CIRCULAR:-

A reference is invited to the Syllabi relating to the M.Sc.(Part I & II) degree course , **vide** this office Circular No. UG/263 of 2008, dated 20th June, 2008 and the Directors/Heads of the recognized Science Institutions concerned and the Principals of affiliated colleges in Science are hereby informed that the recommendation made by the Faculty of Science at its meeting held on 22nd June, 2015 has been accepted by the Academic Council at its meeting held on 26th June, 2015 **vide** item No. 4.3 and that in accordance therewith, the revised syllabus as per Credit Based Semester and Grading System for the M.Sc. degree course in Bio-Informatics, which is available on the University's web site (www.mu.ac.in) and that the same has been brought into force with effect from the academic year 2014-15.

MUMBAI – 400 032   REGISTRAR

30th September, 2015

To,

The Directors/Heads of the recognized Science Institutions concerned and the Principals of affiliated colleges in Science.

A.C/4.3/26/06/2015

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No. UG/87-A of 2015-16   MUMBAI-400 032   30th September ,2015

Copy forwarded with compliments for information to :-

3) The Dean, Faculty of Science.
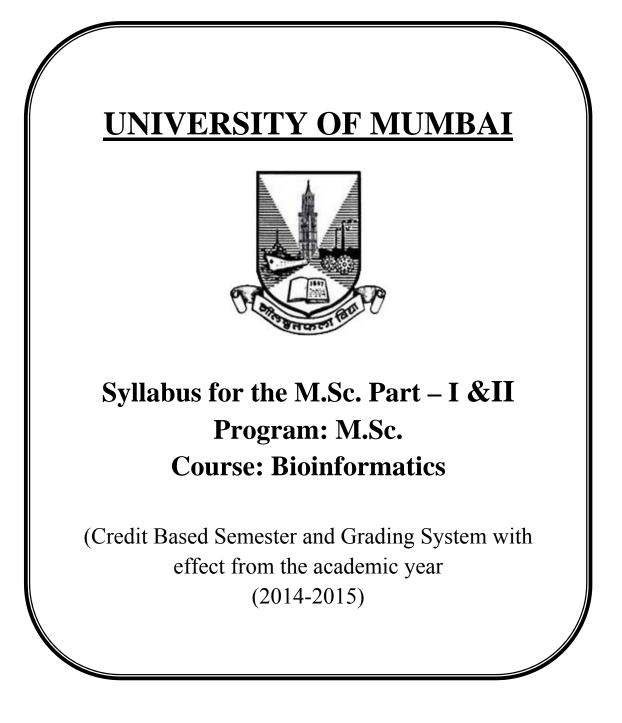2) The Director, Board of Colleges and University Development,
3) The Controller of Examinations,
4) The Co-Ordinator, University Computerization Centre.

REGISTRAR

..PTO

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
(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

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.

Scheme Of Examination:

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.

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

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.

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.

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.

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.

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.

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.

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.

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)
ΣCG: sum of product of credits & grades
ΣC: sum of credit points GPA: ΣCG/ ΣC
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.

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.

Marks Out Of 100 Grade Grade Point:

Grades	Marks	Grade Points
O	70 and above	7
A	60 to 69.99	6
B	55 to 59.99	5
C	50 to 54.99	4
D	45 to 49.99	3
E	40 to 44.99	2
F (FAIL)	39.99 and below	1

- 'B' Grade is equivalent to at least 55% of the marks as per circular No. UGC- 1298/ [4619] UNI-4 dated December 11,1999.
- 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.
- 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.
- 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')
- 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.

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.

Programme Structure:

R. ____ Number of Students:	20 per batch
R. ____ No of lectures:	• 60 lectures / paper / semester including Seminars, Assignments and Presentations. • 4 papers in Part-I • 4 papers in Part-II
R. ____ No of practical periods:	4 practical of four periods each per week
Work load:	• Four periods per week per paper where each period is of ONE hour duration. • Four practical's per week. Each practical is of four periods where each period is of ONE hour duration. • One Seminar per Week. Each seminar is of ONE hour Duration for a batch of TEN students. • Guidance to the students for projects.
R. ____ Passing standard:	Minimum 25 % marks in each paper and each practical and minimum 40 % marks in aggregate in Theory and Practical separately.
R. ____ Duration:	2 Years
Selection :	Entrance test & personal interview.

SYLLABUS IN BRIEF

Distribution of Credits -
Semester I

	Code	Lectures	Credits	Code	Practical	Credits
Fundamentals of Biology	PSBI101	60	4	PSBIP101	60	2
Sequence analysis & taxonomy	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
Sequence analysis & taxonomy	PSBI202	60	4	PSBIP202	60	2
Immunology and Bioinformatics	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
Proteomics and Genomics	PSBI302	60	4	PSBIP302	60	2
Application of Bioinformatics	PSBI303	60	4	PSBIP303	60	2
Concepts of computing	PSBI304	60	4	PSBIP304	60	2
TOTAL		240	16	-	180	8
TOTAL CREDITS				24		

Semester IV

Paper	Code	Lectures	Credits	Code	Practical	Credits
Molecular Modeling & Drug Designing	PSBI401	60	4	PSBIP401	60	2
Proteomics and Genomics	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	-	300	8
TOTAL CREDITS			24			

*Lectures allotment includes periods for seminar & presentations.
*Units equally distributed between two terms.

MODULAR DISTRIBUTION OF TOPICS

FIRST SEMESTER	SECOND SEMESTER
(PSBI101: Fundamentals of Biology)	**(PSBI201: Fundamentals of Biology)**
101.1 Structure of Major Biomolecules	**201.1** Concept of central dogma of life
101.2 Cell biology and Genetics	**201.2** Genomics organization
101.3 Metabolism	**201.3** Cell–Cell communication and Signal transduction
101.4 Protein chemistry	**201.4** Applied genomics
(PSBI102: Sequence analysis and taxonomy)	**(PSBI202: Sequence analysis and taxonomy)**
102.1 Sequence and Structure Databases	**202.1** Heuristic Methods of Sequence alignment
102.2 Composite Databases	**202.2** Multiple Sequence Alignments
102.3 Pair wise sequence alignment	**202.3** Taxonomy and Phylogeny
102.4 Dynamic programming Algorithm	**202.4** Data mining
(PSBI103: Biostatistics)	**(PSBI203: Immunology And Bioinformatics)**
103.1 Basics of Mathematics	**203.1** Introduction to Immune systems
103.2 Statistical Measures	**203.2** Receptors and MHC
103.3 Bivariate Distribution	**203.3** Immunoinformatics and vaccinology
103.4 An Introduction to Statistical inference	**203.4** Patinformatics
(PSBI104: Programming language and databases)	**(PSBI204: Programming language and databases)**
104.1 Fundamentals of Computing and Database systems	**204.1** SQL
104.2 Introduction to C	**204.2** Introduction To Linux
104.3 Introduction to C++	**204.3** HTML & XML
104.4 RDBMS	**204.4** Advanced C++

MODULAR DISTRIBUTION OF TOPICS

THIRD SEMESTER	FOURTH SEMESTER
(PSBI301: Molecular modeling and drug designing)	**(PSBI 401: Molecular modeling and drug designing)**
301.1 Introduction to Molecular Modelling	**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
(PSBI302: Proteomics and Genomics)	**(PSBI402: Proteomics and Genomics)**
302.1 Tools to study Structure of molecules	**402.1** Global profiling technologies
302.2 Techniques for separation	**402.2** Genomics
302.3 Detection of known molecules	**402.3** Applied Genomics
302.4 Sequencing of Nucleic acids and proteins	**402.4** Functional proteomics
(PSBI303: Applications of bioinformatics)	**(PSBI403: Applications of bioinformatics)**
303.1 Secondary Structure Prediction of Protein	**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
(PSBI304: Concepts in computing)	**(PSBI404: Concepts in computing)**
304.1 Introduction to OOPs concept and JAVA	**404.1** Introduction to Perl and data types

304.2	Core JAVA	**404.2**	Regular Expressions in Perl
304.3	JDBC	**404.3**	File Handling and Directories in Perl
304.4	BioJava	**404.4**	CGI Perl and Database connectivity

<u>**SEMESTER I**</u>

<u>PSBI101 FUNDAMENTALS OF BIOLOGY</u>

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
- o Viral genomes
- o Archeal and Bacterial Genomes
- o Eukaryotic genomes with special reference to model organisms (yeast,
- o 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 Pair wise 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:**
o Fitting of a straight line by Least Squares
o 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

PSBI104PROGRAMMING 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:
- o Entity and entity sets
- o Relations and relationship sets
- o E – R Diagram
- o 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)
- 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 minimum one visits –

PSBIP104
- SQL: Creating databases in Oracle, using various data types and granting privileges, Use of SQL Server and mySQL
- Writing programs on C viz:-
  - Finding prime numbers, Fourier series.
  - Reading a DNA sequence, Translating into RNA sequence.
  - 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.

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, bacteriophage 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: 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

PSBI303APPLICATION 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

SEMESTER 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

SEMESTER IV

PSBI401MOLECULAR 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)
- 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 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

- Industry oriented practical training/industrial relevant project work.
- A report should be submitted at the time of examination.

PSBIP404

- 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.

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Minimum Infrastructure required for running the course

Sr. No.	Item
a.	Laboratory Space & Furniture – of ~ 900 sqft carpet area with about 6 sqft 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

Sr. No	Equipment
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 Semester
- Practical Examination
- Successful completion of Industrial Visits
- Successful completion and submission of report of project
- All rules and pattern as per University of Mumbai for M. Sc. Courses.