Rashtreeya Sikshana Samithi Trust

R V College of Engineering
(Autonomous Institution Affiliated to Visvesvaraya Technological University, Belagavi)

Master of Technology (M. Tech.)
Bioinformatics

Scheme and Syllabus

2016

R.V. College of Engineering, Bengaluru – 59

(Autonomous Institution Affiliated to Visvesvaraya Technological University,, Belagavi)

Department of Biotechnology

Vision:

A premier department in Biotechnology Education, Research and Innovation with a focus on sustainable technologies for the benefit of society and environment.

Mission:

- Create state-of-the-art infrastructure for research and training in Biotechnology.
- Develop graduates who are ethical and socially concerned.
- Promoting collaboration with academia, industries and research organizations at National and International level.
- Contribute to socioeconomic development through sustainable and inclusive technologies

Program Educational Objectives (PEO)

M. Tech. in Bioinformatics Program, graduates will be :

Program Educational Objectives (PEO)

M. Tech. in Bioinformatics Program, graduates will be able to :

PEO 1. Demonstrate knowledge and understanding of engineering principles to analyze problems of life science and design solutions using computational techniques.

PEO 2. Apply modern software tools to Explore to simulate problems of healthcare, pharmaceutical and Agriculture industry and provide virtual Bioinformatics. Solutions

PEO 3. Exhibit good communication skills, team work, ethics,, society and environment and sustainability and appreciation of the necessity for lifelong learning.

Program Outcomes (PO)

M. Tech. in Bioinformatics Graduates will be o:

PO 1. Scholarship of Knowledge: Derive scholarship of knowledge in the area of Bioinformatics through mathematics, science and engineering.

PO 2. Critical Thinking: Design and conduct experiments, analyze and interpret biological data by critical thinking..

PO 3.   **Problem Solving:** Problem solving through a system, component, or process to meet desired needs within realistic constraints such as economic, environmental, social, political, ethical, health and safety, manufacturability and sustainability

PO 4.   **Research Skill:** Identify, formulate and solve engineering problems through research skills.

PO 5.   **Usage of modern tools:** Create, select and apply appropriate techniques, resources, and modern prediction and modeling engineering tools to solve complex engineering activities.

PO 6.   **Collaborative and Multidisciplinary work:** Perform tasks at the interface of biotechnology, information technology & other allied fields of technology through Interdisciplinary approach

PO 7.   **Project Management and Finance:** Execute projects taking managerial skills into account to optimize the financial benefits.

PO 8.   **Communication:** Develop managerial, leadership & interpersonal skills honing effective communication techniques.

PO 9.   **Life-long Learning:** Enable to carry the interest & motivation, to learn continuously to be able to contribute for the development of flexible & adoptive technology

PO 10.   **Ethical Practices and Social Responsibility:** Understand the need & importance of ethical practices & social responsibility.

PO 11.   **Independent and Reflective Learning:** Practice independent learning & recognize the value of reflective practice in self improvement.

Program Specific Outcomes (PSO)

M. Tech. in Bioinformatics Graduates will be able to:

PSO 1.   Apply genomic, proteomics and other omics skills to analyze complex biological problems in research or industry either independently or as a part of team.

PSO 2.   Apply modeling, simulation and analytical skills to a evaluate and predict the outcome

PSO 3.   Apply High performance computing, Object oriented programs, data mining and artificial intelligence to solve the unknown of life science systems

R. V. College of Engineering, Bengaluru – 59.

(An Autonomous Institution Affiliated to Visvesvaraya Technological University,, Belagavi)

Department of Biotechnology

M. Tech. Master of Bioinformatics

Sl. No	Course Code	Course Title	BoS	Lecture L	Tutorial T	Practical P	Experiential Learning/ Self Study S	Total Credits
FIRST SEMESTER								
1	16MEM11P	Project Management	IEM	3	1	0	0	4
2	16MBI12	Applied Statistics	BT	4	0	0	0	4
3	16MBI13	Principles of Bioinformatics (Theory and Practice)	BT	4	0	1	0	5
4	16MBI14	Biomolecular Modeling and Simulation	BT	4	0	0	1	5
5	16MBI15X	Elective -1	BT	4	0	0	0	4
6	16HSS16	Professional Practice	BT	0	0	2	0	2
		Total		**19**	**1**	**3**	**1**	**24**
		Number of contact hours		19	2	6	4	31

Elective -1			
16MBI151	Cell and Molecular Biology	16MBI152	Data Structures in C and C++

Sl. No	Course Code	Course Title	BoS	CREDIT ALLOCATION				Total Credits
				Lecture	Tutorial	Practical	Experiential Learning / Self Study	
				L	T	P	S	
1	16MEM21R	Research Methodology	IEM	3	1	0	0	4
2	16MBI22	Genomics, Proteomics, and Genetic Circuits (Theory and Practice)	BT	4	0	1	0	5
3	16MBI23X	Elective - 2	BT	4	0	0	0	4
4	16MBI24X	Elective - 3	BT	4	0	0	0	4
5	16MBI25X	Elective - 4	BT	4	0	0	0	4
6	16MBI26	Minor Project	BT	0	0	5	0	5
		Total		**19**	**1**	**6**	**0**	**26**
		Number of contact hours		19	2	12	0	**33**

The table above is headed **SECOND SEMESTER**.

Elective -2			
16MBI231	Data Warehousing and Mining	16MBI232	Artificial Intelligence
Elective – 3			
16MBI241	*Insilico* Drug Design	16MBI242	Pharmacogenomics
Elective – 4			
16MBI251	Essential Programming for Bioinformatics	16MBI252	High Performance Bio-Computing

R. V. College of Engineering, Bengaluru – 59.
(An Autonomous Institution affiliated to VTU, Belagavi)
Department of Biotechnology

M. Tech. Master of Bioinformatics

Sl. No	Course Code	Course Title	BoS	CREDIT ALLOCATION				Total Credits
				Lecture L	Tutorial T	Practical P	Experiential Learning/ Self Study S	
THIRD SEMESTER								
1	16MBI31	Perl and Python	BT	4	0	1	0	5
2	16MBI32X	Elective -5	BT	4	0	0	0	4
3	16MBI33X	Elective -6	BT	4	0	0	0	4
4	16MBI34X	Elective-7	BT	4	0	0	0	4
5	16MBI35	Internship/ Industrial Training	BT	0	0	3	0	3
6	16MBI36	Technical Seminar	BT	0	0	2	0	2
		Total		**16**	**0**	**6**	**0**	**22**
		Number of Contact Hours		16	0	12	0	28

Elective -5			
16MBI321	Statistical Tools and Techniques	16MBI322	High Throughput Data Analytics
Elective – 6			
16MBI331	DNA chips and Microarray Data Analysis	16MBI332	Software Engineering for Computational Biology
Elective-7			
16MBI341	Next Generation Sequencing Informatics	16MBI342	Graph Theory and Algorithms

FOURTH SEMESTER

Sl. No	Course Code	Course Title	BoS	CREDIT ALLOCATION				Total Credits
				Lecture	Tutorial	Practical	Experiential Learning/ Self Study	
				L	T	P	S	
1	16MBI41	Major Project	BT	0	0	26	0	26
2	16MBI42	Seminar	BT	0	0	2	0	2
		Total		**0**	**0**	**28**	**0**	**28**

Applied Statistics					
Course Code	:	16MBI12		**CIE Marks**	:	100
Hrs/Week	:	L:T:P:S	4:0:0:0	**SEE Marks**	:	100
Credits	:	04		**SEE Duration**	:	03

Course Learning Objectives (CLO):

Graduates shall be able to

1. Understand and analyze different types of data and its structure.
2. Practice the vital statistical methods to prove the hypothesis and find out the relationship between the data sets.
3. Acclimatize to probability principles, applied to advanced bioinformatics data, sampling estimations and predictive analytics.
4. Analyze the sequence and structure data by taking the real time examples.
5. Construct DNA sequence models.

Unit – I	**09 Hrs**

Data types, parametric and non parametric estimations, Measures of central tendency, central limit theory, Measures of Dispersion, Correlation: Karl Pearson and Spearman Correlation coefficient, Regression analysis. Hypothesis testing: t test, Z test, F test,

Unit – II	**07 Hrs**

Probability distributions: Normal, Binomial and Poisson Distributions, Addition, Multiplication and Total probability rules, Joint probability distribution: Discrete and continuous variables, Random Effect Model, Randomized Complete Block Design.

Unit – III	**10 Hrs**

Estimation and Hypothesis testing theory: Estimation theory - Introduction, Criteria for "Good estimators". Methods of estimation - Maximum Likelihood estimation, Least squares, Multiple regression, Multivariate and Bootstrapping. Hypothesis testing theory – Introduction, Fixed sample size test, Composite fixed sample size tests, -2 log λ approximations. ANOVA, Multivariate, Bootstrapping Methods. Sequence analysis.

Unit – IV	**11 Hrs**

Statistical approach for sequence alignment and sequence search: Comparison of two aligned, unaligned sequences and Query sequence against a database. Minimum significance lengths. Gapped BLAST and PSI-BLAST. Hidden Morkov Models: Introduction. Algorithms – Forward and Backward, Verterbi and Estimation algorithms. Applications of Hidden Morkov Models.

Unit – V	**11 Hrs**

Analysis of DNA and Protein sequences: Shotgun sequencing, DNA Modeling, Modeling Signals in DNA, long repeats, rScans. Analysis of patterns. Overlaps counted and not-counted. Analysis of Single Multiple DNA Sequences – Frequency comparison, Sequence alignment, Simple tests for significant similarity in an alignment. Alignment algorithms for two sequences. Protein sequences and Substitution matrices. Multiple sequence alignment.

Expected Course Outcomes:

After going through this course the student will be able to:

CO1. Demonstrate the knowledge of specialized statistical methods.

CO2. Apply the statistical and computational methods for genome and protein data.

CO3: Able to estimate the relevant tests of hypothesis and the probabilities.

CO4: Interpret the data sets using concurrent statistical methods.	

Reference Books:

1.	Warren J. Ewens Gregory Grant. Statistical Methods in Bioinformatics: An Introduction (Statistics for Biology and Health), Springer, 2005.
2.	Douglas C. Montgomery and George C. Runger. Applied Statistics adn Probability for Engineers. John Wiley Publishers, 3rd Edition, 2002. ISBN: 9812-53-058-4.
3.	T. Hastie, R. Tibshirani, J. H. Friedman. The Elements of Statistical Learning, Springer, 2001.
4.	Bioinformatics and Computational Biology Solutions using R and Bioconductor, edited by R. Gentleman, Springer, 2005.
5.	Statistical Analysis of Gene Expression Microarray Data, edited by T.P. Chapman & Hall / CRC, Speed. 2003.

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	M	L	L	H	M	-	-	M	M	M
CO2	M	H	H	L	H	L	-	-	L	M	M
CO3	L	L	H	M	H	L	-	-	L	L	L
CO4	H	L	L	L	M	H	-	-	L	H	L

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	L	H	L
CO2	H	M	H
CO3	M	M	L
CO4	L	H	L

Principles of Bioinformatics (Theory and Practice)						
Course Code	**:**	**16MBI13**		**CIE Marks**	**:**	**100 +50**
Hrs/Week	**:**	**L:T:P:S**	**4:0:1:0**	**SEE Marks**	**:**	**100 +50**
Credits	**:**	**5**		**SEE Duration**	**:**	**3+3 hrs**

<mark>**Course Learning Objectives (CLO):**</mark>

Graduates shall be able to

1. Understanding the basics of bioinformatics and importance of different biological databases.
2. Explore different software's and tools in the field of bioinformatics.
3. Design algorithms and predictive methods.
4. Create customized database and tools for research projects
5. Analyse the

Unit – I	**10 Hrs**

Introduction to Bioinformatics:

Bioinformatics & Biological Databases: Bioinformatics, Goals, Scope, Limitations and Applications of bioinformatics. Types of Databases-Primary and Secondary Databases, Sequence and Structure Databases, Specialized Databases.

Special Databases: Genome, Microarray, Metabolic pathway, motif, Organism specific Databases and domain databases. Applications of these databases. Database Similarity Searching: Unique Requirements of Database Searching. Heuristic Database searching, Scoring Matrices – PAM and BLOSUM, Basic Local Alignment Search Tool (BLAST), FASTA, Comparison of FASTA and BLAST, Database Searching algorithms. Global and local alignment, Dot plots for sequence comparison, Dynamic programming, BLAST and PSI-Blast.

Unit – II	**10 Hrs**

Sequence Analysis:

Sequence Alignment: Evolutionary basis, Sequence similarity, identity, and homology. Concept of Homolog, Paralog and Ortholog Sequences. Types of Sequence alignment - Pairwise and Multiple sequence alignment. Alignment algorithms, Scoring matrices, Statistical significance of sequence alignment. Multiple Sequence Alignment: Scoring function, Exhaustive algorithms, Heuristic algorithms, Practical issues. Profiles and Hidden Markov Models: Position-Specific scoring matrices, Profiles, Markov Model and Hidden Markov Model.

Unit – III	**10 Hrs**

Prediction Methods using Nucleic Acid Sequence:

Sequence logos. Gene and Promoter Prediction: Promoter and Regulatory elements in Prokaryotes and Eukaryotes. Promoter and Regulatory element prediction – algorithms. Gene prediction. Gene prediction in Prokaryotes and Eukaryotes. Categories of Gene Prediction Programs. Prediction algorithms. Discussions with case studies. Predictive methods using Nucleic acid sequence – DNA framework, Masking of repetitive DNA, predicting RNA secondary structure, Finding RNA genes, Detection of functional sites and Codon bias in DNA. Primer design and restriction maps.

Unit – IV	**10 Hrs**

Prediction Methods using Protein Sequence:

Motifs and Domains Prediction: Motif and Domain databases, Identification of Motifs and Domains in Multiple Sequence Alignment using Regular expressions, Motif and Domain Databases statistical models, Protein Family databases, Motif Discovery in unaligned sequences.

Predictive methods using protein sequence – Protein identity and Physical properties. Structure prediction - Prediction of secondary structure of protein, Antigenic sites, Active sites, Folding classes, specialized structures and Tertiary structures. Discussions with case studies.

Unit – V	10 Hrs

Phylogenetic Analysis:

Molecular Phylogenetic: Phylogenetic Basics. Molecular Evolution and Molecular Phylogenetic - Terminology, Gene Phylogeny vs Species Phylogeny. Forms of Tree Representation. Phylogenetic Tree Construction Methods and Programs - Distance-Based Methods, Character-Based Methods. Phylogenetic Tree evaluation methods. Phylogenetic analysis software and algorithms. Bootstrap methods.

Unit – VI (Lab Component)

COURSE OBJECTIVES

1. Gene sequence assembly and contig mapping and identification of Gene.

2. Primer and Promoter design for a given sequences

3. Sequence searches using FASTA and BLAST, and Phylogenetic analysis.

4. Prediction of secondary structure for given protein and RNA sequences.

5. Retrieval of protein structure from PDB and its visualization and modification.

6. Prediction of 3D structure of unknown protein sequence.

7. Prediction of protein-protein interactions.

8. EST clustering and EST mapping, and Genome annotation

9. Microarray data analysis- normalization, clustering.

10. Study of Profiles, Patterns and PSSMs.

Expected Course Outcomes:

After going through this course the student will be able to:

CO1: Understand the basic concepts of bioinformatics.

CO2: Describe Genomics and proteomics analysis using various databases.

CO3: Analyze various Application of software and tools with the understanding of underlying algorithms.

CO4. Design models for biological problems using predictive methods.

Reference Books:

1.	Essential Bioinformatics by Jin Xiong, Cambridge University Press, 2006.
2.	Essentials of Drug Designing by V. Kothekar, DHRUV Publications, 2005.
3.	Systems Biology: Applications and Perspectives by Bringmann, Springer, 2007.
4.	Bioinformatics and Molecular Evolution by Paul G. Higgs, Teresa K. Attwood, Blackwell, 2005.
5.	Bioinformatics Basics: Applications in Biological Science and Medicine by Lukas, 2005.

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Continuous Internal Evaluation (CIE) for Practical

CIE for the practical courses will be based on the performance of the student in the laboratory, every week. The laboratory records will be evaluated for 40 marks. One test will be conducted for 10 marks. The total marks for CIE (Practical) will be for 50 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Practical

SEE for the practical courses will be based on conducting the experiments and proper results for 40 marks and 10 marks for viva-voce. The total marks for SEE (Practical) will be 50 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	L	-	-	-	M	-	-	H	H	H
CO2	H	H	H	L	H	H	-	-	H	L	M
CO3	M	H	H	H	H	H	L	L	H	L	M
CO4	M	H	H	M	H	M	L	L	H	M	H

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	M	M	L
CO2	H	H	L
CO3	M	M	H
CO4	L	H	M

Biomolecular Modeling and Simulation						
Course Code	:	**16MBI14**		**CIE Marks**	:	**100**
Hrs/Week	:	**L:T:P:S**	**4:0:0:1**	**SEE Marks**	:	**100**
Credits	:	**5**		**SEE Duration**	:	**3 hrs**

Course Learning Objectives (CLO):

Graduates shall be able to

1. Explore the knowledge of the fundamental areas of molecular modeling and simulation and study the role of computer science in life sciences.
2. Acquire knowledge of the Protein structural hierarchy and their diversity.
3. Study Molecular and Quantum mechanics and explore their applications in the mimic of physical phenomenon.
4. Understand the importance of molecular and quantum mechanics in the area of modeling and simulation of biological phenomenon by projecting microscopic environment at macroscopic level.
5. Understand the role modeling and simulation in the study of energetics of biological systems along with their dynamics.
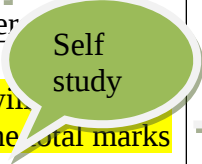
Unit – I	09Hrs

Biomolecular Structure and Modeling: Historical Perspective, Introduction to Molecular Modeling, Roots of Molecular modeling in Molecular mechanics. Structure Hierarchy: Helices – Classic α-Helix and π Helices, Left-Handed α-Helix and Collagen Helix. β-Sheets - Turns and Loops. Super secondary and Tertiary structure. Complex 3D Networks. Introduction to X-Ray crystallography and NMR spectroscopy. Introduction to PDB and 3D Structure data, Structure of

PDB and other 3D Structure record. Classes in Protein Architecture – Folds, α-Class, Bundles, Folded leaves, Hairpin arrays. β-Class folds, Anti-parallel β domains, parallel and Anti-parallel Combinations. α/β and α+β-Class, α/β Barrels, Open twisted α/β folds, Leucine-rich α/β folds. α+β folds. Quaternary structure.

Unit – II	10Hrs

Force Fields: Formulation of the Model and Energy, Quantifying Characteristic Motions, Complex Biomolecular Spectra, Spectra as force constant sources, In-Plane and Out-of-Plane Bending. Bond Length Potentials, Bond Angle Potentials, Cross bond stretch / Angle bend terms. Torsional potentials, Improper torsion, Cross dihedral/Bond angle, Dihedral terms. Van der Waals potentials. Rapidly decaying potential. Coulomb potential, Slowly decaying potential, Dielectric function and Partial charges. 3D QSAR Methods. Free energy calculations in Biological Systems - Drug design, Signal transduction, Peptide folding, Membrane protein association, Numerical methods for calculating the potential of mean force, Replica-Exchange-Based Free-Energy Methods.

Unit – III	9 Hrs

Molecular modeling: Modeling basics. Generation of 3D Coordinates Crystal data, Fragment libraries, and conversion of 2D Structural data into 3D form. Force fields and Geometry optimization. Energy minimizing procedures - Use of Charges, Solvent effects and Quantum Mechanical methods. Computational tools for Molecular modeling. Methods of Conformational analysis - Systematic search procedures, Monte Carlo and molecular dynamics methods.

Unit – IV	10 Hrs

Dynamical and Stochastic-Dynamical Foundations for Macromolecular Modeling: Bimolecular sampling: Algorithms, Test molecules, and metrics. Approach to thermal equilibrium in Biomolecular simulation, Hybrid Monte Carlo and Newton Raphson methods. Langevin equation for generalized coordinates, Meta stability and Dominant Eigen values of Transfer operators. Implicit solvent electrostatics in Biomolecular Simulation, New distributed multipole methods.

Unit – V	10 Hrs

Quantum-Chemical Models for Macromolecular Simulation: Fast and Reliable Quantum Chemical Modeling of Macromolecules, Quantum chemistry simulations of Glycopeptide antibiotics. **Membrane Protein Simulations:** Membrane proteins and their importance, Membrane protein environments in Vivo and in Vitro. Modeling a complex environment - Simulation methods for membranes, Membrane protein systems, Complex solvents, Detergent micelles, Lipid bilayers, Self-Assembly and Complex systems. Modeling and Simulation of Allosteric regulation in enzymes – Modeling and Simulation of sGC.

Expected Course Outcomes:
After going through this course the student will be able to:
CO1: Define and explain concepts of Object Oriented Programming along with the possible data
                structures
CO2: Apply Object Oriented programming and data structures to solve the problems in the area
                of Big Data Analytics
CO3: Analyze and evaluate both set of sorting and searching algorithms with case studies
CO4: Design and implement algorithms to perform high throughput data analysis in the field
                Sequence and structure analysis

Reference Books:

1.	Tamar Schlick. Molecular Modeling and Simulation: An Interdisciplinary Guide, Published by Springer, 2nd edition, 2010.
2.	IsidoreRigoutsos, G. Stephanopoulos. Systems Biology, Published by Oxford University Press US, 2006.
3.	Timothy J. Barth, Michael Griebel, David E.Keyes, Risto M. Nieminen, Dirk Roose, Tamar Schlick. New Algorithms for Macromolecular Simulation, Published by Springer, 2006.
4.	Peter T. Cummings, Phillip R. Westmorland, Brice Carnahan. Foundations of Molecular Modeling and Simulation, Published by American Institute of Chemical Engineer~

Scheme of Continuous Internal Evaluation (CIE) for Theory
CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will~
marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Self study

Scheme of Semester End Examination (SEE) for Theory
The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	M	H	M	L	L	-	-	L	-	L
CO2	M	H	H	H	M	M	-	-	L	-	L
CO3	M	H	H	H	M	H	-	-	L	-	L
CO4	M	H	M	H	M	H	-	-	L	-	L

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	L	L	H
CO2	M	L	H
CO3	L	M	M
CO4	H	L	H

Cell and Molecular Biology						
Course Code	**:**	**16MBI151**		**CIE Marks**	**:**	**100**
Hrs/Week	**:**	**L:T:P:S**	**4:0:0:0**	**SEE Marks**	**:**	**100**
Credits	**:**	**4**		**SEE Duration**	**:**	**3 hrs**

Course Learning Objectives (CLO):
Graduates shall be able to
1. Obtain a solid foundation in cellular and molecular concepts and understand the structures and functions of different biomolecules, their interaction and associated bioenergetics.
2. Get an overview of different membrane transport process and signal transduction
3. Understand the concept of central dogma and with special emphasis on prokaryotic and eukaryotic DNA replication, DNA Damage and repair
4. Get an insight of the concepts of transcription, translation and the post transcriptional and translational process
5. Understand the regulation of gene expression in prokaryotes and eukaryotes.

Unit – I	10 Hrs

Introduction to Cell and Molecular Biology: Basic properties of cells, Structure and function of prokaryotic and eukaryotic cells. Cell cycle, Chromosome structure and functions, Cellular fates- malignant growth, cell differentiation, programmed cell death, aging and senescence Biomolecules- Carbohydrates, Lipids, Proteins, nucleic acids. Bioenergetics- The Laws of Thermodynamics and the Concept of Entropy Free Energy.

Unit – II	9 Hrs

Membrane Transport phenomena: Types, Transport proteins, Transport process, Membrane channels. Cell signaling and signal transduction- Basic elements of cell signaling, G protein-coupled receptors and their second messengers, protein-tyrosine phosphorylation as a mechanism for signal transduction, calcium as an intracellular messenger.

Unit – III	9 Hrs

Concept of Central Dogma: DNA replication - Semiconservative Replication, Replication in Prokaryotes and eukaryotes, telomere replication. DNA repair- Nucleotide excision repair, Base excision repair, Mismatch repair, Double-strand breakage repair. Mutations, Oncogenes and tumor suppressor genes.

Unit – IV	10 Hrs

Gene Expression: Overview of transcription in both prokaryotic and eukaryotic cells. Small regulatory RNAs and RNA silencing pathways. Post transcriptional modification. Genetic Code. Translation mechanism in prokaryotes and eukaryotes, mRNA Surveillance and quality Control, Post translation modifications.

Unit – V	10 Hrs

Control of Gene Expression: Operons, Transcriptional-level control- Role of Transcription Factors in Regulating Gene Expression, Enhancers and supressors. Ribo switches. Translational-level control- Control of mRNA Translation, mRNA Stability and the role of MicroRNAs in Translational-Level Control. Epigenetics and gene regulation.

Expected Course Outcomes:
After going through this course students will be able to:
CO1: Remember and explain the cell and molecular biology concepts such as structures,

functions and interactions of biologically important molecules
CO2: Explain the relationship between genes, proteins and their functions
CO3: Compare and contrast between various cells, physiological processes and inheritance
       pattern
CO4: Apply the molecular biology concepts to understand complex biological process

Reference Books:	
1.	David P. Clark, Nanette J. Pazdernik., "Molecular Biology", Academic Press, 2nd edition, 2013. ISBN: 9780123785947.
2.	Lodish H, Berk A, Kaiser CA, Krieger M, Scott MP, Bretscher A, Ploegh H, Matsudaira. Molecular Biology, Freeman, 7th edn, 2013. ISBN: 13:9781464109812.
3.	Gerald Karp, Cell and Molecular Biology, Wiley, 7th edn , 2013, ISBN-13: 978-1118301791
4.	Donald Voet, Charlotte W. Pratt, Judith G. Voet.," Principles of Biochemistry: International Student Version". Wiley John and Sons, 2012. ISBN: 1118092449.

Scheme of Continuous Internal Evaluation (CIE) for Theory
CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory
The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	L	L	L	L	L	L	-	-	L	-	L
CO2	M	H	H	M	L	L	-	-	M	-	L
CO3	L	M	M	L	L	L	-	-	H	L	L
CO4	L	H	H	L	L	L	-	-	M	-	L

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	M	M	L
CO2	H	M	L
CO3	M	H	L
CO4	L	M	M

Data Structures in C and C++						
Course Code	:	16MBI152		**CIE Marks**	:	100
Hrs/Week	:	L:T:P:S	4:0:0:0	**SEE Marks**	:	100
Credits	:	4		**SEE Duration**	:	3 hrs

Course Learning Objectives (CLO):

Graduates shall be able to

1. Explore the knowledge of the fundamental areas of computer science such as Programming languages and study the role of computer science in life sciences.
2. Acquire knowledge of the Object Oriented Programming
3. Study data structures Stack, Queue, Linked Stack and queues, Trees and Tables
4. Understand the importance of various data structures to solve the problems related to High throughput Data analysis
5. Explore practically the applications of various data structures along with object oriented programming.

Unit – I	08Hrs

Basic concepts: Variables, Operators, Statements, Functions and Pointers. Introduction to Classes, Objects and Object oriented design, C++ string classes. Features of Object Oriented Programming – Encapsulation, Inheritance and Polymorphism.

Unit – II	10Hrs

Stacks: Stack specifications, Lists and Arrays. Reversing a list, Implementation of Stacks, Specification of methods for Stacks. Class Specification, Pushing, Popping, and Other Methods. Queues: Definitions, Queue Operations, Extended Queue Operations, Implementations of Queues - Circular Implementation of Queues. Linked Stacks and Queues: Pointers and Linked structures, Pointers and Dynamic memory in C++. Basics of linked structures - Linked stacks, Linked stacks with safeguards, Destructor, Overloading Assignment Operator, Copy Constructor, Modified linked-stack specification. Linked queues - Basic declarations, Extended linked queues.

Unit – III	10Hrs

Recursion: Introduction to Recursion, Stack Frames for Subprograms, Tree of Subprogram Calls, Factorials: A Recursive Definition, Divide and Conquer (Towers of Hanoi). Principles of Recursion - Designing recursive algorithms. Tail Recursion, Refinement. Lists and Strings: List definition, Method specifications, Implementation of lists, Class templates, Contiguous implementation, Simply linked implementation. Variation: Keeping the Current Position, Doubly Linked Lists, Comparison of Implementations. Strings - Strings in C++, Implementation of strings, String operations. Linked lists in Arrays.

Unit – IV	10Hrs

Searching: Introduction Basic search types - Sequential search, Binary search, Ordered lists. Algorithm Development. Asymptotics – Introduction, Orders of Magnitude, Big-O and Related Notations. Sorting: Introduction, Storable Lists. Sort types – Bubble sort, Insertion sort, Merge sort, Selection sort, Shell sort, Divide-and-Conquer sorting, Merge sort for linked lists, Ordered insertion. Linked version. Analysis - Algorithm, Contiguous implementation and Comparisons. Analysis of Merge sort. Quick sort for Contiguous lists, Partitioning the list, Analysis of Quicksort, Comparison with Merge sort. Heaps and Heapsort, Analysis of Heapsort. Two-Way trees as lists.Priority Queues.

Unit – V	10 Hrs

Tables and Information Retrieval: Introduction. Tables of various shapes, Triangular tables, Rectangular tables Jagged tables, Inverted tables. Tables: New Abstract Data Type, Hashing, Sparse tables. Collision resolution with Open Addressing, Collision Resolution by Chaining. Trees: Basic terminology. Binary trees - Binary tree representation, algebraic Expressions, Complete binary tree, Extended binary tree, Array and Linked representation of Binary trees. Traversing binary trees, threaded binary trees. Traversing Threaded binary trees, Huffman algorithm. Graphs: Terminology & Representations, Graphs &Multi-graphs, Directed Graphs, Sequential representations of graphs - Adjacency matrices, Traversal, Connected component and Spanning Trees, Minimum Cost Spanning Trees.

Expected Course Outcomes:
After going through this course students will be able to:
CO1: Define and explain concepts of Object Oriented Programming along with the possible data structures
CO2: Apply Object Oriented programming and data structures to solve the problems in the area of Big Data Analytics
CO3: Analyze and evaluate both set of sorting and searching algorithms with case studies
CO4: Design and implement algorithms to perform high throughput data analysis in the field Sequence and structure analysis

Reference Books:

1.	Nell B. Dale. C++ plus data structures, Jones Learning & Bartlett, 2007
2.	Vinu V. Das. Principles Of Data Structures Using C And C++, New Age International, 2006.
3.	Robert Kruse, Alexander Ryba, Data Structures and Program Design in C++, Prentice Hall, 2001.
4.	Jean-Paul Tremblay, Paul. G. Soresan. An introduction to data structures with Applications, TataMc-Graw Hill International Editions, 2nd edition, 1984.
5.	A. Michael Berman. Data structures via C++, Oxford University Press, 2002.

Scheme of Continuous Internal Evaluation (CIE) for Theory
CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory
The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	M	H	M	L	L	-	-	L	-	L
CO2	M	H	H	H	H	M	-	-	L	-	L
CO3	M	H	H	H	H	H	-	-	L	-	L
CO4	M	H	M	H	H	H	-	-	L	-	L

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	L	M	M

CO2	M	L	H
CO3	L	M	H
CO4	H	M	H

Genomics, Proteomics and Genetic Circuits (Theory and Practice)						
Course Code	:	16MBI22		**CIE Marks**	:	100 +50
Hrs/Week	:	L:T:P:S	4:0:1:0	**SEE Marks**	:	100 +50
Credits	:	5		**SEE Duration**	:	3 +3 hrs

Course Learning Objectives (CLO):
Graduates shall be able to
1. Understand the molecular aspects of the genome.
2. Develop the concepts and principles underlying the human genome project and plant genome program.
3. Differentiate between the different structures and functions of the proteome.
4. Get insights on protein identification and sequencing methods
5. Understand the dynamic models and regulatory networks at cellular level

Unit – I	**9 Hrs**

Introduction to Genomics: Genome evolution and organization in prokaryotes and eukaryotes, Genome mapping: Genetic and physical mapping. Molecular markers and protein markers, Genome sequencing, basics, strategies and methodology. Comparative and Functional genomics; Model systems- Arabidopsis, Human, Drophila and *E coli*. Serial analysis of gene expression (SAGE) and targeting induced local lesions in genome (TILLING). Genome Wide Association Studies (GWAS)

Unit – II	**10 Hrs**

Tools for Genomics: Computational analysis of sequences- finding genes and regulatory regions; Gene annotation; Alignment statistics; Prediction of gene function using homology, context, structures. Expression sequence tags (ESTs), Microarrays technology- Principles and applications, FISH, transcriptome analysis and SNPs determination. Allele mining and single nucteotide polymorphisms (SNPs).Transcriptomics; Cancer Genomics, Epigenomics, Chemical Genomics; Metabolomics, Nutrigenomics, interactomics, Metagenomics. Personal Genomics; Social, Legal and Ethical Implications of Human Genome Research.

Unit – III	**9 Hrs**

Introduction and Scope of Proteomics: Protein separation techniques: Ion exchange, Size exclusion and affinity chromatographic techniques, Poly acrylamide gel electrophoresis, isoelectric focusing, two dimensional poly acrylamide gel electrophoresis, Mass spectrometry based techniques for protein identification.

Unit – IV	**10 Hrs**

Protein Sequencing: Edman degradation, mass fingerprinting, protein synthesis and post translational modifications. Identification of phosphorylated proteins, characterization of multi-protein complexes, protein - protein interactions (Immunoprecipitation) and quantitative proteomics- Characterization of interaction clusters using two-hybrid systems. Protein arrays- definition, applications- diagnostics, expression profiling, Functional proteomics, Protein structure analysis, Clinical and biomedical applications of proteomics.

Unit – V	10 Hrs

Basic Principles of Systems Biology: Scope, Concepts and Applications, Current Progress in Static and Dyanamic Modelling of Biological networkds, Models and Modeling in Systems Biology, Advantages of Computational Modeling, Modeling of Gene Expression- Lactose, Lac Operon, tRNA. Analysis of Gene Expression Data- Support Vector Machines, Identifying Gene Regulatory Networks and Gene Expression Data. Modeling and Analysis of Gene Networks using Feedback Control. Global Gene Expression Assays, Interactomics in Network pharmacology and Toxicology.

Unit – VI (Lab Component)

1. Homology Modeling of Receptors
2. Protein-Ligand Docking Studies
3. Modeling Protein-Protein Interactions
4. Modeling mutations and Single Nucleotide Polymorphisms
5. Modeling Nanopores for Sequencing DNA
6. Simulation of lipid bilayer.
7. Gene Prediction
8. Secondary and Tertiary Protein Structure Prediction
9. Analysis of NGS (next generation sequencing) data
10. Genome annotation and Comparative Genomics studies

Expected Course Outcomes:

After going through this course the student will be able to:

CO1: Understand the construction concepts of various genome maps and large scale sequencing

CO2: Develop diagnostic tools for plant, animal and human diseases

CO3: Understand how proteomics application in biological research can benefit in solving the complex biological and biochemical processes regardless of the type of organism which is the model for the research.

CO4: Analyze dynamic models and regulatory networks at cellular level

Reference Books:

1.	Sangdun Choi. Systems Biology for Signaling Networks, Publisher-Springer, New York , 2010. ISBN 978-1-4419-5796-2
2.	Andres Kriete, Roland Eils. Computational Systems Biology: From Molecular Mechanisms to Disease:, 2nd Edition , Academic Press, 2013. ISBN 978-0-12-405926-9
3.	Edda Klipp, Ralf Herwig, Axel Kowald, ChristophWierling, Hans Lehrach Systems biology in practice: concepts, implementation and application, Wiley-VCH Verlag GmbH &Co.KGaA,Weinhein 2005.ISBN 978-3-527-31078-4
4.	Corrado Priami (Ed.). Transactions on Computational Systems Biology I. Springer-Verlag– Publisher, 2005.ISBN 3-540-25422-6
5.	Glenn Rowe. Theoretical Models in Biology, Oxford University Press – Publisher,Oxford 1994. ISBN 0 19 859687 1.

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Continuous Internal Evaluation (CIE) for Practical

CIE for the practical courses will be based on the performance of the student in the laboratory, every week. The laboratory records will be evaluated for 40 marks. One test will be conducted

| for 10 marks. The total marks for CIE (Practical) will be for 50 marks. |

Scheme of Semester End Examination (SEE) for Theory
The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Practical
SEE for the practical courses will be based on conducting the experiments and proper results for 40 marks and 10 marks for viva-voce. The total marks for SEE (Practical) will be 50 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	M	M	H	M	L	H	H	H	M	H
CO2	H	H	H	H	M	M	M	H	L	H	H
CO3	M	L	L	H	H	M	M	M	L	H	M
CO4	H	H	L	L	M	M	M	H	H	H	H

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	H	L	L
CO2	H	H	H
CO3	H	M	M
CO4	H	H	H

Data Warehousing and Mining					
Course Code	:	**16MBI231**	**CIE Marks**	:	**100**
Hrs/Week	:	**L:T:P:S** **4:0:0:0**	**SEE Marks**	:	**100**
Credits	:	**4**	**SEE Duration**	:	**3 hrs**

Course Learning Objectives (CLO):
Graduates shall be able to:
1. Understand and analyse the architectures of RDBMS and their models.
2. Comprehend the issues in the warehousing design and patterns.
3. Retrieve the data from different sources, organize and present the data in different formats.
4. Practice the data analytical methods to prove the hypothesis and find out the relationship between the data sets.
5. Accustomed to data mining algorithms and apply in the field of bioinformatics

Unit – I	**11 Hrs**

Introduction to Data Warehousing: Heterogeneous information, integration problem, Warehouse architecture, warehouse vs DBMS. **Aggregations:** SQL and Aggregations, Aggregation functions and Grouping. Data Warehouse Models and OLAP Operations: Decision support; DataMarts, OLAP vs OLTP. Multi-Dimensional data model. Dimensional Modeling. ROLAP vs MOLAP; Star and snowflake schemas; the MOLAP cube; roll-up, slicing, and pivoting.

Unit – II	**9 Hrs**

Issues in Data Warehouse Design: Monitoring, Wrappers, Integration, Data cleaning, Data

loading, materialized views, Warehouse maintenance, OLAP servers and Metadata. Building Data Warehouses: Conceptual data modeling, Entity-Relationship (ER) modeling and Dimension modeling. Data warehouse design using ER approach. Aspects of building data warehouses.

Unit – III	9 Hrs

Introducing Data Mining: KDD Process, Problems and Techniques, Data Mining Applications, Prospects for the Technology. CRISP-DM Methodology: Approach, Objectives, Documents, Structure, Binding to Contexts, Phases, Task, and Outputs

Unit – IV	9 Hrs

Data Mining Inputs and Outputs: Concepts, Instances, Attributes. Kinds of Learning, Kinds of Attributes and Preparing Inputs. Knowledge representations - Decision tables and Decision trees, Classification rules, Association rules, Regression trees & Model trees and Instance-Level representations.

Unit – V	11 Hrs

Data Mining Algorithms: One-R, Naïve Bayes Classifier, Decision trees, Decision rules, Association Rules, Regression, K-Nearest Neighbor Classifiers. Evaluating Data Mining Results: Issues in Evaluation; Training and Testing Principles; Error Measures, Holdout, Cross Validation. Comparing Algorithms; Taking costs into account and Trade-Offs in the Confusion Matrix.

Expected Course Outcomes:

After going through this course the student will be able to:

CO1. Demonstrate the knowledge of specialized data warehousing methods

CO2: Apply the statistical and computational methods for genome and protein data.

CO3: Able to work with the mining tools to help the decision support system

CO4: Interpret the data sets using concurrent statistical method.

Reference Books:

1.	Jiawei Han, Micheline Kamber and Jian Pei. Data Mining: Concepts and Techniques, 3rd edition. Elsevier, 2011. ISBN 0123814804, 9780123814807
2.	Fundamentals of Data Warehouses, Matthias Jarke, Maurizio Lenzerini, Yannis Vassiliou, Panos Vassiliadis 2nd edition. Springer Science & Business Media, 2002. ISBN 3540420894, 9783540420897
3.	Ian H. Witten, Eibe Frank and Mark A. Hall. Data Mining: Practical Machine Learning Tools and Techniques, 3rd edition Morgan Kaufman, 2011. ISBN 9780123748560
4.	Ralph Kimball, Margy Ross, Bob Becker, Joy Mundy, Warren Thornthwaite**.** Kimball's Data Warehouse Toolkit Classics: The Data Warehouse Toolkit, 2nd Edition; Wiley, 2009. ISBN 0470479574, 9780470479575
5.	Data Mining: Introductory and Advanced Topics byMargaret H. Dunham., Pearson Education India, 2006. ISBN 8177587854, 9788177587852

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	L	H	H	M	H	H	L	-	L	-	-
CO2	H	M	H	H	H	H	-	M	H	-	-
CO3	H	H	H	H	H	H	L	-	H	-	H
CO4	H	H	M	H	H	M	L	M	M	L	M

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	L	L	L
CO2	H	H	H
CO3	L	M	H
CO4	L	H	H

Artificial Intelligence						
Course Code	:	16MBI232		**CIE Marks**	:	100
Hrs/Week	:	L:T:P:S	4:0:0:0	**SEE Marks**	:	100
Credits	:	4		**SEE Duration**	:	3 hrs

Course Learning Objectives (CLO):
Graduates shall be able to
1. Understand the basic concepts of Artificial Intelligence
2. Explore the applications of artificial intelligence in bioinformatics
3. Apply basic search algorithms for problem solving; knowledge representation and reasoning.
4. Perform pattern recognition and processing with the application of fuzzy logic and neural nets.
5. Design the intelligent systems that can solve general purpose problems, represent and process knowledge, plan and act, reason under uncertainty.

Unit – I	**10 Hrs**

Introduction to Artificial Intelligence: Introduction to Artificial Intelligence, Problems, Approaches and tools for Artificial Intelligence. Introduction to search, Search algorithms, Heuristic search methods, Optimal search strategies. Use of graphs in Bioinformatics. Grammers, Languages and Automata. Current Techniques of Artificial Intelligence: Probabilistic approaches: Introduction to probability, Bayes' theorem, Bayesian networks and Markov networks.

Unit – II	**10 Hrs**

Classification Methods: Linear Classifiers & Logistic Regression, Linear Classifiers, Overfitting & Regularization in Logistic Regression, Decision Trees, Preventing Overfitting in Decision Trees, Handling Missing Data, Clustering and retrieval of data, Nearest Neighbor Search, Clustering with k-means, Hierarchical Clustering.

Unit – III	**10 Hrs**

Introduction –Agents– Problem formulation– uninformed search strategies – heuristics – informed search strategies – constraint satisfaction. Study of Ethical, legal and social issues associated with AI.

Unit – IV	**10 Hrs**

Supervised learning (parametric/non-parametric algorithms, support vector machines, kernels, neural networks, Unsupervised learning (clustering, dimensionality reduction, recommender

systems, deep learning, Best practices in machine learning (bias/variance theory; innovation process in machine learning and AI, Support vector machines (SVMs), case studies and applications.

Unit – V	10 Hrs

Genetic programming – Method, Applications, Guidelines and Bioinformatics applications. Boolean Networks, Bayesian Networks and Fuzzy Neural Networks with case studies. Learning from observation - Inductive learning – Decision trees – Explanation based learning – Statistical Learning methods - Reinforcement Learning

Expected Course Outcomes:

After going through this course the student will be able to:

CO1: Learn about concepts of artificial intelligence and their applications in Bioinformatics

CO2: Understand the basic ideas and techniques underlying the design of intelligent computer systems

CO3: Use the knowledge acquired for both problem solving and for reasoning.

CO4: Focus on problems, the ethical, legal and social issues involved in the field of AI and use the techniques and algorithms to address those problems.

Reference Books:

1.	Intelligent Bioinformatics: The Application of Artificial Intelligence Techniques to Bioinformatics Problems by Edward Keedwell, Ajit Narayanan, published by John Wiley and Sons, 2005. ISBN 9780470021750.
2.	Artificial Intelligence: A Modern Approach by Stuart Jonathan Russell and Peter Norvig. Prentice Hall, 2010. ISBN 0-13-604259-7
3.	Machine Learning Approaches to Bioinformatics by Zheng Rong Yang. World Scientific Publishing Co. Pte. Ltd, 2010.ISBN 981-4287-30-X
4.	Computational Intelligence in Biomedicine and Bioinformatics: Current Trends and Applications. by Tomasz G. Smolinski, Mariofanna G. Milanova, Aboul Ella Hassanien. (Eds.) Published by Springer-Verlag Berlin Heidelberg, 2009.ISBN 978-3-540-70776-9
5.	Artificial Intelligence: Structures and Strategies for complex problem solving by George F. Luger, Fourth Edition, Pearson Education, 2002.ISBN 9780201648669

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	L	L	M	L	H	L	-	H	M	L
CO2	H	H	H	H	H	H	L	L	H	-	M
CO3	M	M	H	H	H	M	-	M	L	L	H
CO4	-	M	H	-	M	L	-	M	M	H	M

Mapping of COs with PSOs

	PSO1	PSO2	PSO3

	CO1	L	M	L	
	CO2	L	M	M	
	CO3	M	H	H	
	CO4	L	L	H	

Insilico Drug Design						
Course Code	**:**	**16MBI241**		**CIE Marks**	**:**	**100**
Hrs/Week	**:**	**L:T:P:S**	**4:0:0:0**	**SEE Marks**	**:**	**100**
Credits	**:**	**4**		**SEE Duration**	**:**	**3 hrs**

Course Learning Objectives (CLO):

Graduates shall be able to

1. Understand the underlying principles of molecular modeling and simulation involved in drug design and discovery.
2. Explore conceptually the techniques employed in Model building, Library design and Molecular interaction studies
3. Synchronize computational tools and techniques to empower the insights and advances in the field of Pharmacy
4. Apply Evolutionary, Machine leaning and numerical techniques to cope up with the current picture in pharmaceutical research.
5. Design and develop workflows for building molecular complexes

Unit – I	**10 Hrs**

Drug Design Process: Computer - Assisted Drug Discovery: Drug Discovery and Development process. Compound searching, Target Identification, Target characterisation, Study of molecular interactions between target and compound (docking), ADMET Studies and Study of drug resistance. Drug design process for a known protein target – Structure based drug design process, Finding initial hits, Compound refinement, ADMET Studies and Study of drug resistance. Drug design process for unknown protein target – Ligand based drug design process, Finding initial hits, Compound refinement, ADMET Studies and Study of drug resistance. Case studies

Unit – II	**9 Hrs**

Compound Library Design: Target library vs Diverse libraries, Non-Enumerative techniques, Drug likeliness and Synthetic accessibility, Analyzing diversity and Spanning known chemistries. Compound selection techniques.

Unit – III	**10 Hrs**

Homology Modeling and Drug Design: Structure Generation, Retrieval, Structure Visualization. Homology modeling - Constructing an initial model, Refining the model, Manipulating the model, Navigation of the model. Model evaluation – Model evaluation techniques, Concept of energy minimization and Energy minimization techniques. Conformation generation, Deriving bioactive conformations, Molecular superposition and alignment, Deriving the Pharmacophoric pattern, Receptor mapping and estimating biological activities. Structural similarities and Superimposition techniques. Rational Drug Design and Chemical Intuition, Important Key and the Role of the Molecular Model, Limitations of Chemical Intuition.

Unit – IV	**10 Hrs**

Molecular Mechanics: Introduction to Molecular mechanics, Force fields for drug design. Study of protein folding: Algorithms, Conformation analysis. Docking: Introduction, Search algorithms, Scoring functions, Docking Process – Protein Preparation, Building the ligand, Setting the bounding box, Running the docking calculations. Building the Pharmacophore Models: Components of Pharmacophore model, Creating a Pharmacophore model from active compounds, Creating Pharmacophore model from Active site and Searching compound databases.	
Unit – V	**9 Hrs**
Quantum Mechanics in Drug Design: QSAR: Conventional QSAR vs 3D-QSAR, QSAR Process, Molecular descriptors, Automated QSAR Programs. 3D-QSAR – 3D-QSAR Process. Quantum Mechanics algorithms in Drug design, ADMET and Toxicity studies. New Lead Discovery Strategies. Composition of Drug Discovery teams, Current Practice of CADD in the Pharmaceutical industry, Management structures of CADD groups, Contributions and achievements of CADD groups, Limitations of CADD support, Inherent Limitations of CADD support. State of Current Computational Models, Software and Hardware constraints	

Expected Course Outcomes:

After going through this course the student will be able to:

CO1: Demonstrate the knowledge of physical and chemical properties of pharmacological compounds.

CO2: Apply the drug designing methods for screening and inventing the new targets and drugs.

CO3: Able to estimate the relevant drug capabilities of known and unknown compounds.

CO4: To equip with the drug design skills and patenting ability and spread awareness about the compounds.

Reference Books:

1.	Cancer Drug Design and Discovery *by Stephen Neidle,* Academic Press *– Publisher, 2008. ISBN 0123694485, 9780123694485*
2.	Bioinformatics Technologies by Yi-Ping Phoebe Chen, Springer Science & Business Media, 2005. ISBN 354026888X, 9783540268888
3.	Textbook of drug design and discovery *by Kristian Stromgaard, Povl Krogsgaard-Larsen, Ulf Madsen, 5th edition.* Published by CRC Press, LLC, 2016. ISBN1498702783, 9781498702782
4.	*Computational Drug Design: A Guide for Computational and Medicinal Chemists by David. C. Young, Wiley-Interscience, 2009. ISBN: 978-0-470-12685-1*
5.	Drug Discovery Strategies and Methods by Alexandros Makriyannis, Diane Biegel and Marcel Dekker, CRC Press, 2003. ISBN 0203913272, 9780203913277

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	L	-	H	H	H	-	-	L	-	M
CO2	H	M	L	H	H	H	L	L	M	L	L
CO3	M	-	-	M	M	H	-	-	M	-	L
CO4	H	M	-	H	M	H	-	-	H	-	M

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	M	-	-
CO2	H	H	M
CO3	H	H	L
CO4	M	H	M

Pharmacogenomics						
Course Code	:	**16MBI242**		**CIE Marks**	:	**100**
Hrs/Week	:	**L:T:P:S**	**4:0:0:0**	**SEE Marks**	:	**100**
Credits	:	**4**		**SEE Duration**	:	**3 hrs**
Course Learning Objectives (CLO): Graduates shall be able to						

1. Understand the role of genetic variability in phase II metabolizing enzymes on drug pharmacokinetics, efficacy, and toxicity.

2. Apply knowledge to explain or predict the role of genetic variability in drug targets on drug efficacy and toxicity.

3. Describe the molecular basis for a genetic variation influencing the functional activity of phase II metabolizing enzymes.

4. Discuss clinical data supporting a role for efflux transporters in bioavailability, CNS exposure and tumor resistance.

5. Analyse the allele-specific variation in human gene expression.

Unit – I	10 Hrs

Concepts of Pharmacogenetics: Introduction, basic concepts about genetic diseases. Personalized medicine- introduction and importance. The genetics of therapeutic targets and gene-based targets. Pharmacogenomics necessity in drug designing. Detoxification and poisoning. Drug discovery and approval. Pharmacogenomics and Pharmacognosy. Polygenic Nature of Drug Response: Antidepressants. Metabolic changes of drugs and related organic compounds - Ayurgenomics - Genomics and Modern Medicine.

Unit – II	9 Hrs

Polymorphisms-Introduction, types and importance in Drug targets. Prediction of structural changes among sequences by the influence of polymorphisms. Genetic analysis of human variation, Microsatellite for studying genetic variation. Critical analysis of genomic association. Pharmacogenomics and Drug Transport. Approaches to pharmacogenomics studies

Unit – III	10 Hrs

Pharmacogenomics and Drug response: Structural influence in the Drug response. Dose dependent and independent drug response, Efficacy and metabolism of drugs. Drug metabolism pathways and adverse drug reactions. hematotoxicity :leukopenia, pancytopenia, hepatotoxicity and case studies, pancreatitis, gastrointestinal disturbances (eg. nausea, vomiting, diarrhoea), flu-like symptoms such as fever, headache. Rash: Arthralgia, Myalgia. Crohn's Disease and Severe Myelosuppression

Unit – IV	10 Hrs

Pharmacogenomics Analysis Tools: Pharmacokinetics (PK), Pharmacodynamics (PD). Process in Structural Pharmacogenomics- Target Structure optimization, Validation, lead identification, ADME prediction, synthesis, assays and Clinical trials, Treatment of Cancer and Infectious Diseases. Pharmacogenomics of Adverse Drug Reactions. Warfarin, immune suppressants and hepatitis C Pharmacogenomics related Case studies and discussion.

Unit – V	9 Hrs

Allele-Specific Variation in Human Gene Expression: Genome-Wide Analysis of Allele Specific Gene Expression Using Oligo Microarrays, Roche Ampli Chip, HaploChIP: An in vivo Assay. Association Studies in Pharmacogenomics-Pharmacogenomics of Anticoagulation drugs. Ethical issues for Pharmacogenomics; Pharmacogenomics and recent trends of Pharmaceuticals.

Expected Course Outcomes:

After going through this course the student will be able to:

CO1. Demonstrate an understanding of the complexity of most drug responses (i.e. the drug response cascades), and the influence this has on the contribution of genetic variability to drug response.

CO2.Evaluate the current and future potential applications of drug target pharmacogenetics to

individualization of drug therapy.

CO3: Describe the risks and values that genomic information brings to the drug discovery and development process

CO4: Identify key regulatory issues that pharmacogenomics raises in the drug development process

Reference Books:	
1.	Pharmacogenomics: Challenges and Opportunities in Therapeutic Implementation by Yui-Wing Francis Lam, Larisa H. Cavallari. Academic Press, 2013. ISBN: 0123983037, 9780123983039
2.	Pharmacogenomics in Clinical Therapeutics by Pharmacogenomics in Clinical Therapeutics. John Wiley & Sons, 2012. ISBN: 1119959586, 9781119959588
3.	Pharmacogenomics An Introduction and Clinical Perspective by Joseph S. Bertino, Angela Kashuba, Joseph D. Ma, Uwe Fuhr, C. Lindsay DeVane. McGraw Hill Professional, 2012. ISBN: 0071813713, 9780071813716
4.	Pharmacogenomic Testing in Current Clinical Practice: Implementation in the Clinical Laboratory Molecular and Translational Medicine by Alan H. B. Wu, Kiang-Teck J. Yeo. Springer Science & Business Media, 2011. ISBN:1607612836, 9781607612834
5.	Concepts in Pharmacogenomics EBSCO ebook academic collection by Martin M. Zdanowicz. ASHP, 2010. ISBN 1585282340, 9781585282340

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	-	M	-	H	L	H	-	-	-	-	M
CO2	M	M	M	L	H	M	-	-	M	M	M
CO3	H	H	M	M	H	M	-	-	M	H	L
CO4	L	L	M	L	M	H	-	-	L	H	-

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	M	-	-
CO2	H	H	M
CO3	H	H	L
CO4	M	H	M

Essential Programming in Bioinformatics

Course Code	**:**	**16MBI251**		**CIE Marks**	**:**	**100**
Hrs/Week	**:**	**L:T:P:S**	**4:0:0:0**	**SEE Marks**	**:**	**100**
Credits	**:**	**4**		**SEE Duration**	**:**	**3 hrs**

Course Learning Objectives (CLO):

Graduates shall be able to

1. Explore conceptually programming applications in the domains of Life sciences and in general study the role of computer science in life sciences

2. Acquire knowledge of the Object Oriented Programming and Advanced programming skills in Java

3. Study Threading, Event management, Database connectivity as well as Web programming in Java

4. Understand the importance of Threading, Event management, Database connectivity as well as Web programming to High throughput data analysis

5. Explore practically the applications of BioJava to sequence, structure and micro-array data analysis

Unit – I	10 Hrs

Introduction to Java: Java and Java applications. Java Development Kit (JDK). Java Basics – Data Bytes, Operators, Statements and Object-oriented programming. Classes, Inheritance, Exceptions: Classes. Classes in Java - Declaring a class, Class name, Super classes, Constructors. Creating instances of class. Inner classes. Inheritance: Simple, multiple, and multilevel inheritance; Overriding, overloading. Exception Handling in Java.

Unit – II	9 Hrs

Multi-Threaded Programming, Event Handling: Multi Programming: Extending threads; Implementing rentable. Synchronization, Changing state of the thread. Bounded buffer problems, Read-write problem, Producer-Consumer problems. Event Handling: Two event handling mechanisms, Delegation event model, Event classes; Sources of events; Event listener interfaces. Delegation event model; Adapter classes; Inner classes.

Unit – III	10 Hrs

Applets: The Applet Class: Two types of Applets, Applet basics, Applet Architecture, An Applet skeleton; The HTML APPLET tag; Passing parameters to Applets, Simple Applet display methods; Requesting repainting; Using the Status Window. getDocumentbase() and getCodebase(); ApletContext and showDocument(); The AudioClip Interface; The AppletStub Interface;

Drawing Lines; Drawing Other Stuff; Color; Mouse Input; Keyboard Input and Output to the Console. Threads and Animation, Backbuffers, Graphics and Painting; Clocks. Playing with text: Introduction to 2D arrays and hyperlinks, 3D Graphics - Basic classes.

Unit – IV	10 Hrs

Java 2 Enterprise Edition Overview, Database Access: The Concept of JDBC; JDBC Driver Types; JDBC Packages; A Brief Overview of the JDBC process; Database Connection; Associating the JDBC/ODBC Bridge with the Database; Statement Objects; ResultSet; Transaction Processing; Metadata, Data types; Exceptions. Servlets: Background; The Life Cycle of a Servlet; Simple Servlet; The Servlet API. The Javax.servlet Package. Reading Servlet Parameter, Handling HTTP Requests and Responses. Cookies and Session Tracking.

Unit – V	9 Hrs

BioJava: Working with Nucleic Acid and Protein Sequences – create, read, compare sequences. Working with Protein Structures – fetching, parsing PDB structures, Calculating structure alignment, interacting with Jmol. Sequence alignment – performing global, local and multiple sequence alignment. BioJava and Nextgen sequencing.

Expected Course Outcomes:

After going through this course the student will be able to:

CO1: Define and explain concepts of Object Oriented Programming along with Threading, Event management, Database connectivity as well as Web programming

CO2: Apply Threading, Event management, Database connectivity as well as Web programming to solve the problems in the area of Big Data Analytics

CO3: Analyze and evaluate efficiency threading and multithreading with case studies

CO4: Design and implement basic algorithms to perform high throughput data analysis in the field Sequence and structure analysis

Reference Books:

1.	Java - The Complete Reference, 9th edition, by Herbert Schildt, McGraw Hill Education, 2014. ISBN: 0071808558 ISBN-13: 978-0071808552
2.	Introduction to Java Programming, Comprehensive Version, 10th edition by Y. Daniel Liang, Prentice Hall of India, 2013. ISBN-13: 978-0133761313
3.	BioJava: A Programing Guide by Kaladhar D.S.V.G.K. LAP LAMBERT Academic Publishing 2012 ISBN-13: 978-3659167508

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	L	-	H	H	H	-	-	L	-	M
CO2	H	M	L	H	H	H	L	L	M	L	L
CO3	M	-	-	M	M	H	-	-	M	-	L
CO4	H	M	-	H	M	H	-	-	H	-	M

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	L	M	M
CO2	H	H	H
CO3	M	H	H
CO4	H	H	H

High Performance Bio-Computing						
Course Code	:	**16MBI252**		**CIE Marks**	:	**100**
Hrs/Week	:	**L:T:P:S**	**4:0:0:0**	**SEE Marks**	:	**100**
Credits	:	**4**		**SEE Duration**	:	**3 hrs**
Course Learning Objectives (CLO):						
Graduates shall be able to						

1. 1. To impart the basic concepts of High performance computing in applied bioinformatics. 2. To understand and explain the role of HPC in large data driven operations. 3. To compare the difference in normal computing and HPC processing speed. 4. To develop basic scripts to run the commands in HPC 5.	
Unit – I	**10 Hrs**
Introduction to HPC Introduction to Linux operating system, Basic commands used in HPC cluster, Major components and its functions in HPC Cluster- head node, login node, interactive node, compute node, I/O node, Hardware architecture of HPC-processor design, cache architectures, design and evaluation techniques, operating systems and compilers, communications libraries, programming strategies for vector and parallel computers, optimization strategies, grid computing.	
Unit – II	**9 Hrs**
Introduction to shell scripting Basics of shell scripting, invocation, variables, if-then-else. Loops, Workflows and nested workflows, How to submit and monitor workflow execution. HPC Data Storage, Serial and parallel batch jobs and scripting to run processes in parallel.	
Unit – III	**10 Hrs**
Big Data analytics Introduction of Cloud computing, Hadoop architecture. MIKE2.0, Multiple layer architecture, Distributed Parallel architecture, NGS data analysis using Hadoop.	
Unit – IV	**9 Hrs**
Installation of Software Packages Install R packages, Perl modules, Python modules and general software packages. Molecular dynamics and use of VMD Software's and tools used to access HPC cluster with examples. Applications of High performance Computing in the field of Bioinformatics.	
Unit – V	**10 Hrs**
High throughput data analysis with HPC Conversion of SRA files, FASTQC analysis using HPC – Command and tools required, interpretation of results. Adapter trimming, Alignment, Variant calling, Performing BLAST search, interpretation of results. Comparison of the results from various tools using HPC.	

Expected Course Outcomes:
After going through this course the student will be able to:
CO1: Understand the basic knowledge of High Performance Computing
CO2: Describe architectural hardware for high performance computing systems and installation
        of software packages
CO3: Analyze and apply the appropriate tools and techniques to perform high throughput data
        analysis
        CO4. Develop parallel software tools using High Performance Computing	

	Reference Books:
1.	Bioinformatics for High Throughput Sequencing By Naiara Rodríguez-Ezpeleta, Michael Hackenberg, Ana M. Aransay.| ISBN-13: 9781461407812
2.	Review of "Next-generation DNA sequencing informatics" by Stuart M. Brown 2013. Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York. ISBN-13: 978-1936113873
3.	High-Throughput Next Generation Sequencing Methods and Applications Series: Young Min

	Kwon, Steven C. Ricke ISBN: 978-1-61779-088-1 (Print) 978-1-61779-089-8
4.	High Performance Computing by Kevin Autor Dowd, Michael Kosta Loukides.O'Reilly & Associates, 1993.ISBN 1565920325, 9781565920323
5.	Introduction to Parallel Computing, Ananth Grama, Anshul Gupta, George Karypis, and Vipin Kumar, 2nd edition, Addison-Welsey, ISBN-13: 978-0201648652

Scheme of Continuous Internal Evaluation (CIE) for Theory

CIE will consist of TWO Tests, TWO Quizzes and ONE assignment. The test will be for 30 marks each and the quiz for 10 marks each. The assignment will be for 20 marks. The total marks for CIE (Theory) will be 100 marks.

Scheme of Semester End Examination (SEE) for Theory

The question paper will have FIVE questions with internal choice from each unit. Each question will carry 20 marks. Student will have to answer one question from each unit. The total marks for SEE (Theory) will be 100 marks.

Mapping of COs with POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11
CO1	H	M	M	M	M	M	L	-	L	L	M
CO2	M	H	H	M	H	M	M	L	M	L	M
CO3	M	H	H	H	M	H	H	M	H	M	H
CO4	L	L	H	M	M	H	M	M	H	M	M

Mapping of COs with PSOs

	PSO1	PSO2	PSO3
CO1	L	-	-
CO2	L	M	M
CO3	M	H	H
CO4	H	H	H