, Control files; Oracle memory Management
- Security, Grants, Roles, Privileges
- DBA – Oracle server Manager; Export- Import/ SQL Monitor Backup & recovery( Archiving); Physical storage & Logical storage
- Oracle – Reports – Reports Features; Full Integration with Forms and graphics
- Data Normalization

SEMESTER I
PRACTICAL SYLLABUS

PSBIP101
- Identification of various stages in mitosis and meiosis from permanent slides
- Biochemical estimation of carbohydrates
- Biochemical estimation of proteins

PSBIP102
- Search methods viz. Basic, Advanced and LIMITS w.r.t NCBI, EBI, Swiss-Prot, PDB etc.
- Submission Of Biological Sequences
- Biological Databases: Study of different Biological databases (esp. the ones given below), Format, their distinguishing features, Uses and Applications
- Sequence databases: EMBL, DDBJ, GenBank, UniProt, PIR, TrEMBL
- Domain database: Prosite, PRINT, Pfam, BLOCK
- Structure database: PDB, protein explorer
- Specialized database: KEGG, PUBMED, OMIM

PSBIP103
- Report on Industrial visits – minimum one

PSBIP104
- SQL: Creating databases in Oracle, using various data types and granting privileges, Use of SQL Server and mySQL
- Writing programs on C viz:-
  o Finding prime numbers, Fourier series.
  o Reading a DNA sequence, Translating into RNA sequence.
  o From DNA or RNA to Polypeptide sequence.
- Use of statistical packages such as SPSS or Matlab or R statistics packages etc.
- Population distribution studies, Performing statistical tests such as chi square, ANOVA etc.
PSBI201 FUNDAMENTALS OF BIOLOGY

201.1 Enzyme Kinetics (15)
- Introduction to Enzymes
- Units of activity, coenzymes and metal cofactors.
- Temperature and PH effects
- Michaelis – Menten Kinetics
- Feedback inhibition and activation
- Ribozyme and abzymes

201.2 Concept of Central Dogma / Concept of Gene & Gene Organization (15)
- DNA Replication, various enzymes involved, DNA topology, super coiling of DNA, origin of replication
- Operon model in prokaryotes and eukaryotes, lac operon, trp operon
- Transcription – enzymes involved, sigma factor, DNA binding sites, initiation, elongation and termination
- Translation or protein synthesis – enzymes or factors involved polyribosome
- Gene splicing, post translation modifications etc.

201.3 Cell – Cell communication and Signal transduction (15)
- Signaling Pathways differentiation and programmed cell death (apoptosis)
- Cell Junctions, Cell Adhesion, Extracellular Matrix and integrins
- Cell–Cell interaction and signal transduction, signaling by hormones and
- Neurotransmitters

201.4 Recombinant DNA Technology (15)
- History of rDNA Technology, enzymes involved – restriction endonucleases, ligases etc.
- Cloning vectors – plasmids, bacteriophage vectors for eukaryotes- YAC.
- DNA manipulation–cutting and joining DNA using nuclease and ligases, linkers and adapters
- Cloning strategies, construction of libraries
- Transformation of DNA into host cells, Screening for recombinants, blue white screening
- Application of recombinant DNA technology

PSBI202: SEQUENCE ANALYSIS & TAXONOMY

202.1 Heuristic Methods of Sequence Alignment (15)
- BLAST algorithms
- Psi blast and PHI Blast algorithm
- FASTA algorithms
- Various versions of basic BLAST and FASTA.
- Online use of the tools and interpretation of the results.

202.2 Multiple sequence alignment (15)
- Concept of multiple sequence alignment and various applications of MSA.
- Concept of dendograms and its interpretation.
- Algorithm in MSA and its application
- Profiles, PSSM and its application

202.3 Taxonomy and Phylogeny (15)
- Basic concepts in Systematics, taxonomy and phylogeny
- Nature of data used in taxonomy and Phylogeny
- Definition and description of Phylogenetic trees and various methods
- Clustering method - UPGMA
- Cladistic method - Parsimony
- Phylogenetic Analysis softwares Phylip, PAUP

202.4 Data Mining (15)
- Concept of Data mining and definition of sequence patterns, motifs, blocks
- Various types of pattern representation
- Applying Data mining to global database
- Applying Microarray Data
- Data warehousing

PSBI203: IMMUNOLOGY AND BIOINFORMATICS

203.1 Introduction to Immune systems (15)
- Innate and adaptive immunity in vertebrates
- Antigen processing and presentation
- Contemporary challenges to the immune system
- Autoimmune diseases
- Antibodies
- Immunoglobulin classes and subclasses
- CDR and LDR regions and sequence numbering
- Immunogenetics & immunogenomics
- Hybridoma technology : applications
- Humanization of antibodies by design

203.2 Receptors and MHC (15)
- Membrane receptors for antigen
- The B-cell, T-cell surface receptor- BCR and TCR
The major histocompatibility complex (MHC) its polymorphism, Causes polymorphism, supertypes
Epitopes
Affinity Maturation
Recognition of Antigen by B cells
Neutralizing Antibody

203.3 Immunoinformatics and Vaccinology (15)
- Overview of immunoinformatics.
- Databases & tools: IMGT & IEDB, BciPep, Epitome, CED, Ag-Ab.
- Molecular interactions
- Specificity, characterization
- Ag-Ab: Sequential and conformational epitopes
- MHC- peptide designing tool.
- T cell, B cell epitope prediction tool.
- Categories of vaccines
- Reverse vaccinology
- Rational Vaccine design
- Evolution and escape due to variations

203.4 Patinformatics (15)
- IPR: Patents and reading the patent.
- Patinformatics
- Patent prosecution
- Copyrights

PSBI204 PROGRAMMING LANGUAGE & DATABASES

204.1 SQL (15)
- Select statement
- Data definition statement; Data Manipulation Statements
- Data Control Statement
- Other Database Objects (Views, Sequences, Synonyms); Introduction to Application
- Program Executor; Standard Controls; Data Access Using data Control
- Connecting to Oracle

204.2 Introduction to Linux (15)
- History and design
- Principles of Linux
- Functions of Linux OS
- Basic shell commands
• Understanding Linux file permissions
• Basic script building
• File creation in Linux

204.3 HTML & XML (15)
• Introduction to HTML and XML, basic HTML tags
• Tables, hyperlinks, Image Insertion, marquee image mapping, Frame set
• HTML forms, Get and Post methods
• Basics of XML
• XML syntax and semantics
• XML Programming (in Java)
• XML software & its applications

204.4 Advanced C++ (15)
• Basics of object oriented programming
• Concept of Object, class, Constructor and Destructors
• Inheritance, Data encapsulation
• Polymorphism
• Virtual function and friend function

SEMESTER II
PRACTICAL SYLLABUS

PSBIP201
• Biochemical estimation of lipids
• Biochemical estimation of DNA
• Biochemical estimation of RNA

PSBIP202
• Use of BLAST and its variants (specialy PSI and PHI Blast) for the identification of very similar and divergent sequences
• Use of FASTA and its comparison with BLAST
• Multiple sequence alignment using ClustalW and preparation of simple phylogenetic trees using Tree View etc.

PSBIP203
• Report on Industrial visits – minimum one

PSBIP204
• Linux: Basic Shell scripting: Files and directories (Listing, viewing, copying, making.)
- Using gcc compiler (Programming using C/C++).
- Preparing a sample web pages in HTML and XML
- Writing programs based on advanced C++ viz: Demonstrate hybrid inheritance using C++, Runtime Polymorphism using Virtual Functions, Friend Function, friend class, Function overloading, Constructor overloading, this pointer
SEMESTER III

PSBI301 MOLECULAR MODELLING & DRUG DESIGNING

301.1 Introduction to Molecular Modeling (15)
- Concepts of Molecular modeling, chirality and stereochemistry
- Theory and Practice of Energy minimization, Monte Carlo. Definition of the potential energy surface of a molecule, force field and generic form of a forcefield.
- Differences between molecular mechanics energy and the quantum mechanical energy of a system.
- Differences between Class I, Class II and Class III forcefields.
- Parametrization of a forcefield.
- Molecular Dynamics simulation: Major steps, Simulation models such as coarse grained, bead rod & bead spring models, Ensembles- microcanonical, canonical, isobaric-isothermal & grand canonical ensembles

301.2 Cheminformatics (15)
- Storage & Retrieval methods
- Modeling of small molecules and conformer generation
- Databases of small molecules (PubChem, ZINC etc.)
- Structure activity
- Chemo-informatics tools for drug discovery

301.3 Combinatorial Chemistry (15)
- Analysis and design of combinatorial libraries
- Combinatorial chemistry
- Chemical Database Preparation for Compound Acquisition or Virtual Screening
- Preparing a Dataset for Compound Acquisition using Similarity and Diversity

301.4 Drug Designing (15)
- Physicochemical properties of drugs & Introduction to drug designing
- Concept of receptor/target site
- Lead identification and structure modification
- Concepts in molecular recognition, Drug like properties and associated empirical rules, structure based drug design
- Conformational search technique
- Target structure based Drug Design (Active site identification),
- The identification of novel drug targets (e.g. via the de-orphanisation of G-protein coupled receptors)
- Pharmacophore maps and filters for drug-likeliness and ADME
PSBI302 PROTEOMICS AND GENOMICS

302.1 Tools to study structure of Molecule (15)
- Microscopic techniques
- UV visible spectroscopy,
- X-ray diffraction, Bragg’s law.
- Crystallography.
- IR, ESR and NMR

302.2 Techniques for separation (15)
- Gel-Electrophoresis, PAGE, 2-D electrophoresis
- Gel filtration chromatography, ion-exchange chromatography, HPLC etc.
- Centrifugation techniques

302.3 Detection of known molecule (15)
- Protein/DNA/RNA probes, southern and western blotting, In situ hybridization
- Flow cytometry
- Principles of thermal cyclers, Primer designing
- Polymerization chain reaction, Real time PCR etc. gDNA and cDNA amplification using PCR, screening of gene libraries & their uses
- Introduction to next generation sequencing (Tools like Chip-seq at Expasy)

302.4 Sequencing of nucleic acids and proteins (15)
- Principle of DNA and protein sequencing
- Protein extraction & purification
- Protein separation and identification
- Protein fingerprinting for medicinal plants
- Concepts of post transitional modifications w.r.t to proteins

PSBI303 APPLICATION OF BIOINFORMATICS

303.1 Secondary Structure Prediction of Protein (15)
- Secondary structure: basic principles on which the prediction methods of first, second and third generation are based
- Algorithm of Chou-Fasman, GOR methods, other methods, predicting secondary structures using these methods and analysis
- Concepts in measuring the accuracy of prediction (Q3, segment overlap, Mathew’s correlation coefficient etc.)
303.2 Tertiary Structure Prediction of Protein (15)
- Tertiary structure: theoretical basis of the methods for structure prediction (sequence similarity / identity of target protein with protein of known structure, fundamental of protein folding etc.) and choice of appropriate prediction approach
- Basic principles and protocol of homology modeling, databases of models
- Concepts in 3D structure comparison
- Prediction of structural classes, motifs, folds and domains; HSSP, SCOP, FSSP and CATH.
- Algorithm such as FSSP, VAST, and DALI etc.

303.3 Bioinformatics Perspectives on Human Diseases (15)
- Predictions of genes, promoters, splice sites, regulatory regions: basic principles, application of methods to prokaryotic and eukaryotic genomes and interpretation of results. (Synteny and gene order) Mutations and diseases
- Basic concepts on identification of disease genes; role of bioinformatics –OMIM database, reference genome sequence, integrated genomic maps, gene expression profiling

303.4 Markov and Hidden Markov models (HMM) (15)
- Markov chains: The Markov property, transition probabilities, classification of states, estimation of transition probabilities
- Hidden Markov models: model structure, transition and emission probabilities
- Hidden Markov models for Pair wise alignment: Global and local alignment models
- Generalized pair HMM used in gene prediction

PSBI304 CONCEPTS IN COMPUTING

304.1 Introduction to OOPs concept and JAVA (15)
- An introduction to Object-Oriented Programming
- Object-oriented programming and Java
- Introduction to Java basics

304.2 Core JAVA (15)
- Working with objects, Arrays, Conditionals and Loops
- Creating Classes and Applications in Java, methods
- Java Applets Basics, Graphics, Fonts and Color
- Simple Animation and Threads
- Managing Simple Events and Interactivity
- Creating User Interfaces with AWT
- Modifiers, Access Control and Class Design
- Packages and Interfaces
• Exception, Multithreading, Streams and I/O
• Using Native Methods and Libraries

**304.3 JDBC (15)**
• Introduction to JDBC
• Client Server Application
• Java Drivers
• java.sql Package
• Executing SQL Statements

**304.4 BioJava (15)**
• Installing BioJava
• Symbols, reading sequences
• Basic Sequence Manipulation (DNA to RNA, Reverse Complement, motif as regular expression)
• Translation (DNA to Protein, Codon to amino acid, Six frame translation)
• Proteomics (Calculate the mass and pI of a peptide)
• Sequence I/O (File Formats conversions)
• Locations and Features (Point Location, Range Location, Feature modifications), BLAST and FASTA (BLAST and FASTA Parser, extract information from parsed results)
• Counts and Distributions, Weight Matrices and Dynamic Programming, User Interfaces

**SEMMETER III**

**PRACTICAL SYLLABUS**

**PSBIP301**
• PAGE separation of human serum proteins
• 2D separation of amino acids, plant pigments using paper chromatography
• IR analysis of a modern drug (e.g. Diclofenac Sodium)

**PSBIP302**
• Detection of general signals, regulatory regions and promoter prediction
• Secondary structure prediction using various available tools
• Tertiary structure and function prediction using homology modeling and *ab initio* method
• Validation of predicted structure by SAVS server or verify 3d.
• Visualization of 3D protein structure using Rasmol, VMD, PyMol etc.
PSBIP303
- Industry Oriented Practical Training / Industrially relevant Project work. A report should be submitted at the time of examination

PSBIP304
- Creation of classes and use of different types of datatypes and functions.
- Write programs on interfaces, packages, constructor and function overloading.
- Programs using inheritance, IO streams, file manipulations, exception handling mechanism.
- Programs using Applet, AWT and Frames
- Programs using JDBC with MySql and Oracle
- BioJava practicals w.r.t to mentioned theory syllabus
PSBI401 MOLECULAR MODELLING & DRUG DESIGNING

401.1 Drug Delivery systems (15)
- Types of drug delivery system
- Dendrimers
- Molecularly imprinted polymers (MIPs), MIPs in Drug delivery
- Introduction to Biomedical micro- and nano-technology
- Liposomes: Enzyme-activated, Photo triggering, Thermo sensitive

401.2 Orphan receptors and reverse pharmacology (15)
- Orphan GPCRs
- Identification of Orphan GPCRs
- Reverse Pharmacology
- Reverse Pharmacology for Orphan GPCRs
- Deorphanisation

401.3 QSAR (15)
- Docking technique
- QSAR (Quantitative Structure Activity Relationship)
- 2D QSAR: Linear free energy relationships descriptors for QSAR - experimental and theoretical, Hansch analysis, statistical parameters and their significance, correlation coefficient, cross-validated correlation coefficient, standard error, F-value, boot-strap analysis, randomization
- 3D QSAR: CoMFA and CoMSIA

401.4 Molecular modeling and drug designing Softwares (15)
- Gromocs and NAMD
- Autodock
- HEX
- Discovery studio Visualizer
PSBI402 PROTEOMICS AND GENOMICS

402.1 Global Profiling Technologies (15)
- Technologies used to detect differential expression of genes: DNA Microarray
- Designing a microarray experiment - the basic steps
- Mass spectrometry systems: Liquid chromatography/ tandem
- Mass Spectrometry (LC/MS/MS) Systems

402.2 Genomics (15)
- Prokaryotic and Eukaryotic genome & their expression
- Comparative eukaryotic genomics: chloroplast, mitochondrial and nuclear genomes
- Gene organization and control of gene expression; manipulation and exploitation in biotechnology
- Major techniques in gene manipulation of plants, Genetic manipulation of chloroplasts
- Genetically modified organism and their applications

402.3 Applied Genomics (15)
- siRNA technology
- Microarray databases: GEO (gene expression omnibus), MAML, the benefits of GEO and MAML
- Promises of microarray technology in treating disease.
- Tools for analysis of human genome w.r.t to NCBI database, FISH technique,
- Human genome project, Features identification and process of genome annotation

402.4 Functional Proteomics (15)
- Protein-protein interaction: Experimental based and in silico based predictions (w.r.t tools)
- Yeast two hybrid system
- Study of tools and database for protein-protein interaction: STRING, MIPS

PSBI403 APPLICATION OF BIOINFORMATICS

403.1 Machine Learning Techniques (15)
- Introduction to Support Vector Machines and their applications
- Introduction to Neural Networks Classifying Samples from two populations using Multilayer Perceptron and back propagation
- Using genetic algorithm and Perceptron for feature selection and supervised classification
- Recurrent and feed forward associative neural networks
- Applications of ANN, SVM etc.
- Random Forest
403.2 Algorithms and techniques for Microarray analysis (15)
- Introduction to discrimination or classification concept
- Microarray Data Preprocessing the Data, Measuring Dissimilarity of expression pattern
- Distance and dissimilarity measures Visualizing microarray data, Principal Component analysis, PCA and
- Microarray Data Cluster Analysis and Microarray Data-means Clustering, Hierarchical Clustering, Self Organizing Maps (SOM)

403.3 Medical Informatics (15)
- Ethics, patient confidentiality and data protection
- Sources of medical data
- Clinical data: application of linear based models, search algorithms, ANNs, SVMs to case study data
- EHR, Electronic patient records
- Data protection act
- Databases of medical informatics: VISTA, OPEN EMR, OPEN EHR

403.4 Bioinformatics and systems biology (15)
- The search for biomarkers: use of the genome; use of the proteome; sequence etc. analysis of biomarkers Interrogation and investigation of molecular pathways
- Bioinformatics and systems biology
- Systems biology and modeling, system level understanding of biological systems
- Virtual cell

PSBI404 CONCEPTS IN COMPUTING

404.1 Introduction to Perl and data types (15)
- Arrays and List Data: What Is a List or Array? Literal Representation, Variables, Array Operators and Functions, Scalar and List Context
- Control Structures: Statement Blocks, basic I/O
- Hashes, Hash Variables, Literal Representation of a Hash, using Hashes.
- Subroutines, System and User Functions, The local Operator
- Using Bioperl

404.2 Regular Expressions in Perl (15)
- Concepts of Regular Expressions, Simple Uses of Regular Expressions, metacharacters, quantifiers etc.
- Pattern matching, substitution
- split and join Functions, Formatting Data, Sorting, Transliteration
Syllabus for M.Sc. Bioinformatics

- Finding a Substring, Extracting and Replacing a Substring, Variable-length Parameter Lists, Notes on Lexical Variables

**404.3 File Handling and Directories in Perl (15)**
- File handles and File Tests, Opening and Closing a File handle, die, Using File handles
- Directory Access, Moving Around the Directory Tree, Globbing, Directory Handles, Opening and Closing a Directory Handle, Reading a Directory Handle
- Process Management

**404.4 CGI Perl and Database connectivity (15)**
- System Information: Getting User and Machine Information, Packing and Unpacking Binary Data, Getting Network Information
- Database Manipulation: DBM Databases and DBM Hashes, Opening and Closing DBM Hashes, Fixed-Length Random-Access Databases, Variable-Length (Text) Databases, Win32 Database Interfaces
- CGI Programming: environment variables, CGI.pm Module, Simple CGI Programs, Passing Parameters via CGI, Perl and the Web
- Object oriented Perl: Introduction to modules, Creating Objects
- BioPerl: Introduction, Installation procedures, Architecture, Uses of BioPerl

**SEMESTER IV**
**PRACTICAL SYLLABUS**

**PSBIP401**
- Blood film preparation and Identification of various cells
- Isolation of plasmid DNA and chromosomal DNA
- Restriction digestion of DNA
- Ligation

**PSBIP402**
- Microarray and clinical data analysis
- Use of ANN or SVM as a prediction server
- Target Structure Based Drug Design
- Active site identification
- Docking
- Analysis
- Systems Biology Tool: Pathway Commons
PSBIP403

- Uses of Scalar and Array Variables.
- Uses of common Array Operators, loops
- Reading a sequence data from a file and writing the results to a file
- Opening and closing a Directory Handle, Reading a Directory and other directory manipulation functions.
- Uses of Subroutines (eg. to read FASTA files)
- Uses of Hashes for the genetic code: translating codons into amino acids
- Uses of Regular Expressions
- Extract sequence chains from PDB file
- Uses of CGI.pm Module and Passing Parameters via CGI, Debugging CGI programs
- Installing Bioperl, Uses of Bioperl modules using ppm for sequence manipulation, accessing local Database etc.

LIST OF REFERENCE BOOKS

5. The “Practical Approach” series of books on a variety of topics (published by Oxford University press.) - Available on-line through the electronic library
13. Das and Mookerjee. Outline of biology
14. Roy and De. Cell biology
15. Wilson, & Walker. 1905. Principles and techniques of practical Biochemistry
17. Lanhinger. Principles of biochemistry
19. Plumner. An introduction to practical Biochemistry
22. Zube's Biochemistry. Macmillan
29. Proteomics, Daniel C. Leibler
30. Proteins: Structures and Molecular Principles (2d ed.), TE Creighton
31. Organic spectroscopy, William Kemp
32. Proteome Research: Two-Dimensional Gel Electrophoresis and Detection Methods (Principles and Practice), T. Rabilloud (Editor), 2000, Springer Verlag
45. SQL, PL/SQL: The programming languages of Oracle, Bayross Iyan
46. Learning HTML, Robbins C.
47. Oracle SQL, Kreines David C.
48. Oracle 9i: The complete reference, Loney Kevin, Koch G
49. Linux command by Bryan Pfaffemberger
50. Red Hat Linux by Negus
51. Learning C++ by Boardman
52. Computer Fundamentals by Sinha
53. The Wait Groups "C" Programing Using Turbo by Lafore
54. Let us C – Yashavant Kanetkar
56. Morgan Kaufmann Series in Evolutionary Computation, Morgan Kaufmann
59. Investigating Biological System using Modeling: Strategies and software, Meryl E. Wastney
60. Dale G. Deutsch. Analytical Aspects of Drug Testing, John Wiley and Sons
61. Karel Eckschlager, Klans Danzer, Information Theory in Analytical Chemistry, John Wiley and Sons
64. Higgs, P.G & Attwood. T.K., Bioinformatics and Molecular Evolution, 2005, Blackwell Publishing
69. Proteins: Structures and Molecular Principles (2d ed.), TE Creighton
70. Bioinformatics: Sequence and Genome Analysis, David W. Mount
71. Sequence Analysis in a Nutshell: A Guide to Common Tools and Databases, Scott Markel, Darryl Leon
72. Current Topics in Computational Molecular Biology (Computational Molecular Biology), Tao Jiang, Ying Xu, Michael Zhang (Editors),
74. Bioinformatics: Sequence, Structure and Databases: A Practical Approach (The Practical Approach Series, 236), Des Higgins (Editor), Willie Taylor (Editor)
75. Fundamental Concepts of Bioinformatics, Dan E. Krane Michael L. Raymer
76. Introduction to Bioinformatics Algorithms, Neil C. Jones, Pavel Pevzner
77. Data Mining: Multimedia, Soft Computing, and Bioinformatics, Mitra, Sushmita Acharya, Tinku
78. Statistical Methods in Bioinformatics: An Introduction (Statistics for Biology and Health), Warren Ewens, Gregory Grant
Syllabus for M.Sc. Bioinformatics

79. Microarrays for an Integrative Genomics (Computational Molecular Biology), Isaac S. Kohane, Alvin Kho, Atul J. Butte
82. SQL, PL/ SQL: The programming languages of Oracle, BayrossIyan
83. Mastering Perl for Bioinformatics, James D. Tisdall
84. Genomic Perl: From Bioinformatics Basics to Working Code, Rex A.Dwyer
85. Beginning Perl for Bioinformatics, James Tisdall
86. Developing Bioinformatics Computer Skills, Cynthia Gibas, Per Jambeck, 2001
87. Kuby Immunology, Thomas J. Kindt, Richard A. Goldsby, Barbara A. Osborne, Janis Kuby

Minimum Infrastructure required for running the course

<table>
<thead>
<tr>
<th>Sr. No.</th>
<th>Item</th>
</tr>
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<tbody>
<tr>
<td>a.</td>
<td>Laboratory Space &amp; Furniture – of ~ 900 sqft carpet area with about 6 sqft table space /student (Batch of 20 students)</td>
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<td>b.</td>
<td>Air-conditioned Room</td>
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<td>c.</td>
<td>Library Facilities</td>
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<tr>
<td>d.</td>
<td>Computational Facilities – 42 computers ,softwares</td>
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<td>e.</td>
<td>Internet Facilities</td>
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<td>f.</td>
<td>Water &amp; Electricity</td>
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<td>g.</td>
<td>Instrumental Support</td>
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Recommended equipment and accessories

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<thead>
<tr>
<th>Sr. No</th>
<th>Equipment</th>
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<tbody>
<tr>
<td>1.</td>
<td>Agarose and PAG Electrophoresis systems</td>
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<td>2.</td>
<td>Analytical Balance</td>
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<td>3.</td>
<td>Autoclave</td>
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<td>4.</td>
<td>Capillary Electrophoresis (with PDA &amp; UV detectors)</td>
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<td>5.</td>
<td>Computers</td>
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<td>6.</td>
<td>Deep Freezer</td>
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<td>Dissolution Test Apparatus</td>
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<td>8.</td>
<td>Fourier Transform Infrared Spectrometer</td>
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<td>LC/MS/MS</td>
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<td>pH - meter</td>
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<td>11.</td>
<td>Refrigerators</td>
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<td>12.</td>
<td>Top pan balance</td>
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<td>13.</td>
<td>Ultrasonic bath with Temperature control</td>
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<td>14.</td>
<td>UV-Vis Scanning Spectrophotometer</td>
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<td>15.</td>
<td>Water Distillation Apparatus</td>
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<td>16.</td>
<td>Water Purification System</td>
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<tr>
<td>17.</td>
<td>Light microscope</td>
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