

## Course Structure: B. Tech & M.Tech. Integrated (Bioinformatics)

Department of Bioinformatics, Singhania University, Rajasthan

Subject Code	Subject Title	Internal Assessment	External Assessment	Total
<b>Semester - III</b>				
BTBI-211	Introduction of Bioinformatics	60	40	100
BTBI-221	Operating System (Windows, Linux)	60	40	100
BTBI-231	Database Management System	60	40	100
BTBI-241	Molecular Biology and Genetics	60	40	100
BTBI-251	Statistics and Probability	60	40	100
BTBI-261	C - Language	40	30	70
BTBI-271	C - Language Lab	-	30	30
<b>Semester - IV</b>				
BTBI-212	Computational Method for Sequence Analysis	60	40	100
BTBI-222	Biological Databank	60	40	100
BTBI-232	Oracle	60	40	100
BTBI-242	C++ Language	60	40	100
BTBI-252	Animal and Plant Biotechnology	60	40	100
BTBI-262	C++ Lab	-	50	50
BTBI-272	Oracle Lab	-	50	50
<b>Semester - V</b>				
BTBI-311	Genomics, Proteomics and HGP	60	40	100
BTBI-321	Information Theory & Stochastic Process	60	40	100
BTBI-331	Data Warehousing and Data Mining	60	40	100
BTBI-341	Perl Programming for Bioinformatics	60	40	100
BTBI-351	Computer Networking, HTML, and Website Designing	60	40	100
BTBI-361	Perl Programming Lab	-	50	50
BTBI-371	Networking & HTML Lab	-	50	50
<b>Semester - VI</b>				
BTBI-312	Gene Expression & MicroArray Analysis	60	40	100
BTBI-322	Pharmacogenomics & Pharmacogenetics	60	40	100
BTBI-332	Microsoft Visual Basic	60	40	100
BTBI-342	Artificial Neural Network	60	40	100
BTBI-352	Advance Networking and Multimedia	60	40	100

BTBI-362	Bioinformatics Lab	-	50	50
BTBI-372	Microsoft Visual Basic Lab	-	50	50
<b>Semester - VII</b>				
BTBI-411	Advanced Algorithm for Computational Biology	60	40	100
BTBI-421	Environmental Engineering	60	40	100
BTBI-431	Molecular Imaging & Drug Designing	60	40	100
BTBI-441	Asp .Net	60	40	100
BTBI-451	Core Java	60	40	100
BTBI-461	ASP Lab	-	50	50
BTBI-471	Java Lab.	-	50	50
<b>Semester - VIII</b>				
BTBI-412	Major Project	300*	100	400
	* (Project Report Evaluation: 150 & Comprehensive Viva-voce: 150)			
<b>Semester - IX</b>				
BTBI-511	Introduction of Nanotechnology	40	60	100
BTBI-521	Image Processing	40	60	100
BTBI-531	Data Structure using C	40	60	100
BTBI-541	Software Engineering	40	60	100
BTBI-551	Enzymology and Enzyme Technology	40	60	100
BTBI-561	Data Structure Lab	20	30	50
BTBI-571	Image Processing Lab	20	30	50
<b>Semester - X</b>				
BTBI-512	Major Project (Dissertation with one National or International Paper)	100	300 *	400
	* (Project Report Evaluation: 150 & Comprehensive Viva-voce: 150)			
<b>Grand Total:</b>				<b>3400</b>

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester

**Subject:** Introduction of Bioinformatics (BTBI - 211)

### COURSE CONTENTS

#### **Unit I:**

The nature of chemical bonds, Introduction to Genes and Proteins, Nucleotides, Orientation, Base pairing, The central dogma, Promoter sequences, Genetic Code, ORFs, Introns and Exons, Slice variants, Protein structure, Primary, Secondary, Tertiary and Quaternary, The notation of homology.

#### **Unit II:**

Introduction to Data Generating Techniques: Restriction Enzymes, Gel Electrophoresis, Blotting and Hybridization, Cloning, PCR, DNA Sequencing.

#### **Unit III:**

Biological databases, Search engines, Public databases: PubMed, EMBL, GenBank, PDB, Swiss-Port, Data Visualization, Data Mining, Entry and retrieval of data from public databases.

#### **Unit IV:**

Genomics and Proteomics: Prokaryotic genomes, Eukaryotic Genomes, Gene Structure, ORFs, GC Content in Eukaryotic genomes, Gene Expression, Protein Classification, 2D-Electrophoresis, Mass spectrometry, Microarray technology, X-ray crystallography, NMR, Sequence and Phylogeny Analysis, Detecting ORFs, Outline of sequence alignment, Mutation matrices, Pairwise alignments, Introduction to BLAST, Multiple sequence alignment, Phylogenetic analysis.

#### **Text / Reference Books:**

1. Fundamental Concepts of Bioinformatics, D.E. Krane and M.L. Raymer, Person Education, 2003.
2. Bioinformatics Computing by B. Bergeron, Prentice - Hall, 2003.
3. Bioinformatics: A practical guide to the analysis of genes and proteins, D. Baxivanis and F. Oulette, Wiley Indian Edition, 2001
4. Bioinformatics: Sequence and Genome analysis, D.W. Mount, Cold Spring Harbour Laboratory Press, 2001

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester

**Subject:** Operating System -Windows, Linux (BTBI - 221)

### COURSE CONTENTS

**Unit I:**

Introductory concepts, Operating systems, Mainframe systems, Multiprocessors, Distributed systems, Real – Time systems, Computing environments

**Unit II:**

Computer system structure, Computer system organization, I/O structure, Storage structure, Storage hierarchy, Hardware protection, Network structure

**Unit III:**

Operating system structures, System components, OS Services, System calls, System programs, System structure, Virtual machines Processes, Process concepts, Process scheduling, Operations on processes, Process states, Cooperating processes, Inter-process communication, Common OS problems.

**Unit IV:**

DOS and Windows, Introductory concepts, Architecture and special features, Useful DOS commands, DOS – Editor, EDIT & writing Batch Files, Different Versions and their Distinguishing features, Managing Operations with Windows

**Unit V:**

Linux: Introductory concepts, Architecture and special features, Useful Linux commands, Related operating system and their Introduction

**Text / Reference Books:**

1. Operating Systems by Glavin, Addison Wessely, 2000
2. Modern Operating Systems by S. Tanenbaum, Prentice Hall (India), 1999
3. Operating Systems Concept and Design by Milan Milenkovic, Tata McGraw Hill, 2000

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester

**Subject:** DataBase Management System (BTBI - 231)

**COURSE CONTENTS**

**Unit – 1:**

Introduction, Characteristics of Data base approach, Database users, Intended uses of databases, Implication of database approach.

**Unit II:**

Database System Concepts and Architecture, Data Models, Schemas and Instances, DBMS Architecture and data independence, database languages, Classification of DBMS.

**Unit III:**

Database Design: Informal Design guidelines for relation Schemas, functional Dependencies, Normal forms based on primary keys, general Definition of 2<sup>nd</sup> and 3<sup>rd</sup> Normal forms, BCNF, Need of further Normalization.

**Unit IV:**

Data Modeling using ER diagram, ER Model Concepts, Notation for ER Diagrams.

**Unit V:**

The Relational Model, Relational Model Concepts, Relational Model Constraints, Introduction to Relational Algebra.

**Text/Reference Books:**

1. Fundamentals of Database System by Elmasari and Navathe, Prentice Hall (India), 2001
2. Data Mining Concepts and techniques- Jiawei Han, Micheline Kamber, Morgan Kaufmann publisher, 2001

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester

Subject: Molecular Biology and Genetics (BTBI - 241)

### COURSE CONTENTS

**Unit I:**

Concepts in Biology: Characteristics of living organisms, Structure of cells, Energy flow; Nutrition and Metabolism; Information storage and expression, Reproduction and Inheritance,

**Unit II:**

Biomolecules: Carbohydrates, Amino Acids, Proteins, Lipids, Nucleic acids.

**Unit III:**

Enzymes; Properties, Activation energy, Reaction kinetics, Intercellular Communication, Flow of genetic information, DNA expression and replication

**Unit IV:**

Genes; Changing size of Genes, Gene synthesis, Cloning (Plant and Animal), Mutation, Gene Targeting, Gene Therapy

**Unit IV:**

Level of secondary structure, Motifs, Basic concepts of molecular dynamics, Molecular simulation studies

**Unit V:**

Protein structure determination by X-ray Diffraction, NMR, Introduction to nucleic acid structure, Genome organization, HGP

**Text / Reference Books:**

1. Molecular Biology by David Friefelder, Jones & Burtlett Publishers inc, 2000
2. Molecular Cell Biology by Alberts, Bruce Bray, Watson & James, Garland Publishing, 1999.

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester  
Subject: Statistics and Probability (BTBI - 251)

COURSE CONTENTS

**Unit I:**

Probability, Conditional Probability, Random Variables, Expected Value

**Unit II:**

Continuous and Discrete distributions: Binomial, Geometric, Poisson, Pascal, Uniform Exponential and Normal, Poisson Process

**Unit III:**

Multidimensional random variables, Multidimensional and bivariate normal distribution, Moment generating functions

**Unit IV:**

Law of large numbers, Central limit theorem, Sampling distribution, Point and Interval Estimation Testing of hypothesis, Goodness of fit, Linear regression

**Unit V:**

Principal component analysis, Discriminant analysis, Cluster analysis, Multivariate analysis of variance

**Text / Reference Books:**

1. Statistical Methods in Bioinformatics: An Introduction by W. Evans & G. Grant, Springer, 2001
2. First course in Probability by Sheldon Ross, Prentice-Hall (India), 2001

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester

Subject: C - Language (BTBI - 261)

### COURSE CONTENTS

#### Unit I:

Introduction to programming: The basic model of computing, Algorithm and Flow-charts, Programming Languages, Compilation, Linking, Testing, Debugging and Documentation.

#### Unit II:

Introduction to C language: Character set, variables and Identifiers, Built in data types, Arithmetic operators and expression, constant and literals, Relational operator and logical connectivity, Sample assignment statement, Basic input/output statement, Sample C program.

#### Unit III:

Conditional statement and Loops: Decision making within a program, different conditional statements in C, Looping statement in C, Structured programming, Nested loop, Infinite loop.

#### Unit IV:

Arrays and Pointers: Definition and purpose, Difference between arrays and pointers, Static and dynamic memory allocation.

#### Unit V:

Functions: Modular programming and Functions, Standard library of C function, Function prototype and function definition, Calling a function, Recursive function.

#### Unit VI:

Structure, Union, and File: Definition of structure, Union and File, difference between structure and union.

#### Text / Reference Books:

1. Programming with C, K.R.Venugopal & Sudeep R. Prasad, Tata McGraw Hill
2. Programming in C, Herbert Schildt, THM, Fifth Edition, 2002
3. C How to program, Deitel & Deitel, Pearson Edition, Third Edition, 2001
4. Programming in C, Denis Ritchie, THM, Fourth Edition, 2000

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – III Semester

Subject: C – Language Lab (BTBI - 271)

COURSE CONTENTS

- Problem Solving using C language using built in data types and operators.
- Practice on Conditional and Decision making statement with biological problems.
- Programs on Nucleotide sequence by using array and pointer such as to show mutation, to find motifs, etc.
- Program to translate DNA into RNA using C.
- Program to make Open Reading Frame by using C.
- Above all exercise by using Functions.

Sri Hanuman University (Department of Bioinformatics)

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester  
Subject: Computational Methods for Sequence Analysis (BTBI - 212)

### COURSE CONTENTS

#### Unit – I:

Introduction to sequence databases: DDBJ / EMBL / GenBank; Information retrieval from databases; Analysis of DNA and Protein sequences: distribution, pattern and motif searches, Segmentation

#### Unit – II:

Sequence alignment: Scoring matrices, PAM, BLOSUM, Local and global alignment concepts; Dynamic programming; Needleman - Wunch algorithm, Smith - Waterman algorithm; Statistics of alignment score; Multiple sequence alignment

#### Unit – III:

Database searches for homologous sequences: FASTA, BLAST and CLUSTALW, Comparison, Artificial Neural Network concepts, Preceptron, Multilayer preceptron, Secondary Structure Prediction using ANN, Back propagation Algorithm, Training and testing ANNs.

#### Unit – IV:

Evolutionary analysis: Distances, Clustering methods, Tree representation, Genome sequence assembly; Gene finding methods; Analysis and prediction of regulatory regions.

#### Unit – V:

Profiles and Hidden Markov Model, Gene identification and prediction, DNA Microarrays, Gene Expression, Clustering gene expression profiles.

#### Text / Reference Book:

1. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, A. D. Baxevanis and B. F. F. Ouellette John Wiley and Sons (ASIA) Pvt. Ltd. 2002
2. Bioinformatics methods and applications - Genomes, Proteomics and Drug Discovery, S. C. Rastogi, N. Mendiratla and P. Rastogi, Prentice Hall (India), 2004
3. BLAST, by I. Korf, M. Yandell & Joseph Bedell, O'Reilly, 2003
4. Biological Sequence Analysis – Probabilistic Models of Proteins and Nucleic acids, R. Durbin, S. Eddy, A. Krogh, G. Mitchison, Cambridge University Press, 1998

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester

Subject: Biological Databank (BTBI - 222)

### COURSE CONTENTS

#### Unit I:

Overview of Database, Need of database, Application in Biological field

#### Unit II:

Introduction, Documentation and Application of listed Database

#### Primary Sequence Database:

1. DDBJ (DNA Data Bank of Japan) -
2. EMBL Nucleotide DB (European Molecular Biology Laboratory) -
3. GenBank (National Center for Biotechnology Information) -

#### Meta-databases:

1. Entrez (National Center for Biotechnology Information)
2. euGenes (Indiana University)
3. GeneCards (Weizmann Inst.)
4. SOURCE (Stanford University)
5. mGen containing four of the world biggest databases GenBank, Refseq, EMBL and DDBJ
6. GenSolution (Bioinformatics Tools and Database of Inflammatory genes & Pathways and PolyHydroxyAlkanoate genes Database) - [www.gensolution.co.in](http://www.gensolution.co.in)

#### Genome Databases:

1. Ensembl provides automatic annotation databases for human, mouse, other vertebrate and eukaryote genomes.
2. JGI Genomes of the DOE-Joint Genome Institute provides databases of many eukaryote and microbial genomes.
3. CAMERA Resource for microbial genomics and metagenomics
4. MGI Mouse Genome (Jackson Lab.)
5. Corn, the Maize Genetics and Genomics Database

#### Protein Sequence Databases:

1. UniProt Universal Protein Resource (UniProt Consortium: EBI, ExPasy, PIR)
2. PIR (Protein Information Resource)
3. Swiss-Prot Protein Knowledgebase (Swiss Institute of Bioinformatics)
4. DIP Database of Interacting Proteins (Univ. of California)
5. Pfam Protein families database of alignments and HMMs (Sanger Institute)
6. ProDom Comprehensive set of Protein Domain Families (INRA/CNRS)
7. SignalP Server for signal peptide prediction

#### Protein Structure Databases:

1. PDB (Protein Data Bank, Research Collaboratory for Structural Bioinformatics - RCSB)
2. CATH Protein Structure Classification
3. SCOP Structural Classification of Proteins
4. SWISS-MODEL Server and Repository for Protein Structure Models

Metabolic pathway Databases:

1. BioCyc Database Collection including EcoCyc and MetaCyc
2. KEGG Pathway Database
3. BioCarta Pathway Database

Microarray Databases:

1. ArrayExpress (European Bioinformatics Institute)
2. Gene Expression Omnibus (National Center for Biotechnology Information)
3. SMD (Stanford University)
4. GPX (Scottish Centre for Genomic Technology and Informatics)

Specialized Databases:

1. CGAP Cancer Genes (National Cancer Institute)
2. GDB Hum. Genome Db (Human Genome Organisation)
3. NCBI-UniGene (National Center for Biotechnology Information)
4. OMIM Inherited Diseases (Online Mendelian Inheritance in Man)
5. p53 The p53 Knowledgebase

Text / Reference Books:

1. Bioinformatics: A practical guide to the analysis of genes and proteins, D. Baxivanis and F. Oulette, Wiley Indian Edition, 2001

Internet: <http://en.wikipedia.org>

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester  
Subject: Oracle (BTBI - 232)

### COURSE CONTENTS

#### Unit – I:

Introduction to SQL, SQL \*Plus Commands, SQL Buffer Commands; Creating Tables, Inserting rows to the table, View the rows in the table, Delete rows from a table, Update rows in the table; ROLLBACK, COMMIT and SAVEPOINT; Lock Table; SQL select, Sorting Columns, Additional Operators; Data types in Oracle; Referential Integrity; Join Operator, Table aliases; Column format;

#### Unit – II:

Functions and Operators: Number function, Character Function, Conversion function, aggregate function, Data functions, Some other functions

#### Unit – III:

Alter Table; Constraints; Group By clause; Create Sequence Command; Sub query; SET Operators; SQL \*PLUS Report; Views, SQL \*Plus Input Variables.

#### Unit – IV:

Introduction to PL/SQL, PL/SQL construct, Iteration – Looping commands, Variable Attributes; Cursors, Triggers, Procedures and Functions.

#### Unit – V:

Objects; Abstract Data type, Object Views; Methods; Collectors; Table Space; Basic Database Administration; Data Dictionary; Remote Data Access

Text / Reference Book:

1.

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester

**Subject:** C++ - Language (BTBI - 242)

### COURSE CONTENTS

**Unit – I:**

Methodologies: Concepts of structured and Object-Oriented programming, Advantages of OOPs methodologies. Introduction to Object-Oriented programming: Characteristics of OOPs Languages, C++ programming Basics operators, Loops, Arrays, Pointers.

**Unit – II:**

Principle of Object-Oriented programming, Introduction to Abstraction, Encapsulation, Inline function, Reference variable, Access specifier, Information Hiding, Friend Functions, Friend Class.

**Unit – III:**

Operator overloading, Function overloading,

**Unit – IV:**

Inheritance: Extending classes, Types of inheritance, Virtual base class, Problems with multiple inheritance, Containership.

**Unit – V:**

Advanced pointers, Virtual functions, Polymorphism, Pointers to Class, Array pointers to Class, Virtual Function-Abstract Class, Pure Virtual Function, Files and Streams, Building class Libraries in C++.

**Unit – VI:**

File Handling in C++, Template class, Exception Handling.

**Text / Reference Book:**

1. Object Oriented Programming with C++, E. Balagurusamy, Tata McGraw Hill
2. Object Oriented Programming in C++, Robert Lafore, Techmedia 2002
3. C++, How to program by Deitel & Deitel, Person Edition, 2002
4. The C++ Programming Languages by Stroustrup, Addison, Wesley., 2001
5. Problem Solving the object of Programming, Walter Savitch, Pearson Edition, 2003

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester

Subject: Animal and Plant Biotechnology (BTBI- 252)

### COURSE CONTENTS

#### Animal Biotechnology

##### Unit – I:

General metabolism, Special secondary metabolites / products, Insulin growth hormone, interferon, t-plasminogen activator, factor VIII etc. Growth factors promoting proliferation of animal cells (EGF, FGF, PDGF, IL-1, NGF erythropoietin etc).

##### Unit – II:

Expressing cloned proteins in animal cells, Over production and processing of chosen protein. The need to express in animal cells, Production of vaccines in animal cells, Production of monoclonal antibodies, Bioreactors for large scale culture of cells, Transplanting cultured cells.

#### Plant Biotechnology

##### Unit – III:

Introduction to *in vitro* methods, Terms and definitions, Use of growth regulators; *in vitro* pollination and fertilization; Introduction to the processes of embryogenesis and organogenesis and their practical applications; Clonal multiplication of elite species (Micropropagation), axillary bud, shoot-tip and meristem culture.

##### Unit – IV:

Haploids and their applications; Somaclonal variations and application; Endosperm culture and production of triploids; Practical applications of tissue and organ culture; Single-cell suspension cultures and their applications in selection of variants / mutants with or without mutagen treatment (of haploid cultures preferably).

##### Unit – V:

Somatic hybridization - an introduction; Various methods for fusing protoplasts: chemical, electrical, Use of markers for selection of hybrid cells; Practical applications of somatic hybridization (hybrids vs cybrids); Protoplasts and tissue culture for genetic manipulation of plants, Introduction to *A. tumefaciens*, Tumor formation on plants using *A. tumefaciens* (Monocots vs Dicots), Root-formation using *A. rhizogenes*, Practical application of genetic transformation.

Text / Reference Book:

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester

Subject: C++ Lab (BTBI- 262)

COURSE CONTENTS

- Problem Solving using C++ language using built in data types and operators based on Object Oriented Techniques.
- Practice on Conditional and Decision making statement with biological problems.
- Object Oriented Programs on Nucleotide sequence by using array and pointer such as to show mutation, to find motifs, etc.
- Function to translate DNA into RNA using C++.
- Function to make Open Reading Frame by using C++.
- C++ Functions to calculate G+C content and Nucleotide counts.

Singhania University (Department of Bioinformatics)

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – IV Semester

Subject: Oracle Lab (BTBI- 272)

COURSE CONTENTS

- Creating Tables & Applying All Constraints
- Inserting Data into Tables
- Updating Tables
- Alias Table
- Deleting Data From Table, Drop Table
- Working with All SQL Queries using functions (Number, string functions etc.)
- Working with sub queries
- Working with Joins
- Creating Views
- Creating Objects (i.e. Cluster, Synonyms, Indexes etc.)
- Writing PL/SQL programs
- Creation of Cursors
- Creation of Functions.
- Creation of Procedures.
- Creation of Triggers
- Generation of SQL report
- Creating forms and working with different objects.
- Report

Singhania University, (Department of Bioinformatics)

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester

**Subject:** Genomics, Proteomics and HGP (BTBI - 311)

### COURSE CONTENTS

**Unit – I:**

Primer Selection Phylogeny, Protein Sequence Analysis, SAGE, Primer Chain Reaction (PCR).

**Unit – II:**

Genomics, Fragmenting the genomes, Need of markers, Marker Sequencing (RFLP, AFLP & SNP, etc); Genome sequencing: Basic Sanger sequencing, Automated sequence, Gene Identification, MUMmer , Blast2.

**Unit – III:**

Proteomics, Microarray: The technique of microarray design, 2-D gel electrophoresis, Peptide sequencing, Mass spectroscopy.

**Unit – IV:**

Metabolomics, Metabolic pathway databases: KEGG, COG, WIT; Drug target identification.

**Unit – V:**

Functional genomics: Application of sequence based and structure based approach of gene function eg: Sequence comparison, Structure analysis (active site, binding site) and comparison; Approaches for determining gene expression patterns and functions.

**Unit – VI:**

What is HGP: Goals, Progress & History of HGP.

[http://www.ornl.gov/sci/techresources/Human\\_Genome/home.shtml](http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml)

**Text / Reference Book:**

1. Handbook of Comparative Genomics: Principles and Methodology by T.B. Kitano, Graziano Pesole, 2003.
2. Computational Molecular Biology by P. Clate & R. Backofen, Willy Publication, 1998 Proteomics,
3. Timothy Palkill, kluwer Academic Publisher, 2002
4. Introduction to Proteomics: Tools for the new Biology, Daniel C. Liebler, Humana Press, 2001
5. Foundation to systems Biology (Ed) by Hiroaki Kitano, MIT Press, 2001.

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester

**Subject:** Information Theory & Stochastic Process (BTBI- 321)

**COURSE CONTENTS**

**Unit – I:**

Overview: Probabilities defined on events, Random variable, Binomial, Geometric, Poisson variates, Uniform, Exponential, Gamma, Normal Variates, Expectation.

**Unit – II:**

Introduction to stochastic process, Stationary process Poisson process, Non-homogeneous Poisson process, Brownian motion process

**Unit – III:**

Markov Chain: Chapman-Kolmogorov equation, Classification of states, Limiting Probabilities, Time Reversible Markov Chain, Markov Chain Monte Carlo Method, Continuous Time Markov Chain, Birth and Death Process, Time reversibility, Uniformization.

**Unit – IV:**

Information and Entropy, Joint and Conditional Entropies, Mutual information, Chain rules for entropy, Relative entropy.

**Unit – V:**

Entropy rules of stochastic process, Entropy rate, Hidden Markov Models.

**Unit – VI:**

Channel Capacity, Noiseless binary channel, Symmetric, Gaussian channel

**Text / Reference Book:**

1. Element of Information Theory by Cover and Thomas, New York: Wiley, 1991.
2. A First Course in Stochastic Process by Samuel Karlin and Howard M. Taylor, Academic Press Inc. (London) Ltd., 1988.
3. Stochastic Processes by Sheldon M. Ross, John Wiley & Sons, 2000.
4. An Introduction to Stochastic Processes by Edward P. C. Kao, Duxbury, 1999.

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester

**Subject:** Data Warehousing and Data Mining (BTBI- 331)

**COURSE CONTENTS**

**Unit – I:**

Introduction, Data cleaning, Data Preprocessing, Data Intergration , Classification Methods, Cluster analysis methods, Data visualization and Visual data mining, computational mining of biological processes.

**Unit – II:**

Multiple sequence alignment using antipole clustering, AntiClustAl, Comparing Clustal with AntiClustAl, RNA structure comparison and alignment models, algorithm for RNA secondary structure comparison, Structure alignment.

**Unit – III:**

Piecewise constant modeling of sequential data, Bayesian method, Examples, Gene mapping, Haplotype basis of gene mapping, Predicting protein folding pathways.

**Unit – IV:**

Introduction, Methods for locating protein intracellular locations, Chemical compounds, background classification based on frequent sub graphs, Experimental evaluation.

**Unit – V:**

Phyloinformatics, synthesizing bigger trees, Visualizing larger trees, secondary structure querying evaluation techniques, index structure for sequences, protein structure indexing

**Text / Reference Book:**

1. Jason T. L. Wang, *Data Mining in Bioinformatics*, Springer, 2005.
2. Sushmita Mitra, Tinku Acharya, *Data Mining: Multimedia, Soft Computing, and Bioinformatics*, John Wiley and Sons, 2003.
3. Hui-Huang Hsu, *Advanced Data Mining Technologies in Bioinformatics*, Idea Group Inc, 2006.
4. Jiawei Han, Micheline Kamber, *Data Mining: Concepts and Techniques*, Elsevier

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester

**Subject:** Perl Programming for Bioinformatics (BTBI - 341)

### COURSE CONTENTS

#### **Unit – I:**

Getting started with PERL, Perl's Benefits, Versions of Perl, Downloading and installing Perl in Linux/Windows environment, How to run perl programs in Linux/Windows environment, Error Message, Debugging, Perl interpreters, Perl scripts.

#### **Unit – II:**

Scalar values and scalar variables, Strings and numbers, Assignment statements, Blocks, Arrays, Hashes, Operators, Operator precedence, Conditional and logical operators, Binding operators, Loops, IO, Input from file, Input from SDIN, Input from file named in command line, Opposite commands, regular expression, Pattern matching, Meta symbols, Pattern modifiers, Subroutines and modules, Built-in functions.

#### **Unit – III:**

Application of Perl in Bioinformatics: Representing strings and sequenced data in Perl, Program to store a DNA sequence, Concatenating DNA fragments, DNA to RNA transcription, Reading proteins from files, Finding motifs, Counting nucleotides, Exploding strings into arrays, Operating on strings.

#### **Unit – IV:**

Generating random numbers, a program to simulate DNA mutation, Generating random DNA, Analyzing DNA, Translating DNA into proteins, GenBank sequence and annotation, Parsing annotation, Indexing GenBank with database.

#### **Unit – V:**

PDB files, Parsing PDB files, Parsing BLAST output, Introduction to BioPerl, CPAN (Comprehensive Perl Archive Network), Introduction to Python.

#### **Text / Reference Book:**

1. James D.Tisdall, "Beginning Perl for Bioinformatics", O'Rilley and Associates, 2001.
2. Cynthia Gibas & Per Jamesbeck, "Developing ioinformatics Computer skills", O' Rilley & Associates, 2000
3. Rex A.Dawyer, "Genomic Perl", Cambridge University Press.
4. Learning Perl, 3<sup>rd</sup> Edition: Randal L.Schawrtz and Tom Phoneix, O'Rilley

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester  
**Subject:** Computer Networking, HTML, and Website Designing (BTBI - 351)

### COURSE CONTENTS

#### **Unit I:**

Basic concepts of Computer Networking and Internet: Introduction to Internet (History, Terminologies, Technologies); Understanding the Internet, Intranet, Extranet; Hardware requirement to connect to Internet; S/W requirement and Internet service products; Internet addressing scheme.

#### **Unit II:**

Understanding the Web: Introduction to WWW and its resources; Domain System Name- URL; Web surfing (Sites related to Bioinformatics, education, research and commerce); Web search engines; Electronic mailing – SMTP.

#### **Unit III:**

Internet Software: Introduction to TCP/IP and other network protocols (UDP, SNMP, ICMP e.t.c.); DNS – IP Address to name conversion and vice-versa; Basic Functionalities of TCP/IP – Client / Server model; Web servers

#### **Unit IV:**

Internet Programming Tools- HTML, DHTML, JavaScript: Designing and developing web pages using HTML/DHTML (Common Tags, Header, Linking, Images Formatting Text, Unordered list, Basic HTML tables, Basic and Complex HTML forms and Internal linking); Introduction to JavaScript (A simple program, Memory concepts, Decision making, Control structures, Program modules in JavaScript, User defined functions, Arrays, Thinking about objects, Math object, String object, Date object, Boolean and Number objects); Event Model (Event onClick, onLoad, onMouseOver, onMouseMove, onMouseOut, onBlur, onFocus, onSubmit, and onReset)

#### **Unit V:**

Web security: Web security issue (Authentication, Integrity and Security); User – Interface; Security (Symmetric and Public key Cryptography, Digital signatures and Message digest)

#### **Text / Reference Books:**

1. The INTERNET Book- By Douglas E. Comer (PHI Pub.) 2<sup>nd</sup> Edition 2001
2. Internet and World Wide Web- How to Program- By Deitel & Deitel (Pearson Education) 4<sup>th</sup> Edition 2003.
3. HTML, DHTML, JavaScript- By Ivan Bayross (BPB Pub.) 4<sup>th</sup> Edition 2003

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester

**Subject:** Perl Programming Lab (BTBI - 361)

**COURSE CONTENTS**

- Perl scripts to solve biological problems using scalar and array variables.
- Perl script to find motif.
- Perl script to make 2D matrices for two input sequences
- Perl script to make alignment of two sequences
- Perl script to calculate base pairs and G+C contents
- Perl script to find Open Reading Frame
- Perl script for Restriction mapping
- Perl script to translate Nucleotide into Amino acid
- Perl script for Parsing GenBank Flat File

Singhania university, Department of Bioinformatics

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – V Semester  
Subject: Networking, HTML, and Website Designing Lab (BTBI - 371)

### COURSE CONTENTS

- Simple web page designing using basic HTML tags and attributes
- Web page to create tables
- Develop web pages using frames
- Web page to create application forms (e.g. student admission form, form to submit biological information with reference to GenBank Flat File, etc)
- Application form validation by using Java script
- Application of Event Model (Event onClick, onLoad, onMouseOver, onMouseMove, onMouseOut, onBlur, onFocus, onSubmit, and onReset) in web pages and application form's field
- Using META tags to make web page search engine friendly
- Design a simple website to link all bioinformatics database and tools

Sri Gyania University (Department of Bioinformatics)

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester

Subject: Gene Expression & MicroArray Analysis (BTBI - 312)

### COURSE CONTENTS

#### Unit – I:

DNA MicroArray: The Technical Foundations, Why are MicroArray Important? What is a DNA MicroArray

#### Unit – II:

Designing A MicroArray Experiment: The Basic steps, Types of MicroArray, NCBI and MicroArray Data Management, GEO (Gene Expression Omnibus), MAML, The benefits of GEO and MAML, The Promise of MicroArray Technology in Treating Disease

#### Unit – III:

MicroArray Data, Preprocessing the Data, Measuring Dissimilarity of Expression Pattern, Distance Motifs and Dissimilarity measures, Visualizing MicroArray Data: Principal Component Analysis, PCA and MicroArray Data.

#### Unit – IV:

K-Means Clustering, Hierarchical Clustering, Self-Organization Maps (SOM).  
Identifying Genes: Expressed usually in a sample, Expressed significantly in population, Expressed differently in two populations.

#### Unit – V:

Classifying Samples from two populations using Multilayer Perceptron, Support Vector Machines and their applications, Using genetic algorithm and perceptron for feature selection and supervised classification

#### Web Resource (Data, Software, Tutorials)

Web Resources of MicroArray Technology and Gene Expression:

1. <http://www.mged.org/>
2. <http://www.microarrays.org>
3. <http://www.gene-chips.com>
4. <http://cmgm.stanford.edu/pbrown/mguide/>
5. <http://www.ebi.ac.uk/microarray/>
6. <http://www.ncbi.nlm.nih.gov/geo/>
7. <http://www.123genomic.com/files/microarray.html>

8. <http://industry.ebi.ac.uk/alav/microarrays>
9. <http://www.statsoft.com/textbook/starthome.html>
10. <http://linkerockefeller.edu/wli/microarray/>
11. genesight@biodescovery supports PCA, scatter plots, hierarchical clustering.
12. <http://www.pnas.org/cgi/content/full/96/6/2907>

**Text/Reference Books:-**

1. Microarray Data Analysis and Visualization by Arun Jogota, Bioinformatics, The Bay Press, 2001
2. NCBI Science Premier on MicroArrays.
3. Bioinformatics Methods and Application-Genomics, Proteomics and Drug Discovery, by S. C. Rostogi, N. Mendiratla and P. Rostogi, Prentice Hall (India), 2004

Singhania University (Department of Informatics)

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester

**Subject:** Pharmacogenomics & Pharmacogenetics (BTBI - 322)

**COURSE CONTENTS**

**Unit – I:**

Introduction to Pharmacogenomics and Pharmacogenetics, Definition of SNP's, Role of SNP in Pharmacogenomics in clinical trails, Patenting issues in Pharmacokinetics research

**Unit – II:**

Basics of Drug Pharmacokinetics and Pharmacodynamics, How the polymorphism of CYP450 enzymes effects of drug response

**Unit – III:**

Poor metabolizes, Fast metabolizers and drug response.

**Unit – IV:**

Correlation of CYP450 alleles with adverse drug reactions, Pharmacogenomics in the treatment of various diseases

**Text/Reference Books:-**

Singhania University Department of Bioinformatics

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester

Subject: MicroSoft Visual Basic (BTBI- 332)

### COURSE CONTENTS

**Unit – I:**

Introduction to Visual Basic: Introduction, VB Application Development Cycle, Loading VB, VB Current Interface, VB Controls, Drawing Objects on the Form, Event procedures.

**Unit – II:**

Programming Fundamentals: Variables, Scope and Life Time of Variables, Data types; Modules: Form Modules, Standard Modules, Class Module; Procedures: Sub procedures, Function procedures, Property procedures.

**Unit – III:**

Control Structure: Decision structure (If, Select Case), Loop structure (Do While ...Loop, Do...Loop While, For...Next, For Each...Next), Exit statement; Control Array, Arrays; Functions

**Unit – IV:**

Menu Editor, Writing Code for Menu Controls; Dialog Boxes; MDI Application, Menu in MDI Applications; Adding Status bar; Adding a Tool bar; Data Files Handling.

**Unit – V:**

Database Access: accessing Database, Data Control; Data Access Object (DAO), Active Data Objects (ADO), Remote Data Object (RDO); Visual Basic and Oracle.

Text/Reference Books:-

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester

Subject: Artificial Neural Network (BTBI- 342)

### COURSE CONTENTS

#### Unit – I:

**Introduction:** What Is AI, the Foundations of Artificial Intelligence, The History of Artificial Intelligence, Intelligent Agents, How Agents Should Act, Structure of Intelligent Agents, Environments.

#### Unit – II:

**Search Methods:** Solving Problems by Searching, Problem-Solving Agents, Formulating Problems, Search Strategies, Avoiding Repeated States, Constraint Satisfaction Search, Informed Search Methods, Best-First Search, Heuristic Functions, Memory Bounded Search, Iterative Improvement Algorithms, Game Playing, Introduction, Games as Search Problems, Perfect Decisions In Two-Person Games, Imperfect Decisions, Alpha-Beta Pruning, Games That Include An Element Of Chance.

#### Unit –III:

**Logical Reasoning Systems:** First-Order Logic, Syntax and Semantics, Extensions and Notational variations, Using First Order Logic - Introduction to Logical Reasoning system Indexing, Retrieval and Unification, Logical Programming Systems, Theorem Provers, Forward-Chaining Production Systems, Frame Systems and Semantic Networks.

#### Unit –IV:

**Reasoning Under Uncertainty:** Uncertainty, Acting under Uncertainty, Basic Probability Notation, The Axioms of Probability, Bayes' Rule and its Use, Probabilistic Reasoning Systems, Representing Knowledge in an Uncertain Domain, The Semantics of Belief Networks, Inference in Belief Networks, Inference in Multiply Connected Belief Networks, Non monotonic reasoning, Dealing with ignorance, Dempster Shafer theory, Dealing with vagueness- Fuzzy logic and fuzzy sets.

#### Unit –V:

**Planning and Learning:** Planning A Simple Planning Agent, From Problem Solving to Planning, Planning in Situation Calculus, Basic Representations for planning, A Partial-Order Planning Example, A Partial-Order Planning Algorithm- Learning- A General Model of Learning Agents, Inductive Learning, Learning Decision Trees, Neural Networks, Bayesian Methods for Learning Belief Networks, Genetic Algorithms and Evolutionary Programming, Knowledge in Learning, Explanation-Based Learning.

#### Text/Reference Books:-

1. Stuart Russel and Peter Norvig, *Artificial Intelligence- A Modern Approach*, Prentice Hall, 1995.
2. George F Luger, *Artificial Intelligence*, Pearson Education, 4th Edition, 2001.
3. Engene Charniak and Drew Mc Dermott, *Introduction to Artificial Intelligence*, Addison Wesley, 2000.
4. Nils J. Nilsson, *Principles of Artificial Intelligence*, Narosa Publishing House, 2000.
5. Dan W. Patterson, *Introduction to Artificial Intelligence and Expert systems*, Prentice Hall of India, 1992.
6. Robert J Schalkoff, *Artificial Intelligence- An Engineering Approach*, McGraw Hill, 1990.

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester  
**Subject:** Advance Networking and Multimedia (BTBI- 352)

**COURSE CONTENTS**

**Unit – I:**

Introduction, Applications of a Network, Analog and Digital Techniques, Serial and Parallel Transmission, Asynchronous and Synchronous Transmission.

**Unit – II:**

TCP/IP, Telnet, Hypertext Transfer Protocol, Web Servers, Browsers, Search Engines, Web Servers, Firewalls & Intranets, International Organization for Standardization (ISO), OSI Reference Model, TCP/IP Reference Model, LAN Protocols.

**Unit – III:**

Ethernet, Ethernet Limitations, 10 Mbps Switched Ethernet, 100 Mbps Ethernet, Arcnet LAN, IBM Token ring LAN, FDDI.

Introduction to Integrated Services Digital Network (ISDN), Types of ISDN, ISDN Standards.

**Unit – IV:**

Photoshop:

**Unit – V:**

Flash:

**Text/Reference Books:-**

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester  
Subject: Bioinformatics Lab (BTBI - 362)

### COURSE CONTENTS

**1. An introduction to the computing platforms:**

This includes background information on computers in general, all forms of remote computing, text editing, basics of the UNIX operating system, and the X environment, as well as a brief introduction to the GCG Wisconsin Package and its graphical user interface (GUI) SeqLab.

**2. Molecular databases and how they are organized and accessed:**

Internet sequence and structural databases as well as the on-site GCG sequence databases will be reviewed. Access methods such as those available on the WWW, NetEntrez, and GCG's LookUp will be emphasized but data entry and format conversion are also covered.

**3. Unknown DNA -- rational probe design and analysis:**

How to design and analyze oligonucleotide primers for discovering genes in organisms where they have not been identified when the gene's encoded protein sequence is known in other organisms. Techniques used include basic multiple sequence alignment, consensus creation, back translation, and primer discovery and evaluation.

**4. DNA sequencing, the GCG fragment assembly system (FAS), and restriction enzyme mapping:**

How to get sequencing fragment data from an automated sequencer into the computer and assembled into a continuous sequence and then how to perform restriction enzyme mapping and compositional analysis on that contig for subcloning and other purposes.

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – VI Semester

Subject: Microsoft Visual Basic Lab (BTBI - 372)

### COURSE CONTENTS

#### Unit – I:

Introduction to Visual Basic: Introduction Graphical User Interface (GUI), Programming Language(Procedural, Object Oriented, Event Driven), The Visual Basic Environment, How to use VB compiler to compile / debug and run the programs.

#### Unit – II:

Introduction to VB Controls (Textboxes, Frames, Check Boxes , Option Buttons, Images, The Shape Control, The line Control); Working with multiple controls and their properties, Designing the User Interface, Keyboard access, tab controls, Default & Cancel property, Coding for controls.

#### Unit – III:

Variables, Constants, and Calculations Variables, Variables Public, Private, Static, Constants, Data Types, Naming rules/conventions, Constants, Named & intrinsic, Declaring variables, Scope of variables, Val Function, Arithmetic Operations, Formatting Data.

#### Unit – IV:

Decision & Conditions If Statement, If ?then-else Statement, Comparing Strings, Compound Conditions(And, Or, Not), Nested If Statements, Case Structure ,Using If statements with Option Buttons & Check Boxes, Displaying Message in Message Box, Testing whether Input is valid or not. Using Call Statement to call a procedure

#### Unit – V:

Menus, Sub-Procedures and Sub-functions Defining / Creating and Modifying a Menu, Using common dialog box, Creating a new sub-procedure, Passing Variables to Procedures, Passing Argument ByVal or ByRef, Writing a Function Procedure.

#### Unit – VI:

Multiple Forms, Creating , adding, removing Forms in project, Hide, Show Method, Load, Unload Statement, Me Keyword, Referring to Objects on a Different Forms. List, Loops and Printing: List Boxes & Combo Boxes, Filling the List using Property window / AddItem Method, Clear Method, List box Properties, Removing an item from a list, List Box/ Combo Box, Do/Loops, For/Next Loops, Using MsgBox Function, Using String Function, Printing to printer using Print Method.

#### Unit – VII:

Arrays Single-Dimension Arrays, Initializing an Array using for Each, User-Defined Data Types, Accessing Information with User-Defined Data Types, Using List Boxes with Array, Two dimensional arrays.

**Unit – VII:**

OOP in VB, Classes, Creating a new Class, Creating a new object using a class, choosing when to create New Objects, The Initialize & Terminate events.

**Unit – VIII:**

Data Files Opening and Closing Data Files, The Free File Function, Viewing the data in a file, Sequential File Organization (Writing Data to a sequential Disk File, Creating a sequential data file, Reading the Data in a sequential file, Finding the end of a Data file, Locating a file). Trapping Program Errors, The Err Object, Random Data File Opening a random file, Reading and writing a random file(Get, Put, LOF, Seek).

**Text / Reference Book:**

1. Black Book of Visual Basic
2. Mastering in Visual Basic

Singha is University Department of Information

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester  
**Subject:** Advanced Algorithm for Computational Biology (BTBI - 411)

### COURSE CONTENTS

**Unit – I:**

Algorithms and Complexity, Algorithm Design Techniques, Tractable versus Intractable Problems

**Unit – II:**

Restriction Mapping, Graphs, Measuring Fragment Size, Restriction Mapping Algorithms, Double Digest Problem, Classifying multiple solutions, NP-Completeness, Regulatory motifs in DNA Sequences, Profiles, Motif finding Greedy algorithms, Divide and Conquer Algorithms.

**Unit – III:**

Markov Chains, Hidden Markov Models, CG-Islands, Forward & Backward Algorithm, HMM Parameter estimation, Profile HMM, Building viterbi Algorithm, Multiple Sequence Alignment by profile HMM's.

**Unit – IV:**

Graph Algorithms, DNA Sequencing, Shortest Superstring Problem, DNA Arrays as an Alternative Sequencing Technique, Sequencing by Hybridization, SBH as a Hamiltonian Path Problem, SBH as an Eulerian Path Problem, Fragment assembly in DNA Sequencing.

**Unit – V:**

Phylogenetic Reconstruction, Gene Expression Analysis, Hierarchical Clustering, *k*-Mean Clustering, Distance Based Tree Reconstruction, Additive Metrics, Metrics on Tree, Ultrametric Trees, Character-Based Tree Reconstruction, Parsimony Method, Evolutionary Methods, Maximum Likelihood Method, Model Comparison.

**Unit – VI:**

Protein Folding: Levels of Proteins Structures, Prediction by Profile HMMs, Molecular Modeling.

**Text / Reference Book:**

1. An Introduction to Bioinformatics Algorithms, Neil C Jones & Pavel A. Pevzner, Ane Books, 2005.
2. Introduction to Computational Molecular Biology, Setubal and Meidanis, Thomson, 2003.
3. Biological Sequence Analysis Probabilistic Models of Proteins and Nucleic Acid, R. Durbin, Eady, A. Krogh and Mitchison, Cambridge University Press, 1998.
4. Introduction to Mathematical Method in Bioinformatics, Alexcender Isaev, Springer Universitext, 2004

Website <http://www.bioalgorithms.info>

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester

**Subject:** Environmental Engineering (BTBI - 421)

**COURSE CONTENTS**

**Unit – I:**

Air Pollution, sources of pollution, Classification, Effects on Human Beings, Global effects of Air pollution.

**Unit – II:**

Air pollution Control Methods, Particulate control devices, General Methods of Controlling Gaseous Emission; Special Treatment Methods, Adsorption, Reverse Osmosis, Defluoridation, Ion exchange, Ultra Filtration.

**Unit – III:**

Theories industrial waste treatment, Volume reduction, strength reduction, Neutralization, Equalization, Proportioning, Nitrification and Denitrification, Removal of Phosphates.

**Unit – IV:**

Solid waste Management, sources, Composition and properties of solid waste, Collection and handling, Separation and processing.

**Unit – V:**

Solid waste disposal methods, Land filling, Incineration composting; Hazardous Waste, Nuclear waste, Biomedical wastes, chemical wastes, Effluent disposal and Control methods.

**Unit – VI:**

Noise Pollution, effects of noise and control methods, Effluent standards, Air emission standards, Water Act, Air Act, Environment Protection Act.

**Text / Reference Book:**

1. Environmental Science and Engineering by J.G.Henry and G.W.Heinke – Person Education.
2. Environmental Engineering and Management – Dr.Suresh K.Dhameja – S.K.Kartarai & Sons 2nd Edition 2005.

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester

**Subject:** Molecular Imaging & Drug Designing (BTBI - 431)

### COURSE CONTENTS

#### **Unit – I:**

Overview of Drug design, Simulation Methods, Molecular Mechanics, Monte Carlo, Semi-Impirical Method, Ab-initio Method.

#### **Unit – II:**

Analog based drug design: QSAR, Molecular Structure determination, Advance crystallographic techniques, Simulation Anneling (Autodock /Quantum), Peptide Sequencing, EST Clustering.

#### **Unit – III:**

Comparative Protein Modelling: Homology Modeling, Structural Alignment, Ramachandran plot (Side Chain Placement Refinement & Validation of Model), 3D- Pharmacophore modeling.

#### **Unit – IV:**

Computer-aided drug designing: Drug design, Lead discovery, ADMET in drug design, Lipinski "rule of 5", Principle and Methods of Docking, Ligand based drug designing, Target identification, Drug Metabolism, Denovo design of drug Structure based drug design.

#### **Unit V:**

Introduction of Drug discovery, Pharmacogenomics, Analysis of SNP's, Drug discovery technologies and strategies.

#### Text / Reference Book:

1. Molecular Modelling: Principle and Applications, Andrew R. Leach, Longman Singapore Publisher, 1999
2. Bioinformatics: From Genome to Drugs (Vol. I and II), Thomas Lengauer, Wiley- VCH, 2000
3. Structural Bioinformatics, P. E. Bourne and B.H. Weissing, Wiley VCH, 1999
4. Bioinformatics Method and Applications-Genomics, Proteomics and Drug Discovery, S.C. Rastogi, N. Mendiratta and P. Rastogi, Prentice Hall (India), 2004

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester

**Subject:** ASP (BTBI - 441)

**COURSE CONTENTS**

**Unit – I:**

Introduction to Active Server Page, ASP differs from Client-Side Scripting Technologies, Running ASP: Setting Personal Web server (PWS) and Internet Information Server (IIS), Creating ASP Page

**Unit – II:**

ASP Script: Writing ASP Code in different ways, Comments, Return value of Asp script to the Browser; Variables; Data types; Constants; VBScript Operators.

**Unit – III:**

Control Structure: Conditional, Looping, Branching; VBScript Built-in Functions: Formatting Functions, Math Functions, Date Functions, String Functions, Other Functions.

**Unit – IV:**

Building Block of Objects: Properties, Methods, Instances of Objects; Built-in Objects: Response object, Request object, Application object, Session object, Server object, Object Context objects, ASPError object; Events.

**Unit – V:**

Reading and Writing Files on Web Server; Debugging and Error Handling; Database Handling using ASP: Connecting with Database; Reading, Inserting, Updating, and Deleting Database Records.

**Text / Reference Book:**

1. Teach Your Self: Active Server Pages 3.0 by Scott Mitchell and James Atkinson, Techmedia

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester

**Subject:** Core Java (BTBI - 451)

### COURSE CONTENTS

#### **Unit – I:**

Introduction to Java: Importance and Features of Java, Keywords, Constants, Variables and Data Types, Operators and Expressions, Decision Making, Branching and Looping: if..else, switch, while, do, for Statements, Labeled loops, Jump statements: break, continue, return.

#### **Unit – II:**

Introducing Classes, Objects and Methods: Defining a class, Adding Variables and Methods, Creating Objects, Constructors, Class Inheritance; Arrays and String: Creating an array, one and two dimensional arrays, String array and methods; Classes: String and String Buffer classes, Wrapper classes: Basics types, using super, Multilevel hierarchy abstract and final classes, Object class, Packages and interfaces, Access protection, Extending Interfaces, packages.

#### **Unit – III:**

Exception Handling: Fundamentals exception types, Uncaught exceptions, throw, throw, final, built in exception, Creating your own exceptions, Multithreaded Programming: Fundamentals, Java thread model: Priorities, Synchronization, Messaging, Thread classes, Runnable interface, Inter thread Communication, Suspending, Resuming and Stopping threads.

#### **Unit – IV:**

Input/Output Programming: Basics, Streams, Byte and Character Stream, Predefined Streams, Reading and Writing from console and files; Using Standard Java Packages (lang, util, io, net)

#### **Unit – V:**

Event Handling: Different Mechanism, the Delegation Event Model, Event Classes, Event Listener Interfaces, Adapter and Inner Classes, Working with windows, Graphics and Text, Using AWT controls, Layout managers and Menus, Java Applet. Beans: Introduction to Java Beans and Swings; Servlets

#### **Text / Reference Book:**

1. E. Balaguruswamy, "Programming with Java: A Primer", TMH, 1998.
2. Horstmann, "Computing Concepts with Java 2 Essentials", John Wiley.
3. Decker & Hirshfield, "Programming Java: A introduction to programming using JAVA", Vikas Publication, 2000.
4. Patrick Naughton and Herbertz Schildt, "Java-2 The Complete Reference", TMH, 1999.

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester

**Subject:** ASP Lab (BTBI - 461)

**COURSE CONTENTS**

- HTML Form with Java Script validation
- Setting Personal Web server (PWS) and Internet Information Server (IIS)
- Conditional, Looping.
- Application of VBScript Built-in Functions.
- Script to work with Database (MS-Access, Oracle, Sql)
- Database and Operating Tools for Biological (genetic and Proteomic database)
- Exception Handling

Sinhgahi Universt (Department of Bioinformatics)

Course: B.Tech. & M.Tech. Integrated (Bioinformatics) – VII Semester

Subject: Java Lab (BTBI - 471)

COURSE CONTENTS

- HTML Form with Java Script validation
- Simple Java program with Variables, Data Types, Operators, Expressions, Decision Making, Branching and Looping
- Creating Methods, Creating Objects, Constructors, Class Inheritance
- Java program with Arrays and String
- Java program with Exception Handling, Multithreaded Programming,
- Input/Output Programming
- Event Handling, Working with windows, Graphics and Text, Using AWT controls, Layout managers and Menus, Java Applet.

Sri Chaitanya University, Department of Bioinformatics

**Course:** B.Tech. & M.Tech. Integrated (Bioinformatics) – VIII Semester

**Subject:** Major Project (BTBI - 412)

### **Major Project Guideline**

- ❑ The project synopsis should be prepared in consultation with the supervisor(s).
- ❑ Students must submit his/her project synopsis to the Head or Course coordinator along with his/her Name, Father's Name, ID Number, Title of Project, etc and get it approved by them.
- ❑ Project must be done by individually.
- ❑ Approval by the supervisor is based on the directions given by the Department.
- ❑ After scrutinizing the same by the supervisor, students must complete their project and submit the final report within the stipulated time in the form of soft and hard copy to the Department.
- ❑ The Department will evaluate project.
- ❑ Students must demonstrate their project in their Department to the concern persons on the date fixed by the department or examination department.

#### **Synopsis of your Project:**

1. Title of the project
2. Objective of the project
3. Language(s) / Tool to be used
4. A complete structure of program
  - a) Analysis
  - b) Module description
  - c) Data structure (Schema, E-R Diagram, Tables etc.)
  - d) Logic diagram
5. Future scope of the project
6. Any other relevant information

#### **Project category:**

Group 1: Internet based

Group 2: Non Internet based

Group 3: Software based

Group 4: Non Software based

### Project Limited:

- Project must be a complete application such as Biological, Computational, Computational Biology, Genomics, Proteomics, Metabolic pathways, Computational algorithm for biological problems etc.
- It must be clearly divided into modules and properly document.

### Project area and tools:

<u>Case Study:</u>	Biological Problems, Bioinformatics Tools & Databases, etc
<u>GUI Tools:</u>	Visual Studio, SQL Windows, HTML etc.
<u>Languages:</u>	C++, Perl, Python, BioJava, Java etc.
<u>Application:</u>	Database Management / Internet / Client-Server / Multimedia / Graphics etc.
<u>Database:</u>	Oracle, mySQL
<u>Hardware Requirements:</u>	CPU, RAM, Disk space etc.
<u>Software Requirement:</u>	OS, Application Development Packages etc.

### Project Report:

- The length of report may be an about 40 to 50 page, with 1.5 line spacing, 1.25 inches margin on either side, printed on A4 size papers. Ten percent variation on either side is permissible.
- It must contain the following:
  - Preliminary requirement: Title of project, Acknowledgement, Certificate, Index
  - Introduction
  - Objectives
  - Project category
  - Tools / environment used
  - Analysis and design
  - Program structure
  - Coding
  - Documentation
  - Future application
  - References
- Two sets of soft and hard copy must be submitted to the Department by the students along with source code, input data, report generated by used tools/database/software and exe file and the third copy of the project report may be collected back by the students after evaluation.

**Instructions to the supervisor:** (Project guidelines for approval & final evaluation).

**Eligibility of Project guides:**

The Project guide must be a M.Sc. or M.Tech. or equivalent in Bioinformatics, Biotechnology, Biology, Computer Science, or Information Technology with minimum 1 year research experience.

**Objectives of the project proposed:**

- To provide the scope to apply the concept of Bioinformatics, computer programming language, database used and application of computer science in biology.
- To analyze biological problems and provides good exposure to development & implementation of software database by following the software engineering concepts.

**Points to be considered while approving the synopsis:**

- Provide the scope to apply the core concept of Bioinformatics and application of Computer science in Biology.
- Provide the good exposure to software/algorithm/database development & implementation.
- Synopsis should be submitted as per the given instructions.
- Structure of the program must give good understanding of the problem & its implementation. Above-mentioned objectives must be fulfilled.
- Project should not be repeated.

**Project Evaluation (Internal Assessment):**

- Submission date for the project must be strictly followed as per the schedule given.
- Project shall be evaluated and the Department shall award the marks.
- Arrange presentation & demonstration along with viva for each student for their project during the date specified by the Department.
- Department must be arrange for an external evaluator having the above-mentioned qualification and the project certificate. Must have the signature and address of the evaluator.
- Out of 100 marks the project shall have 60 marks for Internal Assessment and 40 marks for Semester Assessment as per the table given:

Marks:

• <b>Internal Assessment:</b>	100 Marks
Project Supervisor:	40
Presentation & Viva Voce Internal	40 + 20 = 60
.....	
Total:	100
• <b>Semester Assessment:</b>	300 Marks

Presentation & Viva Voce - Final:	150 + 50 = 200
Project Report:	100
.....	
Total:	400

- ✦ Department must keep synopsis and project report (hard & soft copy along with program code) of all the students for at least one year after completion for verification by the University.
- ✦ If a project is not up to the expectation or any malpractice is found then such projects have to be repeated.
- ✦ Grand total marks must be sent to Examination department as per Department norms and also the individual marks distribution table.

Singhania University (Department of Bioinformatics)

**Course:** M.Tech. Integrated (Bioinformatics) – IX Semester

**Subject:** Introduction to Nanotechnology (BTBI - 511)

### COURSE CONTENTS

#### **Unit – I:**

Need of quantum mechanics, dual nature of light, heisenberg's uncertainty principle, schrodinger's equation in one and three dimension, particle in a one dimensional box, density of states for particle in a box, density of states for a 1-D quantum wire, tunneling. Revision of crystal structures, quasicrystals, bonding in solids, electronic structure of solids

#### **Unit – II:**

Physical methods for synthesis of nanomaterials: mechanical methods, vapour deposition, cluster beam deposition, laser vapourization, laser pyrolysis, sputter deposition, chemical vapour deposition, electric arc deposition, ion implantation, molecular beam epitaxy

#### **Unit – III:**

Chemical methods for synthesis of Nanomaterials: colloids and colloids in solutions, colloids in vacuum, colloids in medium, synthesis of colloids, growth of nanoparticles, synthesis of metal nanoparticles, synthesis of semiconductor nanoparticles, langmuir-blodgett method, microemulsions, sol-gel method

#### **Unit – IV:**

Biological synthesis of Nanomaterials: synthesis using microorganisms, synthesis using plant extracts, synthesis using proteins and DNA templates.

Review of axioms of quantum mechanics, states and the bra / ket notation, rudiments of quantum theory of the process of measurement, relationship between quantum and classical concepts,

#### **Unit – V:**

WKB approximation, time evolution: Heisenberg, Schrödinger and interaction picture, fluctuations, correlations and eigen-functions, harmonic oscillator, angular momentum and three dimensional wave equation, orbital and spin angular momentum, exclusion principle.

**Text / Reference Book:**

**Course:** M.Tech. Integrated (Bioinformatics) – IX Semester

**Subject:** Image Processing (BTBI - 521)

**COURSE CONTENTS**

**Text / Reference Book:**

1. Digital Image Processing by R. C. Gonzalez and R. E. Woods
2. Mastering Matlab 6: A Comprehensive Tutorial and Reference by D. Hanselman and B. Littlefield

Singhania University (Department of Bioinformatics)

**Course:** M.Tech. Integrated (Bioinformatics) – IX Semester

**Subject:** Data Structure using C (BTBI - 531)

**COURSE CONTENTS**

**Unit – I:**

Linear Structure: Arrays, records, stack, operation on stack, implementation of stack as an array, queue, operations on queue, implementation of queue.

**Unit – II:**

Linked Structure: List representation, operations on linked list - get node and free node operation, implementing the list operation, inserting into an ordered linked list, deleting, circular linked list, doubly linked list.

**Unit – III:**

Tree Structure: Binary search tree, inserting, deleting and searching into binary search tree, implementing the insert, search and delete algorithms, tree traversals

**Unit – III:**

Graph Structure: Graph representation - Adjacency matrix, adjacency list, adjacency multilist representation. Orthogonal representation of graph. Graph traversals - bfs and dfs. Shortest path, all pairs of shortest paths, transitive closure, reflexive transitive closure.

**Unit – IV:**

Searching and sorting: Searching - sequential searching, binary searching, hashing. Sorting - selection sort, bubble sort, quick sort, heap sort, merge sort, and insertion sort, efficiency considerations.

**Text / Reference Book:**

1. Horowitz E Sartaj Sahni, Fundamentals of data structure, Galgotia Publication Private Limited., New Delhi.

Course: M.Tech. Integrated (Bioinformatics) – IX Semester

Subject: Software Engineering (BTBI - 541)

### COURSE CONTENTS

#### Unit – I:

Introduction - S/W Engineering Paradigm, life cycle models (water fall, incremental, spiral, WINWIN spiral, evolutionary, prototyping, object oriented), system engineering, computer based system, verification, validation, life cycle process, development process, system engineering hierarchy.

#### Unit – II:

Functional and non-functional – user, system, requirement engineering process, feasibility studies, requirements, elicitation, validation and management, software prototyping, prototyping in the software process, rapid prototyping techniques, user interface prototyping, S/W document. Analysis and modeling - data, functional and behavioral models, structured analysis and data dictionary.

#### Unit – III:

Design concepts and Principles: Design process and concepts, modular design, design heuristic, design model and document. Architectural design - software architecture, data design, architectural design, transform and transaction mapping, user interface design, user interface design principles. Real time systems - Real time software design, system design, real time executives, data acquisition system, monitoring and control system. SCM – Need for SCM, Version control, Introduction to SCM process, Software configuration items.

#### Unit – IV:

Testing: Taxonomy of software testing – levels, test activities, types of s/w test, black box testing, testing boundary conditions, structural testing, test coverage criteria based on data flow mechanisms, regression testing, testing in the large, S/W testing strategies - strategic approach and issues, unit testing, integration testing, validation testing, system testing and debugging.

#### Unit – V:

Software Project Management: Measures and measurements - S/W complexity and science measure, size measure, data and logic structure measure, information flow measure. Software cost estimation - function point models, COCOMO model, Delphi method. Defining a Task Network – Scheduling, Earned Value Analysis, Error Tracking, Software changes, program evolution dynamics, software maintenance, Architectural evolution. Taxonomy of CASE tools.

#### Text / Reference Book:

1. Roger S.Pressman, Software engineering- A practitioner's Approach, McGraw-Hill International Edition, 5th edition, 2001.
2. Ian Sommerville, Software engineering, Pearson education Asia, 6th edition, 2000.
3. Pankaj Jalote- An Integrated Approach to Software Engineering, Springer Verlag, 1997.
4. James F Peters and Witold Pedryez, "Software Engineering – An Engineering Approach", John Wiley and Sons, New Delhi, 2000.

**Course:** M.Tech. Integrated (Bioinformatics) – IX Semester

**Subject:** Enzymology Enzyme Technology (BTBI - 551)

**COURSE CONTENTS**

**Unit – I:**

Enzyme Techniques: Activity of Enzymes, Handling of Enzymes, Enzyme assays, Analysis of Enzyme activity (Methods), Expression of the activity, Coupled reactions.

**Unit – II:**

DNA Technology: - rDNA Technology, Isolation and purification of Enzymes, Importance of pure enzymes, Separation of Isoenzymes.

**Unit – III:**

Enzyme Kinetics 1: Velocity of a reaction, Order of reaction, progress curve for Enzyme catalyzed reactions, Factors influencing velocity  $V_0$ ; Michaelis Mmenten Kinetics,  $K_M$  and  $V_{MAX}$ , Effect of  $P^H$ ,  $P^H$  Adjustments, Buffer preparation, Temperature on Enzymetic reactions, Anomalous kinetics of competitive and non-competitive, Inhibition, End product Inhibition with examples

**Unit – IV:**

Coenzymes: Coenzymes & Cofactors, Substrate enzyme relationship, Classification of Coenzymestransfer, Hhydrogen transfer, Structure of coenzyme. Functions of Nucleotide coenzymes - CoA, NAD/NADP, FMN/FAD, Biotin, Folic acid, Vitamin B12, Biosynthesis of Puridine and Flavin nucleotides CoA

**Unit – V:**

Enzyme technology: Application in Food and Pharmaceutical industries, Large scale enzyme extraction, Purification and stabilization, Industrial

**Text / Reference Book:**

**Course:** M.Tech. Integrated (Bioinformatics) – X Semester

**Subject:** Final Project (BTBI - 512)

### Major Project Guideline

- ❑ The project synopsis should be prepared in consultation with the supervisor(s).
- ❑ Students must submit his/her project synopsis to the Head or Course coordinator along with his/her Name, Father's Name, ID Number, Title of Project, etc and get it approved by them.
- ❑ Project must be done by individually.
- ❑ Approval by the supervisor is based on the directions given by the Department.
- ❑ After scrutinizing the same by the supervisor, students must complete their project and submit the final report within the stipulated time in the form of soft and hard copy to the Department.
- ❑ The Department will evaluate project.
- ❑ Students must demonstrate their project in their Department to the concern persons on the date fixed by the department or examination department.

#### **Synopsis of your Project:**

5. Title of the project
6. Objective of the project
7. Language(s) / Tool to be used
8. A complete structure of program
  - a) Analysis
  - b) Module description
  - c) Data structure (Schema, E-R Diagram, Tables etc.)
  - d) Logic diagram
7. Future scope of the project
8. Any other relevant information

#### **Project category:**

- Group 1: Internet based
- Group 2: Non Internet based
- Group 3: Software based
- Group 4: Non Software based

### Project Limited:

- Project must be a complete application such as Biological, Computational, Computational Biology, Genomics, Proteomics, Metabolic pathways, Computational algorithm for biological problems etc.
- It must be clearly divided into modules and properly document.

### Project area and tools:

<u>Case Study:</u>	Biological Problems, Bioinformatics Tools & Databases, etc
<u>GUI Tools:</u>	Visual Studio, SQL Windows, HTML etc.
<u>Languages:</u>	C++, Perl, Python, BioJava, Java etc.
<u>Application:</u>	Database Management / Internet / Client-Server / Multimedia / Graphics etc.
<u>Database:</u>	Oracle, mySQL
<u>Hardware Requirements:</u>	CPU, RAM, Disk space etc.
<u>Software Requirement:</u>	OS, Application Development Packages etc.

**Paper publication:** Atleast one paper published in National / International journals related to project work

### Project Report:

- The length of report may be an about 40 to 50 page, with 1.5 line spacing, 1.25 inches margin on either side, printed on A4 size papers. Ten percent variation on either side is permissible.
- It must contain the following:
  - Preliminary requirement: Title of project, Acknowledgement, Certificate, Index
  - Introduction
  - Objectives
  - Project category
  - Tools / environment used
  - Analysis and design
  - Program structure
  - Coding
  - Documentation
  - Future application
  - References

- Two sets of soft and hard copy must be submitted to the Department by the students along with source code, input data, report generated by used tools/database/software and exe file and the third copy of the project report may be collected back by the students after evaluation.

**Instructions to the supervisor:** (Project guidelines for approval & final evaluation).

**Eligibility of Project guides:**

The Project guide must be a M.Sc. or M.Tech. or equivalent in Bioinformatics, Biotechnology, Biology, Computer Science, or Information Technology with minimum 1 year research experience.

**Objectives of the project proposed:**

- To provide the scope to apply the concept of Bioinformatics, computer programming language, database used and application of computer science in biology.
- To analyze biological problems and provides good exposure to development & implementation of software database by following the software engineering concepts.

**Points to be considered while approving the synopsis:**

- Provide the scope to apply the core concept of Bioinformatics and application of Computer science in Biology.
- Provide the good exposure to software/algorithm/database development & implementation.
- Synopsis should be submitted as per the given instructions.
- Structure of the program must give good understanding of the problem & its implementation. Above-mentioned objectives must be fulfilled.
- Project should not be repeated.

**Project Evaluation (Internal Assessment):**

- Submission date for the project must be strictly followed as per the schedule given.
- Project shall be evaluated and the Department shall award the marks.
- Arrange presentation & demonstration along with viva for each student for their project during the date specified by the Department.
- Department must be arrange for an external evaluator having the above-mentioned qualification and the project certificate. Must have the signature and address of the evaluator.
- Out of 100 marks the project shall have 60 marks for Internal Assessment and 40 marks for Semester Assessment as per the table given:

**Marks:**

- **Internal Assessment:** 100 Marks

Project Supervisor:

40



## Course Structure: M. Sc. (Bioinformatics)

Course Code	Course Title	Internal Assessment	Semester Exam	Total
<b>Semester - I</b>				
MSBI-111	Introduction of Bioinformatics	30	70	100
MSBI-121	Statistics and Probability	30	70	100
MSBI-131	Molecular Biology	30	70	100
MSBI-141	Fundamental of Computer	30	70	100
MSBI-151	Operating System (Windows, Linux)	30	70	100
MSBI-161	Computer Lab - I	50	100	150
<b>Semester - II</b>				
MSBI-112	Object Oriented programming in C++	30	70	100
MSBI-122	Computational Method for Sequence Analysis	30	70	100
MSBI-132	Molecular Imaging & Drug Designing	30	70	100
MSBI-142	Database Management System & Data Mining	30	70	100
MSBI-152	Genomics, Proteomics and HGP	30	70	100
MSBI-162	Computer Lab - II	50	100	150
<b>Semester - III</b>				
MSBI-211	Perl programming for Bioinformatics	30	70	100
MSBI-221	Computer Networks and Advanced Multimedia	30	70	100
MSBI-231	Advanced Algorithm for Computational Biology	30	70	100
MSBI-241	Gene Expression & MicroArray Analysis	30	70	100
MSBI-251	Information Theory & Stochastic Process	30	70	100
MSBI-261	Computer Lab - III	50	100	150

Semester - IV				
MSBI-212	Major Project	100	300*	400
	* (Project Report Evaluation: 150 & Comprehensive Viva-voce: 150)			
<b>Grand Total:</b>				<b>2350</b>

**Program Name:** M.Sc. (Bioinformatics) – I Semester

**Course:** Introduction of Bioinformatics (MSBI - 111)

### COURSE CONTENTS

#### **Unit I:**

The nature of chemical bonds, Introduction to Genes and Proteins, Nucleotides, Orientation, Base pairing, The central dogma, Promoter sequences, Genetic Code, ORFs, Introns and Exons, Slice variants, Protein structure, Primary, Secondary, Tertiary and Quaternary, The notation of homology.

#### **Unit II:**

Introduction to Data Generating Techniques: Restriction Enzymes, Gel Electrophoresis, Blotting and Hybridization, Cloning, PCR, DNA Sequencing.

#### **Unit III:**

Biological databases, Search engines, Public databases: PubMed, EMBL, GenBank, PDB, Swiss-Port, Data Visualization, Data Mining, Entry and retrieval of data from public databases.

#### **Unit IV:**

Genomics and Proteomics: Prokaryotic genomes, Eukaryotic Genomes, Gene Structure, ORFs, GC Content in Eukaryotic genomes, Gene Expression, Protein Classification, 2D-Electrophoresis, Mass spectrometry, Microarray technology, X-ray crystallography, NMR, Sequence and Phylogeny Analysis, Detecting ORFs, Outline of sequence alignment, Mutation matrices, Pairwise alignments, Introduction to BLAST, Multiple sequence alignment, Phylogenetic analysis.

#### **Text / Reference Books:**

1. Fundamental Concepts of Bioinformatics, D.E. Krane and M.L. Raymer, Person Education, 2003.
2. Bioinformatics Computing by B. Bergeron, Prentice-Hall, 2003.
3. Bioinformatics: A practical guide to the analysis of genes and proteins, D. Baxivanis and F. Oulette, Wiley Indian Edition, 2001
4. Bioinformatics: Sequence and Genome analysis, D.W. Mount, Cold Spring Harbour Laboratory Press, 2001

**Program Name:** M.Sc. (Bioinformatics) – I Semester  
**Course:** Statistics and Probability (MSBI - 121)

**COURSE CONTENTS**

**Unit I:**

Probability, Conditional Probability, Random Variables, Expected Value

**Unit II:**

Continuous and Discrete distributions: Binomial, Geometric, Poisson, Pascal, Uniform Exponential and Normal, Poisson Process

**Unit III:**

Multidimensional random variables, Multidimensional and bivariate normal distribution, Moment generating functions

**Unit IV:**

Law of large numbers, Central limit theorem, Sampling distribution, Point and Interval Estimation Testing of hypothesis, Goodness of fit, Linear regression

**Unit V:**

Principal component analysis, Discriminant analysis, Cluster analysis, Multivariate analysis of variance

**Text / Reference Books:**

1. Statistical Methods in Bioinformatics: An Introduction by W. Evans & G. Grant, Springer, 2001
2. First course in Probability by Sheldon Ross, Prentice-Hall (India), 2001

**Program Name:** M.Sc. (Bioinformatics) – I Semester

**Course:** Molecular Biology (MSBI - 131)

### COURSE CONTENTS

**Unit I:**

Concepts in Biology: Characteristics of living organisms, Structure of cells, Energy flow; Nutrition and Metabolism; Information storage and expression, Reproduction and Inheritance,

**Unit II:**

Biomolecules: Carbohydrates, Amino Acids, Proteins, Lipids, Nucleic acids.

**Unit III:**

Enzymes; Properties, Activation energy, Reaction kinetics, Intercellular Communication, Flow of genetic information, DNA expression and replication

**Unit IV:**

Genes; Changing size of Genes, Gene synthesis, Cloning (Plant and Animal), Mutation, Gene Targeting, Gene Therapy

**Unit IV:**

Level of secondary structure, Motifs, Basic concepts of molecular dynamics, Molecular simulation studies

**Unit V:**

Protein structure determination by X-ray Diffraction, NMR, Introduction to nucleic acid structure, Genome organization, HGP

**Text / Reference Books:**

1. Molecular Biology by David Friefelder, Jones & Burtlett Publishers inc, 2000
2. Molecular Cell Biology by Alberts, Bruce Bray, Watson & James, Garland Publishing, 1999

**Program Name:** M.Sc. (Bioinformatics) – I Semester

**Course:** Fundamental of Computer (MSBI - 141)

### COURSE CONTENTS

**Unit – I:**

Digital Circuits and Computer Architecture: Transistors – and Integrated Circuits (LSI, VLSI); Operation of processor; Number Systems and Digital Circuits; ALU; Memory Chips (ROM, RAM, DRAM), Storage Devices, Memory Hierarchy; I/O Devices; Bus Systems; Computer Organization and Architecture; Microprocessor; Moore's Law.

**Unit – II:**

Operating Systems and DBMS: Windows and Linux; Basics of relational Databases; SQL.

**Unit – III:**

Programming Languages: Algorithms; Problem Solving Classification; Basics of C Language, Concepts of objects and classes, Introduction to object-oriented Programming.

**Unit – IV:**

Computers Networks: Network communication infrastructure; Protocols; Wireless LAN and Mobile Computing.

**Unit – V:**

Web Technology: HTML and Web pages; The Internet and Intranet; WWW; Java Script and Dynamic Web Pages; Multimedia Application; Computer Network Security, e-Commerce.

**Text/Reference Books:**

1. The Essential Guide to Computing: The story of Information Technology, E. Garrison Walters, PHI, 2001.
2. A Balanced Introduction to Computer science by David Reed, PE, 2000.
3. Introduction to Computing Systems: From Bits to Gates to C and Beyond. Yale N. Patt and Sanjay J. Patel. Prentice Hall India, 1999

**Program Name:** M.Sc. (Bioinformatics) – I Semester  
**Course:** Operating System -Windows, Linux (MSBI - 151)

### COURSE CONTENTS

**Unit I:**

Introductory concepts, Operating systems, Mainframe systems, Multiprocessors, Distributed systems, Real – Time systems, Computing environments

**Unit II:**

Computer system structure, Computer system organization, I/O structure, Storage structure, Storage hierarchy, Hardware protection, Network structure

**Unit III:**

Operating system structures, System components, OS Services, System calls, System programs, System structure, Virtual machines Processes, Process concepts, Process scheduling, Operations on processes, Process states, Cooperating processes, Inter-process communication, Common OS problems.

**Unit IV:**

DOS and Windows, Introductory concepts, Architecture and special features, Useful DOS commands, DOS – Editor, EDIT & writing Batch Files, Different Versions and their Distinguishing features, Managing Operations with Windows

**Unit V:**

Linux: Introductory concepts, Architecture and special features, Useful Linux commands, Related operating system and their Introduction.

**Text / Reference Books:**

1. Operating Systems by Glavin, Addison Wessely, 2000
2. Modern Operating Systems by S. Tanenbaum, Prentice Hall (India), 1999
3. Operating Systems Concept and Design by Milan Milenkovic, Tata McGraw Hill, 2000

**Program Name:** M.Sc. (Bioinformatics) – I Semester  
**Course:** Computer Lab - I (MSBI - 161)

**COURSE CONTENTS**

- Windows and Linux installation, user interface, File management, Data Security, Users management.
- Using Linux and Windows commands.
- Sequence Alignment Software: Searching for sequence databases; Protein databases, PDB, BLAST, FASTA, CLUSTALW

**Program Name:** M.Sc. (Bioinformatics) – II Semester  
**Course:** Object Oriented Programming in C++ (MSBI - 112)

### COURSE CONTENTS

**Unit – I:**

Methodologies: Concepts of structured and Object-Oriented programming, Advantages of OOPs methodologies. Introduction to Object-Oriented programming: Characteristics of OOPs Languages, C++ programming Basics operators, Loops, Arrays, Pointers.

**Unit – II:**

Principle of Object-Oriented programming, Introduction to Abstraction, Encapsulation, Inline function, Reference variable, Access specifier, Information Hiding, Friend Functions, Friend Class.

**Unit – III:**

Operator overloading, Function overloading,

**Unit – IV:**

Inheritance: Extending classes, Types of inheritance, Virtual base class, Problems with multiple inheritance, Containership.

**Unit – V:**

Advanced pointers, Virtual functions, Polymorphism, Pointers to Class, Array pointers to Class, Virtual Function-Abstract Class, Pure Virtual Function, Files and Streams, Building class Libraries in C++.

**Unit – VI:**

File Handling in C++, Template class, Exception Handling.

**Text / Reference Book:**

1. Object Oriented Programming with C++, E. Balagurusamy, Tata McGraw Hill
2. Object Oriented Programming in C++, Robert Lafore, Techmedia 2002
3. C++, How to program by Deitel & Deitel, Person Edition, 2002
4. The C++ Programming Languages by Stroustrup, Addison, Wesley., 2001
5. Problem Solving the object of Programming, Walter Savitch, Pearson Edition, 2003

**Program Name:** M.Sc. (Bioinformatics) – II Semester  
**Course:** Computational Methods for Sequence Analysis (MSBI - 122)

### COURSE CONTENTS

#### **Unit – I:**

Introduction to sequence databases: DDBJ / EMBL / GenBank; Information retrieval from databases; Analysis of DNA and Protein sequences: distribution, pattern and motif searches, Segmentation.

#### **Unit – II:**

Sequence alignment: Scoring matrices, PAM, BLOSUM, Local and global alignment concepts; Dynamic programming; Needleman - Wunch algorithm, Smith - Waterman algorithm; Statistics of alignment score; Multiple sequence alignment

#### **Unit – III:**

Database searches for homologous sequences: FASTA, BLAST and CLUSTALW, Comparison, Artificial Neural Network concepts, Preceptron, Multilayer preceptron, Secondary Structure Prediction using ANN, Back propagation Algorithm, Training and testing ANNs.

#### **Unit – IV:**

Evolutionary analysis: Distances, Clustering methods, Tree representation, Proteomics, Genome sequence assembly; Gene finding methods; Analysis and prediction of regulatory regions.

#### **Unit – V:**

Profiles and Hidden Markov Model, Gene identification and prediction, DNA Microarrays, Gene Expression, Clustering gene expression profiles.

#### **Text / Reference Book:**

1. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, A. D. Baxevanis and B. F. F. Ouellette John Wiley and Sons (ASIA) Pvt. Ltd. 2002
2. Bioinformatics methods and applications - Genomes, Proteomics and Drug Discovery, S. C. Rastogi, N. Mendiratla and P. Rastogi, Prentice Hall (India), 2004
3. BLAST by I. Korf, M. Yandell & Joseph Bedell, O'Reilly, 2003
4. Biological Sequence Analysis – Probabilistic Models of Proteins and Nucleic acids, R. Durbin, S. Eddy, A. Krogh, G. Mitchison, Cambridge University Press, 1988

**Program Name:** M.Sc. (Bioinformatics) – II Semester  
**Course:** Molecular Imaging and Drug Design (MSBI - 132)

### COURSE CONTENTS

**Unit – I:**

Overview of Drug design, Simulation Methods, Molecular Mechanics, Monte Carlo, Semi-Impirical Method, Ab-initio Method.

**Unit – II:**

Analog based drug design: QSAR, Molecular Structure determination, Advance crystallographic techniques, Simulation Anneling (Autodock /Quantum), Peptide Sequencing, EST Clustering.

**Unit – III:**

Comparative Protein Modelling: Homology Modeling, Structural Alignment, Ramachandran plot (Side Chain Placement Refinement & Validation of Model), 3D-Pharmacophore modeling.

**Unit – IV:**

Computer-aided drug designing: Drug design, Lead discovery, ADMET in drug design, Lipinski "rule of 5", Principle and Methods of Docking, Ligand based drug designing, Target identification, Drug Metabolism, Denovo design of drug. Structure based drug design.

**Unit V:**

Introduction of Drug discovery, Pharmacogenomics, Analysis of SNP's, Drug discovery technologies and strategies.

**Text / Reference Book:**

1. Molecular Modelling: Principle and Applications, Andrew R. Leach, Longman Singapore Publisher, 1999
2. Bioinformatics: From Genome to Drugs (Vol. I and II), Thomas Lengauer, Wiley- VCH, 2000
3. Structural Bioinformatics, P. E. Bourne and B.H. Weissing, Wiley VCH, 1999
4. Bioinformatics Method and Applications-Genomics, Proteomics and Drug Discovery, S.C. Rastogi, N. Mendiratta and P. Rastogi, Prentice Hall (India), 2004

**Program Name:** M.Sc. (Bioinformatics) – II Semester  
**Course:** DataBase Management System and Data Mining (MSBI - 142)

### COURSE CONTENTS

**Unit – 1:**

Introduction, Characteristics of Data base approach, Database users, Intended uses of databases, Implication of database approach.

**Unit II:**

Database System Concepts and Architecture, Data Models, Schemas and Instances, DBMS Architecture and data independence, database languages, Classification of DBMS.

**Unit III:**

Database Design: Informal Design guidelines for relation Schemas, functional Dependencies, Normal forms based on primary keys, general Definition of 2<sup>nd</sup> and 3<sup>rd</sup> Normal forms, BCNF, Need of further Normalization.

**Unit IV:**

Data Modeling using ER diagram, ER Model Concepts, Notation for ER Diagrams; The Relational Model, Relational Model Concepts, Relational Model Constraints, Introduction to Relational Algebra.

**Unit V:**

SQL: Introduction, Data definition in SQL, Queries in SQL, Update statement in SQL, Views SQL, Simple program in PL/SQL

**Unit VI:**

Data Mining, Definition, Data Mining and KDD, Data Mining on relational databases, Data Warehouses, Transactional databases etc. Data Mining Functionalities, Pattern Mining.

**Unit VII:**

Association Analysis, Classification and Prediction, Cluster Analysis, Evolution Analysis, Data Mining on Biological data.

**Text/Reference Books:**

1. Fundamentals of Database System by Elmasari and Navathe, Prentice Hall (India), 2001
2. Data Mining Concepts and techniques- Jiawei Han, Micheline Kamber, Morgan Kaufmann publisher, 2001

**Program Name:** M.Sc.(Bioinformatics) – II Semester

**Course:** Genomics, Proteomics and HGP (MSBI - 152)

### COURSE CONTENTS

**Unit – I:**

Primer Selection Phylogeny, Protein Sequence Analysis, SAGE, Primer Chain Reaction (PCR).

**Unit – II:**

Genomics, Fragmenting the genomes, Need of markers, Marker Sequencing (RFLP, AFLP & SNP, etc); Genome sequencing: Basic Sanger sequencing, Automated sequence, Gene Identification, MUMmer , Blast2.

**Unit – III:**

Proteomics, Microarray: The technique of microarray design, 2-D gel electrophoresis, Peptide sequencing, Mass spectroscopy.

**Unit – IV:**

Metabolomics, Metabolic pathway databases: KEGG, COG, WIT; Drug target identification.

**Unit – V:**

Functional genomics: Application of sequence based and structure based approach of gene function eg: Sequence comparison, Structure analysis (active site, binding site) and comparison; Approaches for determining gene expression patterns and functions.

**Unit – VI:**

What is HGP: Goals, Progress & History of HGP.

[http://www.ornl.gov/sci/techresources/Human\\_Genome/home.shtml](http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml)

**Text / Reference Book:**

1. Handbook of Comparative Genomics: Principles and Methodology by T.B. Kitano, Graziano Pesole, 2003.
2. Computational Molecular Biology by P. Clate & R. Backofen, Willy Publication, 1998 Proteomics,
3. Timothy Palkill, kluwer Academic Publisher, 2002
4. Introduction to Proteomics: Tools for the new Biology, Daniel C. Liebler, Humana Press, 2001
5. Foundation to systems Biology (Ed) by Hiroaki Kitano, MIT Press, 2001.

**Program Name:** M.Sc. (Bioinformatics) – II Semester  
**Course:** Computer Lab - II (MSBI - 162)

### COURSE CONTENTS

- Problem solving using C++ programming language.
- Sequence Alignment Software: Searching for sequence databases; Protein databases, PDB, BLAST, FASTA, CLUSTW, Comparing and aligning sequences; Phylogenetic trees for sequences
- Creating database for Biological projects including Schema, E-R Diagram, and Normalization.
- Developing database applications: SQL queries using Oracle.
- Clustering and classification software such as SOM, SVM, PCA; using visualization software such as TreeView, Sammon Mapping

**Program Name:** M.Sc. (Bioinformatics) – III Semester  
**Course:** Perl Programming for Bioinformatics (MSBI - 211)

### COURSE CONTENTS

#### **Unit – I:**

Getting started with PERL, Perl's Benefits, Versions of Perl, Downloading and installing Perl in Linux/Windows environment, How to run perl programs in Linux/Windows environment, Error Message, Debugging, Perl interpreters, Perl scripts.

#### **Unit – II:**

Scalar values and scalar variables, Strings and numbers, Assignment statements, Blocks, Arrays, Hashes, Operators, Operator precedence, Conditional and logical operators, Binding operators, Loops, IO, Input from file, Input from STDIN, Input from file named in command line, Opposite commands, regular expression, Pattern matching, Meta symbols, Pattern modifiers, Subroutines and modules, Built-in functions.

#### **Unit – III:**

Application of Perl in Bioinformatics: Representing strings and sequenced data in Perl, Program to store a DNA sequence, Concatenating DNA fragments, DNA to RNA transcription, Reading proteins from files, Finding motifs, Counting nucleotides, Exploding strings into arrays, Operating on strings.

#### **Unit – IV:**

Generating random numbers, a program to simulate DNA mutation, Generating random DNA, Analyzing DNA, Translating DNA into proteins, GenBank sequence and annotation, Parsing annotation, Indexing GenBank with database.

#### **Unit – V:**

PDB files, Parsing PDB files, Parsing BLAST output, Introduction to BioPerl, CPAN (Comprehensive Perl Archive Network), Introduction to Python.

#### **Text / Reference Book:**

1. James D.Tisdall, "Beginning Perl for Bioinformatics", O'Rilley and Associates, 2001.
2. Cynthia Gibas & Per Jamesbeck, "Developing Bioinformatics Computer skills", O'Rilley & Associates, 2000
3. Rex A.Dawyer, "Genomic Perl", Cambridge University Press.
4. Learning Perl, 3<sup>rd</sup> Edition: Randal L.Schwartz and Tom Phoenix, O'Rilley

**Program Name:** M.Sc. (Bioinformatics) – III Semester  
**Course:** Computer Networks and Advanced Multimedia (MSBI - 221)

### COURSE CONTENTS

**Unit I:**

Basic concepts of Computer Networks: Computer Networks, Networks Hardware, Networks Software, ISO-OSI reference models, Protocols (TCP/IP, application of FTP, HTTP and Telnet).

**Unit II:**

The Physical and Data Link Layer, Different transmission media, Data Link Layer Design Issues, Error Detection and Correction, Elementary Data Link Protocols

**Unit III:**

The Network Layer, Network Layer Design Issues, Routing Algorithms, Shortest Path Routing (Flooding, Flow based Routing), IP Protocols, IP Address

**Unit IV:**

The Transport Layer, The Transport Service, Services Providing to the Upper Layers, Transport Services Primitives

Internet Programming Tools- HTML, DHTML, JavaScript: Designing and developing web pages using HTML/DHTML (Common Tags, Header, Linking, Images Formatting, Events etc.)

**Unit V:**

Overview of Multimedia: Different Views and Perspectives; Multimedia Applications: Video-on-demand, Interactive television, Video conferencing, Hypermedia courseware, Groupware, World Wide Web, Digital libraries; Media and its Types: Static, Continuous, Time-Based.; Visual Communication and Human Perception: visual and auditory; Multimedia Devices and Systems: Audio/Video boards, Support for Media, CMS services; User Interface Design: Need, Significance, Guidelines etc.

**Unit – VI:**

Multimedia Development: Phases, Stages, Team etc, Multimedia Building Blocks, Text: Value and significance, Formats, style, Font Size and Type, use in MM Networking and Applications, Streaming Audio and Video, Best Effort Service, Protocols for Real Time Applications, RTP, RTCP, SIP etc.; Graphics: Significance, different Image Formats, Scheduling Policing Mechanism, Integrated services and Differentiated services

**Text / Reference Books:**

1. Computer Networks by A.S. Tanenbaum, 4<sup>th</sup> Edition, Pearson Education, 2000
2. Multimedia – An Introduction by Villmil:, Prentice Hall (India), 1999
3. Computer Networking by J.F. Kurose and Keith W. Ross, 2<sup>nd</sup> Edition, Pearson Education, 2001

**Program Name:** M.Sc. (Bioinformatics) – III Semester  
**Course:** Advanced Algorithm for Computational Biology (MSBI - 231)

### COURSE CONTENTS

#### **Unit – I:**

Algorithms and Complexity, Algorithm Design Techniques, Tractable versus Intractable Problems

#### **Unit – II:**

Restriction Mapping, Graphs, Measuring Fragment Size, Restriction Mapping Algorithms, Double Digest Problem, Classifying multiple solutions, NP-Completeness, Regulatory motifs in DNA sequences, Profiles, Motif finding Greedy algorithms, Divide and Conquer Algorithms.

#### **Unit – III:**

Markov Chains, Hidden Markov Models, CG-Islands, Forward & Backward Algorithm, HMM Parameter estimation, Profile HMM, Building viterbi Algorithm, Multiple Sequence Alignment by profile HMM's.

#### **Unit – IV:**

Graph Algorithms, DNA Sequencing, Shortest Superstring Problem, DNA Arrays as an Alternative Sequencing Technique, Sequencing by Hybridization, SBH as a Hamiltonian Path Problem, SBH as an Eulerian Path Problem, Fragment assembly in DNA Sequencing.

#### **Unit – V:**

Phylogenetic Reconstruction, Gene Expression Analysis, Hierarchical Clustering, *k*-Mean Clustering, Distance Based Tree Reconstruction, Additive Metrics, Metrics on Tree, Ultrametric Trees, Character-Based Tree Reconstruction, Parsimony Method, Evolutionary Methods, Maximum Likelihood Method, Model Comparison.

#### **Unit – VI:**

Protein Folding: Levels of Proteins Structures, Prediction by Profile HMMs, Molecular Modeling.

#### **Text / Reference Book:**

1. An Introduction to Bioinformatics Algorithms, Neil C Jones & Pavel A. Pevzner, Ane Books, 2005.
2. Introduction to Computational Molecular Biology, Setubal and Meidanis, Thomson, 2003.
3. Biological Sequence Analysis Probabilistic Models of Proteins and Nucleic Acid, R. Durbin, Eddy, A. Krogh and Mitchison, Cambridge University Press, 1998.
4. Introduction to Mathematical Method in Bioinformatics, Alexander Isaev, Springer Universitext, 2004

Website <http://www.bioalgorithms.info>

**Program Name:** M.Sc. (Bioinformatics) – III Semester  
**Course:** Gene Expression & MicroArray Analysis (MSBI - 241)

### COURSE CONTENTS

**Unit – I:**

DNA MicroArray: The Technical Foundations, Why are MicroArray Important? What is a DNA MicroArray

**Unit – II:**

Designing A MicroArray Experiment: The Basic steps, Types of MicroArray, NCBI and MicroArray Data Management, GEO (Gene Expression Omnibus), MAML, The benefits of GEO and MAML, The Promise of MicroArray Technology in Treating Disease

**Unit – III:**

MicroArray Data, Preprocessing the Data, Measuring Disimilarity of Expression Pattern, Distance Motifs and Dissimilarity measures, Visualizing MicroArray Data; Principal Component Analysis, PCA and MicroArray Data.

**Unit – IV:**

K-Means Clustering, Hierarchical Clustering, Self Organization Maps (SOM).  
Identifying Genes: Expressed usually in a sample, Expressed significantly in population, Expressed differently in two populations.

**Unit – V:**

Classifying Samples from two populations using Multilayer Perceptron, Support Vector Machines and their applications, Using genetic algorithm and perceptron for feature selection and supervised classification

#### **Web Resource (Data, Software, Tutorials)**

Web Resources of MicroArray Technology and Gene Expression:

1. <http://www.mged.org/>
2. <http://www.microarrays.org>
3. <http://www.gene-chips.com>
4. <http://cmgm.stanford.edu/pbrown/mguide/>
5. <http://www.ebi.ac.uk/microarray/>
6. <http://www.ncbi.nlm.nih.gov/geo/>
7. <http://www.123ggenomic.com/files/microarray.html>
8. <http://industry.ebi.ac.uk/alav/microarrays>
9. <http://www.statsoft.com/textbook/starthome.html>
10. <http://linkerockefeller.edu/wli/microarray/>

11. genesight@biodiscovery supports PCA, scatter plots, hierarchical clustering.
12. <http://www.pnas.org/cgi/content/full/96/6/2907>

**Text/Reference Books:-**

1. Microarray Data Analysis and Visualization by Arun Jogota, Bioinformatics, The Bay Press, 2001
2. NCBI Science Premier on MicroArrays.
3. Bioinformatics Methods and Application-Genomics, Proteomics and Drug Discovery by S. C. Rostogi, N. Mendiratla and P. Rostogi, Prentice Hall (India), 2004

**Program Name:** M.Sc. (Bioinformatics) – III Semester  
**Course:** Information Theory & Stochastic Process (MSBI - 251)

### COURSE CONTENTS

**Unit – I:**

Overview: Probabilities defined on events, Random variable, Binomial, Geometric, Poisson variates, Uniform, Exponential, Gamma, Normal Variates, Expectation.

**Unit – II:**

Introduction to stochastic process, Stationary process Poisson process, Non-homogeneous Poisson process, Brownian motion process

**Unit – III:**

Markov Chain: Chapman-Kolmogorov equation, Classification of states, Limiting Probabilities, Time Reversible Markov Chain, Markov Chain Monte Carlo Method, Continuous Time Markov Chain, Birth and Death Process, Time reversibility, Uniformization.

**Unit – IV:**

Information and Entropy, Joint and Conditional Entropies, Mutual information, Chain rules for entropy, Relative entropy.

**Unit – V:**

Entropy rules of stochastic process, Entropy rate, Hidden Markov Models.

**Unit – VI:**

Channel Capacity, Noiseless binary channel, Symmetric, Gaussian channel

**Text / Reference Book:**

1. Element of Information Theory by Cover and Thomas, New York: Wiley, 1991.
2. A First Course in Stochastic Process by Samuel Karlin and Howard M. Taylor, Academic Press Inc. (London) Ltd., 1988.
3. Stochastic Processes by Sheldon M. Ross, John Wiley & Sons, 2000.
4. An Introduction to Stochastic Processes by Edward P. C. Kao, Duxbury, 1999.

**Program Name:** M.Sc. (Bioinformatics) – III Semester  
**Course:** Computer Lab - III (MSBI - 261)

**COURSE CONTENTS**

- Perl programming for Motif search, Open reading frames, Parsing, etc.
- Signing and Creating Web pages using: HTML, Java Script.
- Multimedia: Introduction to Photoshop, Developing multimedia application using Flash.
- Gene expression and MicroArray: Pre-processing of datasets; using clustering and classification software such as SOM, SVM, PCA using visualization Software such as Tree View, Sammon Mapping

**Program Name:** M.Sc. (Bioinformatics) – IV Semester

**Course:** Major Project (MSBI - 212)

### **Major Project Guideline**

- ❑ The project synopsis should be prepared in consultation with the supervisor(s).
- ❑ Students must submit his/her project synopsis to the Head or Course coordinator along with his/her Name, Father's Name, ID Number, Title of Project, etc and get it approved by them.
- ❑ Project must be done by individually.
- ❑ Approval by the supervisor is based on the directions given by the Department.
- ❑ After scrutinizing the same by the supervisor, students must complete their project and submit the final report within the stipulated time in the form of soft and hard copy to the Department.
- ❑ The Department will evaluate project.
- ❑ Students must demonstrate their project in their Department to the concern persons on the date fixed by the department or examination department.

#### **Synopsis of your Project:**

1. Title of the project
2. Objective of the project
3. Language(s) / Tool to be used
4. A complete structure of program
  - a) Analysis
  - b) Module description
  - c) Data structure (Schema, E-R Diagram, Tables etc.)
  - d) Logic diagram
5. Future scope of the project
6. Any other relevant information

#### **Project category:**

Group 1: Internet based

Group 2: Non Internet based

Group 3: Software based

Group 4: Non Software based

#### **Project Limited:**

- Project must be a complete application such as Biological, Computational, Computational Biology, Genomics, Proteomics, Metabolic pathways, Computational algorithm for biological problems etc.
- It must be clearly divided into modules and properly document.

**Project area and tools:**

<u>Case Study:</u>	Biological Problems, Bioinformatics Tools & Databases, etc
<u>GUI Tools:</u>	Visual Studio, SQL Windows, HTML etc.
<u>Languages:</u>	C++, Perl, Python, BioJava, Java etc.
<u>Application:</u>	Database Management / Internet / Client-Server / Multimedia / Graphics etc.
<u>Database:</u>	Oracle, MySQL
<u>Hardware Requirements:</u>	CPU, RAM, Disk space etc.
<u>Software Requirement:</u>	OS, Application Development Packages etc.

**Project Report:**

- The length of report may be an about 40 to 50 page, with 1.5 line spacing, 1.25 inches margin on either side, printed on A4 size papers. Ten percent variation on either side is permissible.
- It must contain the following:
  - Preliminary requirement: Title of project, Acknowledgement, Certificate, Index
  - Introduction
  - Objectives
  - Project category
  - Tools / environment used
  - Analysis and design
  - Program structure
  - Coding
  - Documentation
  - Future application
  - References
- Two sets of soft and hard copy must be submitted to the Department by the students along with source code, input data, report generated by used tools/database/software and exe file and the third copy of the project report may be collected back by the students after evaluation.

**Instructions to the supervisor:** (Project guidelines for approval & final evaluation).

**Eligibility of Project guides:**

The Project guide must be a M.Sc. or M.Tech. or equivalent in Bioinformatics, Biotechnology, Biology, Computer Science, or Information Technology with minimum 1 year research experience.

**Objectives of the project proposed:**

- To provide the scope to apply the concept of Bioinformatics, computer programming language, database used and application of computer science in biology.
- To analyze biological problems and provides good exposure to development & implementation of software database by following the software engineering concepts.

**Points to be considered while approving the synopsis:**

- Provide the scope to apply the core concept of Bioinformatics and application of Computer science in Biology.
- Provide the good exposure to software/algorithm/database development & implementation.
- Synopsis should be submitted as per the given instructions.
- Structure of the program must give good understanding of the problem & its implementation. Above-mentioned objectives must be fulfilled.
- Project should not be repeated.

**Project Evaluation (Internal Assessment):**

- Submission date for the project must be strictly followed as per the schedule given.
- Project shall be evaluated and the Department shall award the marks.
- Arrange presentation & demonstration along with viva for each student for their project during the date specified by the Department.
- Department must be arrange for an external evaluator having the above-mentioned qualification and the project certificate. Must have the signature and address of the evaluator.
- Out of 100 marks the project shall have 60 marks for Internal Assessment and 40 marks for Semester Assessment as per the table given:

**Marks:**

• **Internal Assessment:** 100 Marks

Project Supervisor:	40
Presentation & Viva Voce Internal	40 + 20 = 60
.....	.....
Total:	100

• **Semester Assessment:** 300 Marks

Presentation & Viva Voce - Final:	150 + 50 = 200
Project Report:	100
.....	.....
Total:	400

- ✦ Department must keep synopsis and project report (hard & soft copy along with program code) of all the students for at least one year after completion for verification by the University.
- ✦ If a project is nit up to the expectation or any malpractice is found then such projects have to be repeated.
- ✦ Grand total marks must be sent to Examination department as per Department norms and also the individual marks distribution table.