

CIRCULAR :-

A reference is invited to the Ordinances, Regulations and syllabi relating to the Master of Science (M.Sc.)(Parts I & II) degree course vide Pamphlet No.175 and the Directors /Heads of the recognized Science Institutions concerned and the Principals of the affiliated colleges in Science are hereby informed that the recommendation made by the Ad-hoc Committee appointed by the Academic Council to advise it on all matters relating to the courses of study and examinations for the M.Sc. degree in Bioanalytical Sciences at its meeting held on 5th January, 2008 has been accepted by the Academic Council at its meeting held on 27th February, 2008 vide item No.4.13 and subsequently approved by the Management Council at its meeting held on 24th April, 2008 vide item No.15 and that, in accordance therewith, the M.Sc. degree course in Bio-Informatics has been introduced by the University from the academic year 2008-2009.

Further that in exercise of powers conferred upon the Management Council under Section 54(1) and Section 55(1) of the Maharashtra Universities Act 1994. it has made the Ordinance 5739 and Regulations 5812, 5813, 5814, 5815, 5816, 5817, 5818 and 5819 including scheme of examinations and detailed syllabus for the M.Sc. degree course in Bio-Informatics is as per Appendix and that the same has been brought into force with effect from the academic year 2008-2009.

MUMBAI-400 032
20th June, 2008


for REGISTRAR

To,

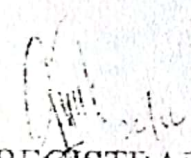
The Directors /Heads of the recognized Science Institutions concerned and the Principals of the affiliated colleges in Science

A.C/4.13/27.02.2008
M.C.15/24.04.2008

No.UG/ 263 -A of 2008 MUMBAI-400 032, 20th June, 2008

Copy forwarded with compliments to :-

1. The Dean, Faculty of Science.
2. The Convener of the Ad-hoc Committee in Bioanalytical Sciences.
3. The Superintendent, Post Graduate Section.
4. The Controller of Examinations,
5. The Co-ordinator, University Computerization Center.


for REGISTRAR
P.T.O.

27.2.08.

UNIVERSITY OF MUMBAI



Ordinances, Regulations

and

Syllabus

in

Bioinformatics

at

M.Sc. degree course

(Introduced from the academic year 2008-2009)

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 in molecular biology, pharmacology, biotechnology, forensic science, drug design, and various other disciplines.

Completion of the human genome project and explosion of genomic information from highthroughput 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 the educational front has 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 bridge this gap and meets the demand of the pharmaceutical industry and strengthens research collaboration

Programme Overview

The proposed programme for Masters in Bioinformatics is a two year degree 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, analyse 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 them a competitive edge in field related to biological sciences, computer and IT.

O. 5739 Eligibility

Bachelors 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

Programme Structure

R. 5813	Number of Students:	20 per batch
R. 5814	No of lectures:	• 120 lectures / paper including Seminars, Assignments and Presentations. • 4 papers in Part I • 4 papers in Part II
R. 5815	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 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. 5816	Passing standard:	Minimum 25 % marks in each paper and each practical and minimum 40 % marks in aggregate in Theory and Practical separately.
R. 5817	Duration:	2 Years
	Selection :	Entrance test & personal interview.

5818 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

PhD degree in the subject of Bioinformatics, computers, Microbiology, Biochemistry, Biotechnology, life science, molecular biology, Botany, Zoology, 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.

M.Sc Part I

120 lectures each

(including Seminars, Assignments and Presentations)

- Four Theory Papers.
- Three Practicals
- Industrial Visits (Practical III)

M.sc Part II

120 lectures each

(including Seminars, Assignments and Presentations)

- Four Theory Papers
- Three Practicals
- One Project (Practical VIII)

M.Sc	PAPER	TITLE	LECTURE
Part I	I	Fundamentals of Biology	120
	II	Proteomics & Genomics	120
	III	Biostatistics	120
	IV	Programming Language & Databases	120
Part II	V	Molecular modelling & Drug designing.	120
	VI	Sequence analysis & Taxonomy.	120
	VII	Application of Bioinformatics	120
	VIII	Concepts in computing	120

**SYLLABUS FOR M.Sc BIOINFORMATICS
MODULAR DISTRIBUTION OF TOPICS**

M.Sc PART I

PAPER I Fundamentals of Biology

UNIT I - FIRST TERM	UNIT I – SECOND TERM
1.1 Cell Biology (15)	1.5 Enzyme Kinetics (15)
1.2 Structure of Major Biomolecules (15)	1.6 Concept of Central Dogma / Concept of gene and gene Organization (15)
1.3 Carbohydrate Metabolism (15)	1.7 Cell-Cell communication and signal transduction(15)
1.4 Integration of Metabolic Pathways and Bioenergetics(15)	1.8 Recombinant DNA technology (15)

PAPER II Proteomics and Genomics

UNIT II – FIRST TERM	UNIT II – SECOND TERM
2.1 Tools to study Structure of molecules (15)	2.5 Global profiling technologies (15)
2.2 Techniques for separation (15)	2.6 Genomics (15)
2.3 Detection of known molecules (15)	2.7 Applied Genomics (15)
2.4 Sequencing of Nucleic acids and proteins (15)	2.8 Functional proteomics (15)

PAPER III Biostatistics

UNIT III – FIRST TERM	UNIT III- SECOND TERM
3.1 Basics of Mathematics(15)	3.5 Stochastic Process (15)

3.2 Probability(i) (15)	3.6 Analysis of variance and Regression (15)
3.7 Probability(ii) (15)	3.7 Analysis of one and multiple DNA (15)
3.8 An Introduction to statistical inference (15)	3.8 BLAST(15)

PAPER IV Programming Language & Databases

UNIT IV – FIRST TERM	UNIT IV – SECOND TERM
4.1 Fundamentals of Computing (15)	4.5 SQL (15)
4.2 Introduction to operating systems (15)	4.6 Electronic Document Management (15)
4.3 Introduction to Database Systems(15)	4.7 Introduction to C (15)
4.4 RDMS (15)	4.8 C++ (15)

SYLLABUS FOR M.Sc BIOINFORMATICS
MODULAR DISTRIBUTION OF TOPICS
M.SC PART II

PAPER V Molecular modelling & Drug designing

UNIT V- FIRST TERM	UNIT V- SECOND TERM
5.1 Introduction to Molecular Modelling (15)	5.5 Drug Delivery systems(15)
5.2 Cheminformatics (15)	5.6 Orphan receptors and reverse pharmacology (15)
5.3 Combinatorial Chemistry (15)	5.7 QSAR (15)
5.4 Drug Designing (15)	5.8 Molecular modelling and drug designing softwares (15)

PAPER VI Sequence analysis & Taxonomy.

UNIT VI – FIRST TERM	UNIT VI – SECOND TERM
6.1 Sequence and Structure Databases (15)	6.5 Heuristic Methods of Sequence alignment (15)
6.2 Derived Databases (15)	6.6 Multiple Sequence Alignments (15)
6.3 Pair wise sequence alignment(15)	4.7 Taxonomy and Phylogeny (15)
6.4 Dynamic programming Algorithm (15)	4.8 Data mining (15)

PAPER VII Application of Bioinformatics

UNIT VII- FIRST TERM	UNIT VII- SECOND TERM
7.1 Secondary Structure Prediction of Protein (15)	7.5 Machine Learning Techniques (15)
7.2 Tertiary Structure Prediction of Protein(15)	7.6 Algorithms and techniques for Microarray analysis (15)
7.3 Bioinformatics Perspectives on	7.7 Medical Informatics (15)

Human Diseases (15)	
7.4 Markov and Hidden Markov models (HMM) (15)	7.8 Bioinformatics and systems biology (15)

PAPER VIII Concepts in computing

UNIT VIII- FIRST TERM	UNIT VIII- SECONDTerm
8.1 HTML &XML (15)	8.5 Introduction to Perl and data types (15)
8.2 Introduction to OOPs concept and JAVA (15)	8.6 Regular Expressions in Perl (15)
8.3 Core.JAVA (15)	8.7 File Handling and Directories in Perl (15)
8.4 JDBC (15)	8.8 CGI Perl and Database connectivity (15)

PAPER I
FUNDAMENTALS OF BIOLOGY

1.1 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.

1.2 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.

1.3 Integration of metabolic Pathway & bioenergetics(15)

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

1.4 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.

1.5 Enzyme Kinetics(15)

- Introduction to Enzymes.
- Units of activity, coenzymes and metal cofactors.
- Temperature and PH effects,
- Michaelis – Menten Kinetics,
- Feed back inhibition and activation.
- Ribozyme and abzymes

1.6 Concept of Central Dogma / Concept of Gene & gene organization (15)

- DNA Replication, various enzymes involved, DNA topology, supercoiling 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.

1.7 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.

1.8 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,

LIST OF REFERENCE BOOK

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

2.1 Tools to study structure of Molecules (15)

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

2.2 Techniques for separation (15)

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

2.3 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

2.4 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-translational modifications

2.5 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.

2.6 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 organisms and their applications.

2.7 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

2.8 Functional proteomics(15)

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

LIST OF REFERENCE BOOK

- Principles of Protein structure, Schultz, G. E., and Schirmer, R. H. Dr. Shakti Sahi
- Proteomics, Daniel C. Leibler
- Proteins: Structures and Molecular Principles (2d ed.), TE Creighton
- Organic spectroscopy, William Kemp
- Proteome Research: Two-Dimensional Gel Electrophoresis and Detection Methods (Principles and Practice), T. Rabilloud (Editor), 2000, Springer Verlag
- Introduction to Protein Architecture: The Structural Biology of Proteins, M. Lesk, 2001, Oxford University Press

3.1 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.

3.2. Probability(i) (15)

- Random variable, Probability distribution
- Important discrete distribution such as Bernouli, 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.

3.3 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, Maximum.
- Introduction to P- Values, P- Values for various distributions
- Large observations and rare events
- Order statistics

3.4 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, likelihood Estimators etc
- Non parametric tests

- Bayesian approach to estimation
- Bayesian approach to testing
- Multiple testing

3.5 Stochastic Process (15)

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

3.6 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
- Mutiway classification model
- Regression analysis

3.7 Analysis of one and multiple DNA (15)

- Shot gun sequencing, Modelling DNA, Modelling Signals in DNA: weight matrices, Independence, Markov dependence, maximal dependence 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: Gapped global comparisons and Dynamic Programming Algorithms.
- Fitting One sequence into another Using Gap model, other Gap models.
- Protein sequences and substitution Matrices.

3.8 BLAST (15)

- Comparison of two Aligned sequences: Ladder points and Excursions, Parameter Calculation, Choice of a score, bounds for P Values, Normalised and the bit score, Number of high scoring Excursions, Karlin – Altschul Sum statistics

- Comparison of a Query Sequence against a database
- Minimum significance length
- BLAST : Parametric or non parametric Test
- Relation to Sequential Analysis

LIST OF REFERENCE BOOK

- Ewens Warren J. and Grant Gregory R.(2004): Statistical Methods in Bioinformatics, Springer.
- Gene H. Golub, Chaless F. Van Loan(1996): Matrix Computation, 3rd Ed.
- James Stewart(2001) : Calculus: Early Transcendent
- Ben hui Liu (2007) : Statistical Genomics : linkage, Mapping & QTL Analysis
- Lange Kenneth (2003): Mathematical and Statistical Methods for Genetic Analysis, 2nd Edition, Springer
- Lange Kenneth (2005): Applied Probability, 1st Edition, Springer.
- Durrett Rick (2001): Essentials of stochastic Processes, Springer.
- Higgins James J. and Keller-McNulty Sallie(1995): Concepts in Probability and Stochastic modeling, Duxbury.
- Wackerly, Dennis D. and Mendenhall III William and Scheaffer Richard L. (2002): Mathematical statistics with Applications, 6th Edition, Duxbury.
- Karlin S. and Taylor H.(1975): A first course in Stochastic Processes, Academic Press
- Norris J.R.(1997): Markov chains, Cambridge University Press

4.1 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.

4.2 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).

4.3 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.

4.4 RDMS (15)

- Relational database design; Oracle objects - Tables, Views, Indexes, Sequences; Synonyms, Snapshots
- Databases – tablespace, Datafile, 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.

2L (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.

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.

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.

7 C++ (15)

- Basics of object oriented programming
- Concept of Object, class, Constructor and Destructors.
- Inheritance, Data encapsulation.

- Polymorphism.
- Virtual function and friend function

LIST OF REFERENCE BOOK

1. SQL, PL/ SQL: The programming languages of Oracle, Bayross Iyan
2. Learning HTML, Robbins C.
3. Oracle SQL, Kreines David C
4. Oracle 9i: The complete reference, Loney Kevin, Koch G
5. Linux command by Bryan Pfaffemberger
6. Red Hat Linux by Negus
7. Learning C++ by Boardman
8. Computer Fundamentals by Sinha
9. The Wait Groups "C" Programing Using Turbo by Lafore
10. Let us C – Yashavant Kanetkar.

PAPER V

MOLECULAR MODELLING & DRUG DESIGNING

5.1 Introduction to Molecular Modelling (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.

5.2 Cheminformatics (15)

- Storage & Retrieval methods
- Modelling of small molecules
- Structure activity.

5.3 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

5.4 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).

5.5 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, Phototriggering, Thermosensitive

5.6 Orphan receptors and reverse pharmacology (15)

- Orphan GPCRs
- Identification of Orphan GPCRs
- Reverse Pharmacology
- Reverse Pharmacology for Orphan GPCRs
- Deorphanisation

5.7 QSAR (15)

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

5.8 Molecular modelling and drug designing softwares (15)

- Dock
- Autodock
- HyperChem
- CDS etc

LIST OF REFERENCE BOOK

1. G. Thomas (2000) Medicinal Chemistry: An Introduction, Wiley
2. Morgan Kaufmann Series in Evolutionary Computation, Morgan Kaufmann
3. Kenneth W. Goodman (1998) Ethics, Computing and Medicine: Informatics and the Transformation of Health Care. Cambridge University Press.
4. R. B. Silverman (2004) The Organic Chemistry of Drug Design and Drug Action, 2nd Edition, Academic Press.
5. Investigating Biological System using Modeling: Strategies and software, Meryl E. Wastney
6. Dale G. Deutsch, Analytical Aspects of Drug Testing, John Wiley and Sons
7. Karel Eckschlager, Klaus Danzer, Information Theory in Analytical Chemistry, John Wiley and Sons
8. Principles of Protein structure, Schultz, G. E., and Schirmer, R. H. Dr. Shakti Sahi

PAPER VI SEQUENCE ANALYSIS & TAXONOMY

6.1 Sequence and Structure Databases (15)

- Major Bioinformatics resources NCBI, EBI, ExPASy
- Open access bibliographic resources and literature Databases
- Nucleic acid : GeneBank, 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

6.2 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 etcWith examples.

6.3 Pairwise Sequence alignment (15)

- Various file formats for bio- molecular sequences.
- Basic Concepts of sequences similarity, Identity and homology.
- Definition of homologues, orthologues, Paralogs
- 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.

6.4 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

6.5 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

6.6 Multiple sequence alignment (15)

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

6.7 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

6.8 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

LIST OF REFERENCE BOOK

1. Westhead, D.R., Parish, J.H. & Twyman, R.M., Instant Notes: Bioinformatics, 2002, BIOS
2. Higgs, P.G & Attwood. T.K., Bioinformatics and Molecular Evolution, 2005, Blackwell Publishing.
3. Campbell, A.M & Heyer, L.J., Discovering genomics, proteomics and bioinformatics, 2003, Benjamin Cummings.
4. Mount, D.W., Bioinformatics sequence and genome analysis, 2nd Ed., 2004 Cold Spring Harbour Laboratory Press.
5. M.Lesk. (2002) Introduction to Bioinformatics Oxford University Press
6. G.B Fogel D.W Corne (2002) Evolutionary Computation in Bioinformatics

PAPER VII APPLICATION OF BIOINFORMATICS

7.1 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.)

7.1 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

7.2 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.
- Application of Bioinformatics in Immunology.

7.3 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

7.5 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 feedforward associative neural networks,
- Applications of ANN, SVM etc.

7.6 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.

7.7 Medical Informatics (15)

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

7.8 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

LIST OF REFERENCE BOOK

1. Proteins: Structures and Molecular Principles (2d ed.), TE Creighton
2. Bioinformatics: Sequence and Genome Analysis, David W. Mount.
3. Sequence Analysis in a Nutshell: A Guide to Common Tools and Databases, Scott Markel, Darryl Leon.
4. Current Topics in Computational Molecular Biology (Computational Molecular Biology), Tao Jiang, Ying Xu, Michael Zhang (Editors),
5. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Second Edition, Andreas D. Baxeavanis, B. F. Francis Ouellette.
6. Bioinformatics: Sequence, Structure and Databanks: A Practical Approach (The Practical Approach Series, 236), Des Higgins (Editor), Willie Taylor (Editor).
7. Fundamental Concepts of Bioinformatics, Dan E. Krane Michael L. Raymer
8. Introduction to Bioinformatics Algorithms, Neil C. Jones, Pavel Pevzner
9. Data Mining: Multimedia, Soft Computing, and Bioinformatics, Mitra, Sushmita Acharya, Tinku
10. Kubly Immunology by Richard A. Goldsby (Editor), Barbara A Osborne, Thomas J/ Kindt, Janis Kubly, Paperback, W H Freeman & Co (June 2006)
11. Statistical Methods in Bioinformatics: An Introduction (Statistics for Biology and Health), Warren Ewens, Gregory Grant,
12. Microarrays for an Integrative Genomics (Computational Molecular Biology), Isaac S. Kohane, Alvin Kho, Atul J. Butte
13. Bioinformatics: The Machine Learning Approach by Pierre Baldi, Soren Brunak, Sren Brunak.
14. Microarray Gene Expression Data Analysis: A Beginner's Guide, Helen C. Causton, John Quackenbush, Alvis Brazma.

PAPER VIII
CONCEPTS IN COMPUTING

8.1 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.

8.2 Introduction to OOPs concept and JAVA (15)

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

8.3 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

8.4 JDBC (15)

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

8.5 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.

8.6 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

8.7 File Handling and Directories in Perl (15)

- Filehandles and File Tests, Opening and Closing a Filehandle, die, Using Filehandles,
- Directory Access, Moving Around the Directory Tree, Globbing, Directory Handles, Opening and Closing a Directory Handle, Reading a Directory Handle
- Process Management,

8.8 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

LIST OF REFERENCE BOOK

1. SQL, PL/ SQL: The programming languages of Oracle, Bayross Iyan
2. Mastering Perl for Bioinformatics, James D. Tisdall
3. Genomic Perl: From Bioinformatics Basics to Working Code, Rex A.Dwyer
4. Beginning Perl for Bioinformatics, James Tisdall
5. Developing Bioinformatics Computer Skills, Cynthia Gibas, Per Jambeck, 2001

PRACTICALS SYLLABUS FOR M. Sc. BIOINFORMATICS
Part I Practicals
PRACTICAL I TO IV

PRACTICAL I

- Identification of various stages in mitosis and meiosis from permanent slides.
- 2D separation of amino acids, plant pigments using paper chromatography
- Biochemical estimation of carbohydrates:-
- Biochemical estimation of proteins:-
- Biochemical estimation of lipids:-
- Biochemical estimation of DNA & RNA

PRACTICAL II

- IR analysis of a modern drug (e.g. Diclofenac Sodium) (optional)
- Blood film preparation and Identification of various cells.
- Isolation of plasmid DNA and chromosomal DNA
- Restriction digestion of DNA
- Ligation
- PAGE separation of human serum proteins

PRACTICAL III

Report on Industrial visits – minimum FOUR.

PRACTICAL IV

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

PRACTICALS SYLLABUS FOR M. Sc. BIOINFORMATICS
Part II Practical
PRACTICAL V TO VIII

PRACTICAL V

- 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.
 - Specialised database: KEGG, PUBMED, OMIM
- 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.

PRACTICAL VI

- Detection of general signals, regulatory regions and promoter prediction.
- Secondary structure prediction using various available tools,
- Tertiary structure and function prediction using homology modelling and *ab initio* method.
- Validation of predicted structure.
- Visualization of 3D protein structure using Rasmol, VMD etc.
- 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

PRACTICAL VII

- 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 servlets.
- JDBC: connecting to a database (mySQL)
- Using perl for writing small scripts like
 - 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

PRACTICAL VIII

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

Evaluation:

- Theory Examination of all four papers for each year
- Practical Examination
- Successful completion of Industrial Visits (Practical III).
- Successful completion and submission of report of project (Practical VIII)
- All rules and pattern as per University of Mumbai for M. Sc. courses

Theory Examination Question Paper Pattern:

- Each Theory paper will be of 75 marks
- Each Theory paper will be of 3 hr. Duration
- Each theory paper will have five question in all divided.
- All will be compulsory questions
- Out of Five. First question will be of mixed type and rest four will be based on eight units of paper.

Paper	Maximum Marks	Duration	Minimum for Passing	Remarks
I	75	3 Hr	19	
II	75	3 Hr	19	
III	75	3 Hr	19	
IV	75	3 Hr	19	
Aggregate	300	---	120	
V	75	3 Hr	19	
VI	75	3 Hr	19	
VII	75	3 Hr	19	
VIII	75	3 Hr	19	
Aggregate	300	---	120	

Practical Examination Question Paper Pattern:

- Each Practical paper will be of 50 marks (i.e. 200 marks in all)
- Each Practical paper will be of 6 hr duration on separate days, i.e. Four days in all
- For each Practical there will be 2 experiments with marks suitably assigned for Viva and Journal.
- For Practical III in Part I the marks will be allotted to the reports on the industrial visits and a presentation by the student on the visit.
- For Practical VIII in Part II the marks will be allotted to the report on the Project carried out by the student and the report submitted on the project.

Practical	Maximum Marks	Minimum for Passing	Remarks
I	50	13	
II	50	13	
III	50	13	Presentation, Submission and Viva on Industrial Visits
IV	50	13	
Aggregate	200	80	
V	50	13	
VI	50	13	
VII	50	13	Presentation, Submission and Viva on Industrial oriented work.
VIII	50	13	
Aggregate	200	80	

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 – 25 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.	DNA Sequencer
9.	Flame Photometer
10.	Fourier Transform Infrared Spectrometer
11.	Gas Chromatograph
12.	Gel Documentation
13.	HPLC with various detectors (UVNIS, E.C.D, PDA) & software
14.	HPTLC Densitometer with CATS 3.0software
15.	HPTLC Spotter
16.	LC/MS/MS
17.	Low Volume Evaporator
18.	Melting Point Apparatus
19.	pH - meter
20.	Refrigerators
21.	Solid Phase Extractor
22.	Top pan balance
23.	Ultrasonic bath with Temperature control
24.	UV-Vis Scanning Spectrophotometer
25.	Water Distillation Apparatus
26.	Water Purification System