

**UNIVERSITY OF MUMBAI**



**Syllabus for the M.Sc. Part - I &II**  
**Program: M.Sc.**  
**Course: Bioinformatics**

(Credit Based Semester and Grading System with  
effect from the academic year  
2012-2013)



## **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

## **Programme Overview**

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.

## **Fee Structure**

Rs.45, 805 per year

**Note:** If there is a change in the examination fee structure then the excess amount will be collected afterwards.

## **No of Lectures**

120 lectures/paper including seminar, assignments and presentations.

## **No of Practicals**

4 practicals of four periods each per week.

## **Duration**

2 Years of full time course.

## **No students**

20 per batch

## **R. 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.

## **Mark-list**

---

The mark-list of the students must indicate titles of papers in the syllabus.

### **Scheme of Examination**

---

**1. Each course will have:**

Term work 40% (internal assessment) and 60% external/University. Written examination of TWO hours and Practical examination (wherever applicable) of six hours duration. All examinations will be held at the end of each semester and will be conducted by the University as per the existing norms.

**2. Term work (40%) and University examination (60%) will be separate heads of passing.**

**3. Standard of passing**

- The learners shall have to obtain a minimum of 40 % marks in aggregate to qualify the each course where the course consists of internal assessment and semester end examination.
- The learners shall obtain a minimum of 40 % marks (i.e. 16 out of 40) in the internal assessment and obtain a minimum of 40 % marks (i.e. 24 out of 60) in semester end examination.
- To pass the course and minimum grade C shall be obtained in each project wherever applicable in the particular semester.

**4. A teacher may select a variety of procedures for internal (Continuous) assessment Examination such as: 40  
marks**

- i. Short Quizzes / Viva / Presentations;
- ii. Assignments / Seminars / Laboratory Journal Work ;
- iii. Extension/Field/experimental Work;
- iv. Research Project by individual students or group of students; or
- v. An open Book Test / Review of Research Papers (with the concerned teacher deciding what books / scientific publications / research papers / Chapters from Reference books are to be allowed for this purpose.)
- vi. Two periodical test/case studies/on-line or combination of these
- vii. Overall conduct as a responsible student, mannerism and exhibition of leader ship qualities in organizing co-curricular activities and attendance.

**5. End semester examination 60 % 60 marks**

- Duration – these examinations shall be of two hours duration.
- Questions paper pattern:-

There shall be four questions each of 15 marks.

All questions shall be compulsory with internal choice within the questions. Question may be sub divided into sub- questions a,b,c,d &e only and allocation of marks depends on the weightage of the topic

#### 6. Method to carry forward the marks

- A learner who passes in the internal assessment but fails in the semester end examination of the course shall reappear for the semester end examination of that course. However his/her marks of the internal assessment shall be carried over and he/she shall be entitled for grade obtained by him/ her on passing.
- A learner who fails in the internal assessment but passes in the semester end examination of the course shall resubmit and reappear for the internal assessment on the form of projects of that course. However his/her marks of the semester end examination shall be carried over and he/she shall be entitled for grade obtained by him/ her on passing.
- The evaluation of internal assessment for students who fails and reappear will consist of one project of 40 marks which will be divided into 20 marks for the documentation of the project, 10 marks for the presentation and 10 marks for the viva.

#### 7. ATKT

- A student shall be allowed to keep term for semester II irrespective of the number of heads of failure on the semester I.
- A student shall be allowed to keep term for semester III if she /he passes each of semester I and semester II

OR

- A student fails in not more than two courses semester I and semester II taken together.
- A student shall be allowed to keep term for semester IV irrespective of the number of heads of failure on the semester III. However the student has to pass each of semester I and semester II in order to appear for semester IV.
- A student shall be allowed to keep term for semester V if she /he passes each of semester I and semester II , semester III , semester IV

OR

- A student shall pass semester I and semester II and fail in not more than two courses semester II and semester IV taken together.
- A student shall be allowed to keep term for semester VI irrespective of the number of heads of failure on the semester V.

- The results of semester VI shall be kept in abeyance until the student passes each of semesters I and semester II, semester III, semester IV and semester V.

#### 8. Additional examinations

Additional class test or assignment for internal assessment:

- There will be one additional class test or assignment for those who have remained absent on valid ground, in such a case student will be allowed to appear for additional class test or assignment by the head of the institution after following necessary formalities.

Semester end examination:

- There will be one additional examination for semester I, II, III and IV for those who have failed or remained absent.
- The absent student will be allowed to appear for the examination by the head of the institution after following necessary formalities.
- This examination will be held 20 days after the declaration of results but not later than 40 days.

#### 9. Project evaluation (if applicable)

- A student who passes in all the courses but does not secure minimum grade of C in project as applicable has to resubmit a fresh project till he/she secures a minimum of grade C.
- The credits and grade points secured by him/her in the other courses will be carried forward and he/she shall be entitled for grade obtained by them on passing.
- The evaluation of project and viva –voce examination shall be by awarding grade in the seven point scale.
- A student shall have to obtain minimum of grade C (or its equivalent marks) in project evaluation and viva-voce taken together to obtain 40 % marks in project work.

#### 10. Conversion of marks to grade and calculations of GPA

##### Abbreviations and formulas used

G: grade    GP: grade points    C: credits    CP: credit points  
 CG: credits X grades (product of credits & grades)  
 $\Sigma$ CG: sum of product of credits & grades  
 $\Sigma$ C: sum of credit points    GPA:  $\frac{\Sigma CG}{\Sigma C}$

SGPA: semester grade point average shall be calculated for individual semester.  
(It is also designated as GPA)

CGPA: cumulative grade point average shall be calculated for the entire course by taking all semesters taken together.

11. The system of evaluation will be as follows; Each term work module mentioned above will be evaluated in terms of marks first and then to letters grades as shown in the following table.

<b>Marks Out Of 100</b>	<b>Grade</b>	<b>Grade Point</b>
70 and above	O	7
60 to 69.99	A	6
55 to 59.99	B	5
50 to 54.99	C	4
45 to 49.99	D	3
40 to 44.99	E	2
39.99 and below	F	1

12. 'B' Grade is equivalent to at least 55% of the marks as per circular No. UGC-1298/[4619] UNI-4 dated December 11,1999.
13. The formula for GPA will be based on Weighted Average. The final GPA will not be printed unless a student passes courses equivalent to minimum 72 credits for B.Sc. and 96 credits for M.Sc.
14. A seen point grade system [guided by the Government of Maharashtra Resolution No.NGV-1298/[4619]UNI.4 dt. December 11, 1999] will be followed. The corresponding grade table is detailed in 09 above.
15. If the GPA is higher than the indicated upper limit in the three decimal digit then the student be awarded higher final grade (e.g. a student getting GPA of 3.491 be awarded 'B')
16. For grade improvement minimum 24 credits (two papers) should be taken by the student for grade improvement. Grade improvement programme will be implemented at the end of the first semester after declaration of the final result. A student can opt for the grade improvement programme only after the declaration of final semester examination.
17. Grade cards
- The grade cards will be printed along with the marks shown for all the concerned courses.



- The grade cards will be issued to all the learners with credits earned and all the remarks
- The SGPA will be calculated only for the learners who will qualify in all the courses and accordingly the grade will be awarded to them.
- The result gazette and the format of the grade cards will be uniform for all the colleges/institutions.

## SYLLABUS IN BRIEF

### M.Sc Part I

60 lectures for each paper per semester  
(Including Seminars, Assignments and Presentations)

- Four Theory Papers.
- Three Practicals
- Industrial Visits (PSBIP103) and (PSBIP203)

### M.sc Part II

60 lectures for each paper per semester  
(Including Seminars, Assignments and Presentations)

- Four Theory Papers
- Three Practical
- One Project (PSBIP303) and (PSBIP403)

### Distribution of Credits -

#### Semester I

	Code	Lectures	Credits	Code	Practical	Credits
Fundamentals of Biology	PSBI101	60	4	PSBIP101	60	2
Proteomics & Genomics	PSBI102	60	4	PSBIP102	60	2
Biostatistics	PSBI103	60	4	PSBIP103	60	2
Programming Language & Databases	PSBI104	60	4	PSBIP104	60	2
TOTAL		240	16		240	8
TOTAL CREDITS			24			

\*Lectures allotment includes periods for seminar & presentations.

\*Units equally distributed between two terms.

**Semester - II**

Paper	Code	Lectures	Credits	Code	Practical	Credits
Fundamentals of Biology	PSBI201	60	4	PSBIP201	60	2
Proteomics & Genomics	PSBI202	60	4	PSBIP202	60	2
Biostatistics	PSBI203	60	4	PSBIP203	60	2
Programming Language & Databases	PSBI204	60	4	PSBIP204	60	2
TOTAL		240	16	-	240	8
TOTAL CREDITS			24			

**Semester - III**

Paper	Code	Lectures	Credits	Code	Practical	Credits
Molecular modeling & drug designing	PSBI301	60	4	PSBIP301	60	2
Sequence analysis & taxonomy	PSBI302	60	4	PSBIP302	60	2
Application of Bioinformatics	PSBI303	60	4	PSBIP303	60	2
Concepts in computing	PSBI304	60	4	PSBIP304	60	2
TOTAL		240	16	-	240	8
TOTAL CREDITS			24			

**Semester IV**

Paper	Code	Lectures	Credits	Code	Practical	Credits
Molecular modeling & drug designing	PSBI401	60	4	PSBIP401	60	2
Sequence analysis & taxonomy	PSBI402	60	4	PSBIP402	60	2
Application of Bioinformatics	PSBI403	60	4	PSBIP403	60	2
Concepts in computing	PSBI404	60	4	PSBIP404	60	2
TOTAL		240	16	-	240	8
TOTAL CREDITS			24			

\*Lectures allotment includes periods for seminar & Presentations.

\*Units equally distributed between two terms.

**MODULAR DISTRIBUTION OF TOPICS**  
**M.Sc PART**

<b>FIRST SEMESTER</b>	<b>SECOND SEMESTER</b>
<b>PSBI101: Fundamentals of Biology</b>	<b>PSBI201: Fundamentals of Biology</b>
101.1 Cell Biology	201.1 Enzyme Kinetics
101.2 Structure of Major Biomolecules	201.2 Concept of central dogma/ gene and gene organization
101.3 Carbohydrate Metabolism	201.3 Cell-Cell communication and signal transduction
101.4 Integration of Metabolic Pathways and Bioenergetics	201.4 Recombinant DNA technology
<b>(PSBI102) Proteomics &amp; Genomics</b>	<b>(PSBI202) Proteomics &amp; Genomics</b>
102.1 Tools to study Structure of molecules	202.1 Global profiling technologies
102.2 Techniques for separation	202.2 Genomics
102.3 Detection of known molecules	202.3 Applied Genomics
102.4 Sequencing of Nucleic acids and proteins	202.4 Functional proteomics
<b>(PSBI103) Biostatistics</b>	<b>(PSBI203) Biostatistics</b>
103.1 Basics of Mathematics	203.1 Stochastic Process
103.2 Probability(i)	203.2 Analysis of variance and Regression
103.3 Probability(ii)	203.3 Analysis of one and multiple DNA
103.4 An Introduction to statistical inference	203.4 BLAST
<b>(PSBI104) Programming Language &amp; Databases</b>	<b>(PSBI204) Programming Language &amp; Databases</b>
104.1 Fundamentals of Computing	204.1 SQL
104.2 Introduction to operating systems	204.2 Electronic Document Management
104.3 Introduction to Database Systems	204.3 Introduction to C
104.4 RDMS	204.4 C++

## MODULAR DISTRIBUTION OF TOPICS

<b>THIRD SEMESTER</b>	<b>FOURTH SEMESTER</b>
<b>(PSBI301) Molecular modeling &amp; Drug designing</b>	<b>(PSBI 401) Molecular modeling &amp; Drug designing</b>
301.1 Introduction to Molecular Modeling	401.1 Drug Delivery systems
301.2 Cheminformatics	401.2 Orphan receptors & reverse pharmacology
301.3 Combinatorial Chemistry	401.3 QSAR
301.4 Drug Designing	401.4 Molecular modeling & drug designing softwares
<b>(PSBI302) Sequence analysis &amp; taxonomy</b>	<b>(PSBI402) Sequence analysis &amp; taxonomy</b>
302.1 Sequence and Structure Databases	402.1 Heuristic Methods of Sequence alignment i.
302.2 Derived Databases	402.2 Multiple Sequence Alignments
302.3 Pair wise sequence alignment	402.3 Taxonomy and Phylogeny
302.4 Dynamic programming Algorithm	402.4 Data mining
<b>(PSBI303) Application of Bioinformatics</b>	<b>(PSBI403) Application of Bioinformatics</b>
303.1 Secondary Structure Prediction of Protein 1.	403.1 Machine Learning Techniques
303.2 Tertiary Structure Prediction of Protein	403.2 Algorithms and techniques for Microarray analysis
303.3 Bioinformatics Perspectives on Human Diseases	403.3 Medical Informatics
303.4 Markov and Hidden Markov Models	403.4 Bioinformatics & systems biology
<b>(PSBI304) Concepts in computing</b>	<b>(PSBI404) Concepts in computing</b>
304.1 HTML & XML	404.1 Introduction to Perl and data types
304.2 Introduction to OOPs concept and JAVA	404.2 Regular Expressions in Perl
304.3 Core JAVA	404.3 File Handling and Directories in Perl
304.4 JDBC	404.4 CGI Perl and Database connectivity

## **SEMESTER I**

---

### **PSBI101 FUNDAMENTALS OF BIOLOGY**

#### **101.1 Cell Biology (15)**

- Cell Membranes- Structure, various models, its function
- Structure and Function of cells and intracellular organelles (of both prokaryotes and eukaryotes)
- Organelles bounded by double membrane viz. nucleus, mitochondria, chloroplast etc., endosymbiont theory
- Organelles bounded by single membrane viz. peroxisomes, lysosome, endoplasmic reticulum, Golgi apparatus, vacuoles etc.
- Cytoskeleton
- Mechanism of cell division including (mitosis and meiosis) and its regulation.
- Cellular transport and concept of motors

#### **101.2 Structure of major Biomolecules (15)**

- Carbohydrates Monosaccharides, Disaccharides and Polysaccharides, Glycoconjugates
- Nucleic acids: Bases, nucleotides, RNA and DNA. Different structural form of DNA, denaturation and renaturation of DNA
- Proteins: Amino acids and peptides; Primary, secondary, tertiary and quaternary structures
- Proteoglycans, Glycoproteins, and Glycolipids

#### **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 Integration of metabolic Pathway & bioenergetics (15)**

- Hormonal Regulation of Fuel Metabolism
- Bioenergetics and Thermodynamics
- Phosphoryl Group Transfers and ATP
- Biological Oxidation-Reduction Reactions

### **PSBI102 PROTEOMICS AND GENOMICS**

### **102.1 Tools to study structure of Molecule (15)**

- Microscopy visible and UV
- X- ray diffraction, Bragg's law
- Crystallography
- IR, ESR and NMR

### **102.2 Techniques for separation (15)**

- Gel-Electrophoresis, PAGE, 2-D electrophoresis
- Gel filtration chromatography, ion-exchange chromatography, HPLC etc.
- Centrifugation techniques

### **102.3 Detection of known molecule(15)**

- Protein/DNA/RNA probes, southern and western blotting, In situ hybridization
- Flow cytometry
- Microscopic techniques
- Principles of thermal cyclers, Primer designing
- Polymerization chain reaction, Real time PCR etc.
- DNA and cDNA amplification using PCR, gene libraries & their uses

### **102.4 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
- Endogenous peptides and concepts of post transitional modifications

## **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

### **103.2 Probability (i) (15)**

- Random variable, Probability distribution
- Important discrete distribution such as Bernoulli, Binomial, Uniform, Geometric, Negative binomial, Poisson
- Moments – mean , Variance
- Probability generating function
- Continuous random variable, Chebyshev's Inequality, moments
- Important continuous distribution



Uniform, Normal, Exponential, Gamma, Beta, Normal approximation to various distributions

- Moment generating function

### **103.3 Probability (ii) (15)**

- Multiple Random variables: Discrete and continuous
- Independence and dependence
- Marginal and conditional, Expected values
- Asymptotic distribution
- Derived R.V: Sums, Averages, Minimum, and Maximum.
- Introduction to P- Values, P- Values for various distributions
- Large observations and rare events
- Order statistics

### **103.4 An Introduction to statistical inference (15)**

- Classical and Bayesian methods
- Classical Estimation Methods: Unbiased Estimators, Maximum likelihood Estimators etc
- Classical hypothesis testing: t, F Z and x square, general Principal, like hood Estimators etc.
- Non parametric tests
- Bayesian approach to estimation
- Bayesian approach to testing
- Multiple testing

## **PSBI104 PROGRAMMING LANGUAGE & DATABASES**

### **104.1 Fundamentals of Computing (15)**

- Overview and functions of a Computer System
- History of Computer: Evolution, classification
- Storage Devices
- Memory: Register, buffer, RAM, PROM, EPROM, EEPROM
- Overview of various computer threats viz. Trojan horses, viruses etc.
- Fundamentals of Computer Graphics and Visualization
- Computer security or network security

### **104.2 Introduction to operating systems (15)**

- Operating systems concepts
- Windows
- UNIX/LINUX
- Internet usage and WWW
- Computer networking /LAN/WAN
- IP address
- Software Development Life cycle (SDLC)

### **104.3 Introduction to Database Systems (15)**

- 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
- Multimedia Databases – Basic concepts and Application
- Text Databases
- Introduction to distributed Database Processing, Data security

#### **104.4 RDMS (15)**

- 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

### **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**

- 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)

#### **PSBIP103**

- Report on Industrial visits – minimum TWO

#### **PSBIP104**

- Introduction and overview of general computer operation (Windows and Linux platforms). Use of various search engines, email etc.
- Creating databases in SQL and Oracle, using various data types and granting privileges
- Use of statistical packages such as SPSS, Matlab etc.
- Population distribution studies
- Performing statistical tests such as chi square, ANOVA etc

## SEMESTER II

---

### **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, bacteriophages vectors for eukaryotes- YAC
- DNA manipulation–cutting and joining DNA using nucleases 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 PROTEOMICS AND GENOMICS**

### **202.1 Global Profiling Technologies (15)**

- Technologies used to detect differential expression of genes
- Mass spectrometry systems: liquid chromatography/tandem mass spectrometry (LC/MS/MS) systems
- Microarray technology

### **202.2 Genomics (15)**

- Prokaryotic and Eukaryotic genome & their expression
- Comparative microbial genomics: microbial circular and linear genomes, mega-plasmids, reduced genomes case studies to include *Campylobacter jejuni*, *Salmonella*, *E. coli*
- 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.

### **202.3 Applied Genomics (15)**

- DNA Microarray, Designing a microarray experiment - the basic steps
- 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, Alternative-splicing models, Probing with EST's
- Human genome project, Features identification and genome annotation

### **202.4 Functional proteomics(15)**

- Protein-protein interaction
- Yeast two hybrid system
- Protein-protein interactions in intact mammalian cells (MAPPIT)

## **PSBI203 BIOSTATISTICS**

### **203.1 Stochastic Process (15)**

- Poisson Process
- Markov chains
- Transition Probabilities
- M.C with Absorbing state and no absorbing state
- Stationary distributions
- Modeling

### **203.2 Analysis of variance and Regression (15)**

- One-way classification
- Two – way classification model with and without interaction effects, one observation per cell and r observations per cell
- Multiway classification model
- Regression analysis

### **203.3 Analysis of one and multiple DNA (15)**

- Shot gun sequencing, Modeling DNA, Modeling Signals in DNA: weight matrices, Independence, Mearkov depence, maximal depence decomposition
- Long repeats, R- Scans, Analysis of Patterns, Overlap Counted: General comments, distance between recurrences; number of recurrences
- Generalizations: arbitrary Nucleotide Probabilities; arbitrary word Length
- Two Sequences: frequency comparisons
- Alignments, Simple tests for significant. Similarity in an Alignment. Alignment algorithms for two sequences: Gaped global comparisons and Dynamic Programming Algorithms
- Fitting one sequence into another Using Gap model, other Gap models.
- Protein sequences and substitution Matrices

### **203.4 BLAST (15)**

- Comparison of two Aligned sequences: Ladder points and Excursions, Parameter Calculation, Choice of a score, bounds for P Values, Normalized and the bit score, Number of high scoring Excursions, Karlin-Atlschual Sum statistics
- Comparison of a Query Sequence against database
- Minimum significance length
- BLAST :Parametric or non parametric Test
- Relation to Sequential Analysi

## **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
- Development using Visual Basic; Working with code and forms; Variables, Procedures and controlling
- Program Executor; Standard Controls; Data Access Using data Control Connecting to Oracle / SQL Database using Visual Basic

### **204.2 Electronic Document Management (15)**

- Electronic Acquisition of data
- Management of data in computers
- Electronic Data Validation and regulatory requirements

- Electronic signature & its regulation
- Generating reports using computers
- Regulatory requirements and Data validation

### **204.3 Introduction to C (15)**

- Introduction to software programming
- Data types in C, *int, flo char* etc.
- Control statements, *if, else, else if*, loops like *for, while, do while, Swich, break, continue* etc.
- Arrays (single and double), Sorting and searching method in array (liner & 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.

### **204.4 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 & RNA

### **PSBIP202**

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

### **PSBIP203**

- Report on Industrial visits – minimum TWO

### **PSBIP204**

- Writing programs based on C and C++
- Finding prime numbers, Fourier series
- Reading a DNA sequence, Translating into RNA sequence
- From DNA or RNA to Polypeptide sequence
- Use of SQL Server and mySQL

- Writing Basic SQL select queries

## **SEMESTER III**

---

### **PSBI301 MOLECULAR MODELLING & DRUG DESIGNING**

#### **301.1 Introduction to Molecular Modeling (15)**

- Concepts of Molecular modeling
- Theory and Practice of Energy minimization, Monte Carlo and Molecular Dynamics simulations
- Protein structure Prediction an overview. Introduction to *ab-initio* structure prediction
- Fold family recognition or threading approaches
- Homology modeling

#### **301.2 Cheminformatics (15)**

- Storage & Retrieval methods
- Modeling of small molecules
- Structure activity

#### **301.3 Combinatorial Chemistry (15)**

- Analysis and design of combinatorial libraries
- Chemo-informatics tools for drug discovery
- 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), Characterization of target site
- Small molecule libraries and the identification of novel drug targets (e.g. via the de-orphanisation of G-protein coupled receptors)

### **PSBI302 SEQUENCE ANALYSIS & TAXONOMY**

### **302.1 Sequence and Structure Databases (15)**

- Major Bioinformatics resources NCBI, EBI, ExPASy
- Open access bibliographic resources and literature Databases
- Nucleic acid : GenBank, EMBL, DDBJ
- Protein sequence: SWISS – PROT, TrEMBL, PIR
- 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
  - PDB, NDB, CCSD

### **302.2 Derived Databases (15)**

- Concepts of derived databases with examples
- History, content, usage, and applications of the following databases  
Prosite, PRODOM, Pfam, PRINTS  
CATH, SCOP, DSSP, FSSP, DALI etc with examples

### **302.3 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 Search

### **302.4 Dynamic Programming Algorithm (15)**

- Concepts of sequence alignments
- Needleman & Wuncsh, Smith & Waterman algorithms for Pairwise alignments
- Use of Pairwise Alignments for analysis of Nucleic acid and Protein Sequences and interpretation of results

## **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
- 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 Pairwise alignment: Global and local alignment models
- Generalized pair HMM used in gene prediction

## **PSBI304 CONCEPTS IN COMPUTING**

### **304.1 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

### **304.2 Introduction to OOPs concept and JAVA (15)**

- An introduction to object-oriented programming
- Object-oriented programming and Java
- Introduction to Java basics

### **304.3 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
- Using Biojava

#### **304.4 JDBC (15)**

- Introduction to JDBC
  - Client Server Application
  - Java Drivers
  - java.sql Package
- Executing SQL Statements

### **SEMESTER III PRACTICAL SYLLABUS**

#### **PSBIP301**

- Different types of search engines & important sites viz NCBI, EBI, Swiss-Prot, PDB etc.
- 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, use of Rasmol, protein explorer
- Specialized database: KEGG, PUBMED, OMIM

#### **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
- Visualization of 3D protein structure using Rasmol, VMD etc.

#### **PSBIP303**

- Industry Oriented Practical Training / Industrially relevant Project work. A report should be submitted at the time of examination.

### **PSBIP304**

- Preparing a sample WebPages for self in HTML (self website)
- Writing simple programs in Java like finding prime numbers, Fourier series etc.
- Java applets and servelets
- JDBC: connecting to a database (mySQL)

---

## **SEMESTER IV**

---

### **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)**

- QSAR (Quantitative Structure Activity Relationship)
- 2D QSAR
- 3D QSAR
- Docking technique

#### **401.4 Molecular modeling and drug designing softwares (15)**

- Dock
- Autodock
- HyperChem
- CDS etc

### **PSBI402 SEQUENCE ANALYSIS & TAXONOMY**

#### **402.1 Heuristic methods of sequence alignment (15)**

- BLAST algorithms

- PSI BLAST algorithm
- FASTA algorithms
- Various versions of basic BLAST and FASTA. Online use of the tools and interpretation of the results

#### **402.2 Multiple sequence alignment (15).**

- Concept of Multiple Sequence Alignment and various approaches of MSA
- Algorithm of CLUSTALW and its application
- Concepts of dendograms and its interpretation

#### **402.3 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

#### **402.4 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

### **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.

#### **403.2 Algorithms and techniques for Microarray analysis (15)**

- Introduction to Bayesian statistics, 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)

- Identifying genes: expressed usually in a sample, Expressed significantly in population, Expressed differently in two populations

#### **403.3 Medical Informatics (15)**

- Ethics, patient confidentiality and data protection
- Sources of medical data
- Populations: ordination and population characterization: error and variance in populations
- Clinical data: application of linear based models, search algorithms, ANNs, SVMs to case study data

#### **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

### **PSBI404 CONCEPTS IN COMPUTING**

#### **404.1 Introduction to Perl and data types (15)**

- Introduction: What is Perl? Why use Perl in Bioinformatics? History of Perl, Availability, Support, Basic Concepts
- Scalar Data: What Is Scalar Data?, Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Operators and Functions
- 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
- 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 bioper

### **SEMESTER IV PRACTICAL SYLLABUS**

#### **PSBIP401**

- Use of BLAST and its variants (especially PSI-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.

#### **PSBIP402**

- Microarray and clinical data analysis
- Use of ANN or SVM as a prediction server
- Target Structure Based Drug Design
- Active site identification
- Characterization of target site
- Docking
- Analysis

#### **PSBIP403**

- Industry Oriented Practical Training / Industrially relevant Project work. A report should be submitted at the time of examination.

#### **PSBIP404**

- Using perl for writing small scripts
- Reading a DNA sequence, Translating into RNA sequence
- From DNA or RNA to Polypeptide sequence etc.
- Using Hashes
- Creating dynamic web pages using CGI perl
- Retrieving and writing to databases (mySQL) using perl database connectivity
- Installing and using Bioperl

## LIST OF REFERENCE BOOKS

---

1. Alberts. Molecular Biology of cell. Garland Pub.
2. Kaufman. Handbook of molecular and cellular methods in biology and science. CRC press.
3. Boyer. 1999. Concepts of biochemistry. Thomson
4. *Principles and Techniques of Practical Biochemistry*. Wilson and Walker (6<sup>th</sup> Ed 2005) Cambridge Scientific Press ISBN-0-521-53581-6
5. The "Practical Approach" series of books on a variety of topics (published by Oxford University press.) - available on-line through the electronic library.
6. Alberts. Molecular Biology of cell. Garland Pub.
7. Kaufman. Handbook of molecular and cellular methods in biology and science. CRC press.
8. Boyer. 1999. Concepts of biochemistry. Thomson Fundamentals of Enzymology: The Cell and Molecular Biology of Catalytic Proteins, 3rd Edition
9. Starr, 1998, Cell biology and genetics. Thomson Harmes. Biochemistry 2nd Ed. Viva Books.
10. Fisher. Chemistry for biologists. Viva Books
11. Turner. Molecular Biology. Viva Books.
12. Enger. Concepts in biology Tata McGraw-Hill.
13. Das and Mookerjee. Outline of biology.
14. Roy and De. Cell biology
15. Wilson, & Walker. 1905. Principles and techniques of practical Biochemistry
16. Davidson V.L. & Sittman. 1993. Biochemistry.
17. Lanhinger. Principles of biochemistry
18. Stryer - Biochemistry. W.H. Freeman & Co.
19. Plummer. An introduction to practical Biochemistry.
20. J.Jayraman. Lab Manual in Biochemistry
21. Cohn and Stumph. Outline of Biochemistry. Wiley eastern.
22. Zube's Biochemistry. Macmillan
23. Blel & Odian. 1999. Organic and Biochemistry
24. Tinoco. and other. 1995. Physical chemistry Principles and applications in biological Sciences. Prentice-Hall
25. Paul H. Teesdale & others 2001. Eventual of Biological chemistry J/W
26. Voet Donald. 1999. Fundamentals of Biochemistry, J/W.
27. Switzer and Gautv. 1995. Experimental Biochemistry WH Freeman.
28. Principles of Protein structure, Schultz, G. E., and Schirmer, R. H. Dr. Shakti Sahi
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

33. Introduction to Protein Architecture: The Structural Biology of Proteins, M. Lesk, 2001, Oxford University Press
34. Ewens Warren J. and Grant Gregory R.(2004): Statistical Methods in Bioinformatics, Sringer.
35. Gene H. Golub, Chaless F. Van Loan(1996): Matrix Computation,3rd Ed.
36. James Stewart(2001) : Calculus: Early Transcendent
37. Ben hui Liu (2007) : Statistical Genomics : linkage,Mapping & QTL Analysis
38. Lange Kenneth (2003): Mathematical and Statistical Methods for Genetic Analysis,2nd Edition, Springer
39. Lange Kenneth (2005): Applied Probability, 1st Edition, Springer.
40. Durrett Rick (2001): Essentials of stochastic Processes, Springer.
41. Higgins James J.and Keller-McNulty Sallie (1995): Concepts in Probability and Stochastic modeling,Duxbury.
42. Wackerly,Dennis D.and Mendenhall III William and Scheaffer Richard L. (2002): Mathematical statistics with Applications,6th Edition,Duxbury.
43. Karlin S. and Taylor H.(1975): A first course in Stochastic Processes, Academic Press
44. Norris J.R.(1997): Markov chains,Cambridge University Press
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
55. G. Thomas (2000) Medicinal Chemistry: An Introduction, Wiley
56. Morgan Kaufmann Series in Evolutionary Computation, Morgan Kaufmann
57. Kenneth W. Goodman (1998) Ethics, Computing and Medicine: Informatics and the Transformation of Health Care. Cambridge University Press.
58. R. B. Silverman (2004) The Organic Chemistry of Drug Design and Drug Action, 2<sup>nd</sup> Edition, Academic Press.
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
62. Principles of Protein structure, Schultz, G. E., and Schirmer, R. H. Dr. Shakti Sahi
  
63. Westhead, D.R., Parish, J.H. & Twyman, R.M., Instant Notes: Bioinformatics, 2002, BIOS
64. Higgs, P.G & Attwood. T.K., Bioinformatics and Molecular Evolution, 2005, Blackwell Publishing.



65. Campbell, A.M & Heyer, L.J., Discovering genomics, proteomics and bioinformatics, 2003, Benjamin Cummings.
66. Mount, D.W., Bioinformatics sequence and genome analysis, 2nd Ed., 2004 Cold Spring Harbour Laboratory Press.
67. M. Lesk. (2002) Introduction to Bioinformatics Oxford University Press
68. G.B Fogel D.W Corne (2002) Evolutionary Computation in Bioinformatics
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),
73. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Second Edition, Andreas D. Baxevanis, B. F. Francis Ouellette.
74. Bioinformatics: Sequence, Structure and Databanks: 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,
79. Microarrays for an Integrative Genomics (Computational Molecular Biology), Isaac S. Kohane, Alvin Kho, Atul J. Butte
80. Bioinformatics: The Machine Learning Approach by Pierre Baldi, Soren Brunak, Sren Brunak.
81. Microarray Gene Expression Data Analysis: A Beginner's Guide, Helen C. Causton, John Quackenbush, Alvis Brazma.
82. SQL, PL/ SQL: The programming languages of Oracle, Bayross Iyan
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

---

**Minimum Infrastructure required for running the course**

Sr. No.	Item
---------	------

a.	Laboratory Space & Furniture – of ~ 900 sq ft carpet area with about 6 sq ft table space /student (Batch of 20 students)
b.	Air-conditioned Room
c.	Library Facilities
d.	Computational Facilities – 42 computers , softwares
e.	Internet Facilities
f.	Water & Electricity
g.	Instrumental Support

### **Recommended equipment and accessories**

---

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

### **Evaluation:**

---

- Theory Examination of all four papers for each year
- Practical Examination
- Successful completion of Industrial Visits ( **PSBIP103**)and (**PSBIP203**)
- Successful completion and submission of report of project ( **PSBIP304**)and (**PSBIP304**)
- All rules and pattern as per University of Mumbai for M. Sc. Courses.