Birla Institute of Technology, Mesra

Ranchi - 835215 (India)

Two -Year

Master Degree Programme

In

Bioinformatics and Computational Biology

Department of Bioengineering & Biotechnology

Birla Institute of Technology, Mesra, Ranchi- 835215 (India)

June 2023

Department of Bioengineering & Biotechnology

Birla Institute of Technology, Mesra, Ranchi - 835215 (India)

Institute Vision

To become a Globally Recognized Academic Institution in consonance with the social, economic and ecological environment, striving continuously for excellence in education, research and technological service to the National needs.

Institute Mission

- To educate students at Undergraduate, Post Graduate Doctoral and Post-Doctoral levels to perform challenging engineering and managerial jobs in industry.
- To provide excellent research and development facilities to take up Ph.D. programmes and research projects.
- To develop effective teaching and learning skills and state of art research potential of the faculty.
- To build national capabilities in technology, education, and research in emerging areas.
- To provide excellent technological services to satisfy the requirements of the industry and overall academic needs of society.

Department Vision

The Department of Bioengineering and Biotechnology has a vision to impart international standard quality education in the field of Bioscience, Biotechnology, Bioinformatics and Bioengineering.

Department Mission

- To create state-of-the-art infrastructure for Research and Training in Biotechnology, Bioinformatics and Bioengineering.
- To provide globally acceptable technical education in Bioscience, Biotechnology, Bioinformatics and Bioengineering.
- To nurture graduates for innovation and creativity in the field of Bioscience, Biotechnology, Bioinformatics and Bioengineering having ethical and social concerns.
- To promote collaboration with Academia, Industries and Research Organizations at National and International level to enhance quality of education and research.
- To contribute to socioeconomic development through education and bioentrepreneurship.

M.Sc. Bioinformatics & Computational Biology

Programme Educational Objectives (PEOs)

PEO1	Students will gain necessary knowledge and develop specialized skills in the different areas of Bioinformatics and Computational Biology.
PEO2	Students will think critically and creatively about the use of Bioinformatics to address local and global problems.
PEO3	Students will be able to implement the scientific skills for development of new databases and tools for industrial applications and entrepreneurship.

Program Outcomes (POs)

PO1	Ability to carry out research /investigation independently in specialized areas of Biotechnology, Bioinformatics and Computational Biology.
PO2	Ability to write and present a substantial technical report/document.
PO3	Able to demonstrate a degree of mastery in the area of Bioinformatics to enable them in collaborative and multidisciplinary research.
PO4	Recognize the need for continuous learning and will prepare oneself to create, select, learn and apply appropriate techniques, resources, and modern bioinformatics methods to solve complex biological problems with an understanding of the limitations.
PO5	Demonstrate knowledge of Bioinformatics & Computational Biology skills in pharmaceutical industries like Vaccine design, new drug molecule design and in healthcare like Genetic diseases & personalized medicines.

BIRLA INSTITUTE OF TECHNOLOGY- MESRA, RANCHI

COURSE STRUCTURE

M.Sc. Bioinformatics & Computational Biology

Based on CBCS & OBE model (NEP2020)

Semester / Session	Course Level	Course Category	Course Code	Course Name	Mode of Delivery and Credits (Period/Week)			
					Lecture	Tutorial	Practical	Credits
Semester - I								
FIRST / Monsoon	FOURTH LEVEL	**THEORY**						
		Program Core	BI101	Cell and Molecular Biology	3	0	0	3
			BI102	Biological Databases and MySQL	3	0	0	3
			BI103	Mathematics and Statistics for Biologist	3	0	0	3
			CA405	Data Structures and Algorithms	3	0	0	3
		Program Elective		PE Subject 1	3	0	0	3
		LABORATORY - I						
		Laboratory	BI104	Cell & Molecular Biology Lab	0	0	3	1.5
			BI105	Biocomputing with Python, PERL & MySQL Lab	0	0	3	1.5
			CA406	Data Structures and Algorithms Lab	0	0	3	1.5
				PE Lab 1	0	0	3	1.5
		NEP Course	MT132	Communication Skills -1	0	0	3	1.5
					Total Semester Credits			**22.5**
Semester - II								
SECOND/ Spring	FOURTH LEVEL	**THEORY**						
			BI201	Biological Sequence Analysis & Algorithms	3	0	0	3
		Program Core	BI202	Computational Structural Biology	3	0	0	3
			BI203	Artificial Intelligence & Machine Learning	3	0	0	3
			BI204	Data Analytics using R	3	1	0	4
		Program Elective		PE Subject 2	3	0	0	3
		Open Elective		OE Subject 1	3	0	0	3
		LABORATORY - II						
		Laboratory	BI205	BioSequence & Structure Analysis Lab	0	0	3	1.5
			BI206	Data Science Lab	0	0	3	1.5
				PE Lab 2	0	0	3	1.5
		NEP Course	MT133	Communication Skills - 2	0	0	3	1.5
		NEP Course	NP202	Community Engagement	0	0	4	2
					Total Semester Credits			**27**
Semester - III								
THIRD/ Monsoon	FIFTH LEVEL	**THEORY**						
		Program Core	BI301	Proteomics, Metabolomics & Biomarker Design	3	0	0	3
			BI302	Cheminformatics and Drug Design	3	0	0	3
			BI303	NGS Data Analysis	3	0	0	3
			CA439	Image Processing	3	0	0	3
		Program Elective		PE Subject 3	3	0	0	3
		Open Elective		OE Subject 2	3	0	0	3
		LABORATORY - III						
		Laboratory	BI304	Cheminformatics and Drug Design Lab	0	0	3	1.5
			BI305	NGS data Analysis Lab	0	0	3	1.5
			BI306	Image Processing Lab	0	0	3	1.5
				PE Lab 3	0	0	3	1.5
			BI307	Mini Project - Dissertation Part-I	0	0	0	1.5
					Total Semester Credits			**25.5**
Semester - IV								
FOURTH/ Spring	FIFTH LEVEL	Research Project	BI401	Dissertation Part-II / Major Project	**Total Credits**			**8**
Grand Total Credits for M.Sc. Bioinformatics Course								**83**

PROGRAM ELECTIVES (PE) FOR M.Sc. LEVEL OFFERED FOR LEVEL 4 - 5

PE / LEVEL	Code no.	Name of the PE courses	Prerequisites/ Corequisites	L	T	P	C
Programme Elective -I							
PE/4 (MO)	BT415	Molecular Biology and rDNA Technology		3	0	0	3
PE/4 (MO)	BT420	Genomics & rDNA Technology Lab		0	0	3	1.5
PE/4 (MO)	BT403	Applied Microbiology		3	0	0	3
PE/4 (MO)	BT406	Microbiology Lab		0	0	3	1.5
PE/4 (MO)	CA409	Object Oriented Design using JAVA		3	0	0	3
PE/4 (MO)	CA410	Object Oriented Design using JAVA Lab		0	0	3	1.5
PE/4 (MO)	IT303	Internet and Web Technology		3	0	0	3
PE/4 (MO)	IT340	Internet and Web Technology Lab		0	0	3	1.5
Programme Elective -II							
PE/4 (SP)	BT407	Genomics		3	0	0	3
PE/4 (SP)	BT408	Genomics Lab		0	0	3	1.5
PE/4 (SP)	CA407	Database Design Concepts		3	0	0	3
PE/4 (SP)	CA408	Database Design Concepts Lab		0	0	3	1.5
PE/4 (SP)	BI207	Systems Biology & Biological Networks		3	0	0	3
PE/4 (SP)	BI208	Systems Biology & Biological Networks Lab		0	0	3	1.5
Programme Elective -III							
PE/5 (MO)	BI308	Medical Genomics		3	0	0	3
PE/5 (MO)	BI309	Medical Genomics Lab		0	0	3	1.5
PE/5 (MO)	BI310	Biocomputing with Perl & BioPerl		3	0	0	3
PE/5 (MO)	BI311	Biocomputing with Perl & BioPerl Lab		0	0	3	1.5
PE/5 (MO)	BI312	Immuno-Informatics and Vaccine Design		3	0	0	3
PE/5 (MO)	BI313	Immuno-Informatics and Vaccine Design Lab		0	0	3	1.5

OPEN ELECTIVES (OE)* FOR M.Sc. LEVEL OFFERED FOR LEVEL 4 - 5

OE / LEVEL	Code no.	Name of the OE courses	Prerequisites/ Corequisites	L	T	P	C
Open Electives - I (MO Session)							
OE/4 (MO)	BI102	Biological Database & MySQL	NIL	3	0	0	3
OE/4 (MO)	BT503	Biosafety, Bioethics and IPR	NIL	3	0	0	3
Open Electives - II (SP Session)							
OE/5 (SP)	BI310	Biocomputing with Perl & BioPerl	NIL	3	0	0	3
OE/5 (SP)	BT418	Analytical Techniques	NIL	3	0	0	3

*** OPEN ELECTIVES TO BE OPTED ONLY BY OTHER DEPARTMENT STUDENT**

NEP 2020 Exit Policy

Students who leave the course after one year, earning 49.5 credits will be awarded with **Post Graduate Diploma in Bioinformatics and Computational Biology**.

M.Sc. Bioinformatics & Computational Biology

Semester - I

Program Core - I:

1. Cell and Molecular Biology (BI101)
2. Biological Databases and MySQL **(**BI102)
3. Mathematics and Statistics for Biologist (BI103)
4. Data Structures and Algorithms (CA405)

Laboratories - I:

1. Cell & Molecular Biology Lab (BI104)
2. Biocomputing with Python, PERL & MySQL (BI105)
3. Data Structures and Algorithms Lab (CA406)
4. Communication Skills -1 (MT132)

Program Electives - I with Labs:

1. Molecular Biology and rDNA Technology (BT415)
    - LAB: Genomics & rDNA Technology Lab (BT420)
2. Applied Microbiology (BT403)
    - LAB: Microbiology LAB (BT406)
3. Object Oriented Programming using JAVA (CA409)
    - LAB: Object Oriented Programming using JAVA Lab (CA410)
4. Internet and Web Technology (IT303)
    - LAB: Internet and Web Technology Lab (IT340)

Course Information Sheet

Course: CELL & MOLECULAR BIOLOGY

Course code: BI101
Course title: Cell & Molecular Biology
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:

This course enables the students to:

1.	Recapitulate the previous knowledge of cell biology and to establish thorough understanding of various cell structure and function at molecular level.
2.	Provide a thorough understanding of the various molecular biology concepts in study of cell biology and to study the different tools and techniques used to study the biology of cells at molecular level.
3.	Provide students with a deep insight about the motility of the cell with emphasis on the molecular motors, cell adhesions, molecular biology involved in the movement process involved in movement of Cilia and Flagella.
4.	Teach our students to have a concrete knowledge about cell-to-cell communication in animals as well as plants and to study about the basis of the interaction as well as the genes involved in it.
5.	Acquire in-depth knowledge of the molecular events involved in cell division which includes mitosis, meiosis, cell cycle and its regulation. Including. To provide a wider and global perspective of cell cycle regulation and cancer, with an ability to discriminate, evaluate, analyze and synthesize existing and new knowledge, and integration of the same for enhancement of knowledge.

Course Outcomes:

At the end of the course, a student should be able to:

CO1	Apply knowledge of cell biology and molecular Biology in various cellular functions, inculcate a knowledge of various issues related to molecular cell biology, the application and research involved in functioning of the different cell organelles.
CO2	Design and analyze the experiments related with the different molecules involved in cell biology and use of the various techniques in molecular cell biology to study the kinetics and rationale behind each phenomenon.

CO3	Identify, formulate, and solve problems that arise due to the inefficient functioning of the various life processes like cell-to-cell communication, cell cycle regulation, movement processes of a cell or system.
CO4	Use the techniques, skills, and modern tools necessary for imbalances in various life processes, design a molecular cell biology research project, collect, and analyze data, and interpret results

SYLLABUS

Module I: Cytology: Origin of Life, Characteristics of life, Chemical Composition of Life, Water and its properties, Theories of Origin of Life, Miller's Experiment, Biological organization, Prokaryotic & Eukaryotic Cells, Cell structure and function, Cell Theory, Cell cycle and Cell Division. (8L)

Module II: Biomolecules: Structure and functions of Proteins, Carbohydrates and Lipids. Structure of DNA and RNA, DNA Conformations (forms of DNA: A, B, Z). Central Dogma of Molecular Biology - DNA Replication, Transcription and Translation. (8L)

Module III: Enzymology & Bioenergetics: Classification of enzymes, Structure and mechanism of enzyme action, Factors affecting enzyme activity, Application of enzymes, Bioenergetics basics, Gibbs free energy and Thermodynamics, Metabolism, Aerobic and Anaerobic respiration, Glycolysis, Krebs cycle, Electron transport chain, Beta-oxidation of Fatty acids. (8L)

Module IV: Genetics: Mendel's Laws of Inheritance, Codominance, and Incomplete Dominance, Overdominance, Epistasis: Non-allelic interactions and modification of Mendelian ratios, Multiple Alleles-ABO Blood Groups in Humans, Inborn Errors of Metabolism, Inheritance of Polygenic Traits with Specific Examples. (8L)

Module V. Gene Expression and Genome Editing - Hybridization based method (Northern Blot, RNA-FISH, DNA microarray), PCR based methods, Real time qRT-PCR, RNA sequencing. DNA Supercoiling, Gene Editing Techniques (Mega nuclease, Zinc finger nuclease, TALENS, CRISPR), Concepts of CRISPR/Cas9 technology, its Versions and working mechanism. Limitations of Gene editing techniques. (8L)

Books recommended:

1. Molecular biology of the gene by Watson et. Al (5th edition) ISBN: 8177581813
2. Molecular biology of the cell by Bruce Albert et al (4th edition) ISBN: 815332181

Reference Book

3. Genes VII by Benjamin Lewin, Oxford University Press ISBN: 019879276X
4. Molecular Cell Biology, by Harvey Lodish, Matthew P. Scott, P Matsudaira, J Darnell, L Zipursky, Chris A. Kaiser, A Berk, M Krieger, publisher: W. H. Freeman; 5th edition, ISBN: 0716743663

Course Evaluation:

Individual assignment, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	2	-	2	2	1
CO2	1	3	3	3	-
CO3	1	3	3	3	-
CO4	1	3	3	2	-

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**
[1: Slight (Low) 2: Moderate (Medium) 3: Substantial (High)]

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD2, CD3, CD6
CO2	CD1, CD2, CD3,CD4, CD6
CO3	CD1, CD2, CD3,CD4, CD6
CO4	CD1, CD3,CD6,CD7

COURSE INFORMATION SHEET

Course: BIOLOGICAL DATABASES AND MYSQL

Course code: BI102
Course title: Biological Databases and MySQL
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 3
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students to:

1.	Learn the fundamental concepts & importance of international repositories and explain the theoretical knowledge of database systems and algorithms.
2.	Extend comprehensive knowledge about Major Databases including Primary and Secondary Databases
3.	Gain knowledge about the techniques for database crosslinking and information retrieval systems.
4.	Demonstrate concept about various specialized & Genome databases in Bioinformatics
5.	Grasp the current fundamental problems of Bioinformatics and challenges of the subject.

Course Outcomes:

At the end of the course, a student should be able to:

CO1	Access various Bioinformatics resources and molecular databases and explain their collaborative effects in the field of Bioinformatics.
CO2	Analyze and discuss the similarity search results of BLAST & FASTA algorithms
CO3	Collect the proficient knowledge about the database cross-linking and integrated information retrieval system.
CO4	Effectively utilize the specialized and genome databases for advanced research.
CO5	Develop the key skills of Bioinformatics fundamental problems related to databases, crosslinking, and mechanism of information retrieval.

SYLLABUS

Module I: Major Information Resources: Biological Data types, Biological Literature Information access, storage, and retrieval systems. Primary and secondary databases of genomics, transcriptomics, proteomics, metabolomics and structural. Major file formats and their conversion tools. Human Genome Project, ENCODE project (8L).

Module II: Database Searching and Sequence Retrieval Methods: Sequence Similarity, Identity, and Homology; Sequence Similarity Searching Tools: BLAST, FASTA, PSI & PHI BLAST etc.. Query Filtering and Limits, Algorithms of BLAST & FASTA and their statistical significance (E value and other parameters), Various flavors of BLAST & FASTA (8L).

Module III: Database Systems: Characteristics of Database, Database Concepts, Schemas & Instances, Database users and Administrators, DBMS architecture. (8L).

Module IV: Database Management using MySQL - Data types, Tables and Queries, Primary and foreign Key, filtering and sorting, Grouping, Joins, SET operator, Constraints and Indexes, views, functions, Operation - Insert, update, delete. MySQL administrations and control. (8L).

Module V: Specialized Databases and Current Challenges: Databases of Genomic Sequences(EST,STS etc), Chemical Structure database. Gene expression and Microarray Databases. Pathway Databases. Gene Ontology (GO) database, Protein-Interaction Databases (STRING, IntAct etc.), Database of Genetic Variations (dbSNP, dbVar etc.). Current Challenges - NGS data generation and handling. (8L).

Textbook

- Bioinformatics: a practical guide to the analysis of genes and proteins, Baxevanis A., Ouellette F.B.F., John Wiley and Sons, New York.
- Introduction to Bioinformatics, Arthur Lesk, Oxford University Press ((Indian Edition).
- Learning MySQL by Saied M.M. Tahaghoghi, Hugh E. Williams, O'Reilly Media, Inc.

Reference Book

- Bioinformatics: Sequence and Genome Analysis, David W Mount, Cold Spring Harbor Laboratory Press, New York.
- Fundamental Concepts of Bioinformatics, Dan E Krane, Michael L Raymer, Benjamin-Cummings Pub Co (ISBN 0805346333)

Course Evaluation:

Individual assignment, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	2	2	2	2
CO2	1	-	2	3	3
CO3	3	1	2	2	-
CO4	3	2	-	2	2
CO5	3	2	2	1	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD2, CD3
CO2	CD1, CD2, CD3,CD4
CO3	CD1, CD2, CD3,CD4, CD6
CO4	CD1, CD2,CD6,CD7
CO5	CD1, CD2, CD3,CD6,CD7

COURSE INFORMATION SHEET

Course: MATHEMATICS AND STATISTICS FOR BIOLOGIST

Course code: BI103
Course title: Mathematics and Statistics for Biologist
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students to:

1.	Present basic concepts and techniques of linear algebra, probability, statistics, and graph theory
2.	Develop mathematical thinking and problem-solving skill
3.	Provide the foundations of probabilistic and statistical analysis
4.	Explain graphs to formulate computational problems

Course Outcomes
After the completion of this course, students will be able to:

CO1	Demonstrate skills in solving mathematical problems
CO2	Apply knowledge of computing and mathematics appropriate to the discipline
CO3	Analyze problems and identify the computing requirements appropriate to its solution
CO4	Explain basic concepts in probability theory and statistical analysis
CO5	Articulate the advanced courses in Computer science such as Coding Theory, Artificial Intelligence, Numerical Computation, etc.

SYLLABUS

Module I: Linear Algebra: Introduction, Matrices and solving set of linear equations, Vector space, Subspace, Linear combination of vectors, Linear dependence and independence of vectors, Bases and dimensions. (8L)

Module II: Inner product spaces, Orthogonal vectors and dual vectors, Eigenvalues and Eigenvectors, Linear programming. (8L)

Module III: Differential Calculus - Intro to Differentiation and Integration, finding Maxima and Minima, first order differential equations. (8L)

Module IV: Graph Theory: Introduction: Graphs and its types, Representation of graphs: Adjacency matrix, Incidence matrix, Adjacency list, Planar graph, Kuratowski's Graphs, Concepts of Clique. (8L)

Module V: Probability and Statistics: Frequency distribution and measures of central tendency mean, median mode, quartiles, measures of dispersions and skewness, standard deviation, mean deviation, coefficient of variation, moments. Probability: definition, Distribution: discrete and continuous, Chi-square test, t-test. (8L)

Books recommended:

1. K. Haffman, and R. Kunze, "Linear Algebra", 2nd Edition, Pearson, 2015.
2. W. Navidi, "Statistics for Engineers and Scientists", 2nd Edition, TMH, 2008.
3. Douglas B. West, "Introduction to Graph theory", Pearson Education, 2002.

Reference Books:

4. G. Williams, "Linear Algebra with Applications", 4th Edition, John & Bartlett.
5. J.K. Goyal, and J. N. Sharma, "Mathematical Statistics", Krishna Prakashan, 2017.
6. Narsingh Deo, "Graph Theory with Applications to Engineering and Computer Science", Prentice Hall of India, 2001.

Course Evaluation:

Individual assignment, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	2	1	1	1
CO2	3	3	1	1	1
CO3	2	3	2	1	1
CO4	3	2	1	1	1
CO5	3	1	1	1	1

If satisfying and **< 34% = 1 (L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Course: DATA STRUCTURE AND ALGORITHMS

Course code: CA405
Course title: Data Structures and Algorithms
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L:3 T:0 P:0
Class schedule per week: 3
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives

This course enables the students to:

1.	Provide knowledge of practical implementations and usage of Data Structures and Algorithms.
2.	Employ knowledge of various data structures during construction of a program.
3.	Develop the logical ability to store and retrieve data efficiently.
4.	Develop an appreciation of graph theory-based solutions for real life problems.
5.	Design and construct object-oriented software with an appreciation for data abstraction.

Course Outcomes

After the completion of this course, students are able to

CO1	Identify various data structures and their usages.
CO2	Apply data structures in the modeling of computer-based systems in a way that demonstrates comprehension of the trade-offs involved in design.
CO3	Demonstrate the usage of optimal trees, heaps and priority queues.
CO4	Implement sorting algorithms.
CO5	Develop programs using algorithms in graph theory.

SYLLABUS

Module I:
Fundamental Data Structures: Using Arrays, Singly Linked Lists, Circularly Linked Lists, Doubly Linked Lists, Asymptotic Analysis. (8L)

Module II:
Stacks, Queues, Dequeues: The Stack, Queue, Dequeue ADTs, Simple Array Based Stack, Queue, Dequeue Implementation, Implementing Stack, Queue with Singly Linked List, Reversing an Array using Stack, Matching Parenthesis and HTML tags, A Circular Queue. (8L)

Module III:
Trees: General Trees, Binary Trees, Implementing Trees, Tree Traversal Algorithms, Binary Search Trees, AVL Trees, B Trees. (8L)

Module IV:
Sorting: Insertion sort, Merge sort, Quick sort, Comparing Sorting Algorithms w.r.t time and space complexities. Heap: Priority Queues, Array Implementation of Heaps, Construction of Heaps, Heap Sort. (8L)

Module V:
Graphs: Computer representation of graphs, Graph Traversals, Transitive Closure, Directed Acyclic Graphs, Shortest Paths, Minimum Spanning Trees. (8L)

Textbooks:

1. Klein Shmuel Tomi, Basic Concepts in Data Structures, Cambridge University Press, 1st Edition, 2016.

Reference books:

1. Brass Peter "Advanced Data Structures", Cambridge University Press, 1st Edition.
2. Goodrich Michael T., Tamassia Roberto, Goldwasser Michael H. "Data Structures and Algorithms in Java", Wiley, 6th Edition, 2014.

Course Evaluation:

Individual assignment, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	2	1	1	1
CO2	3	3	1	1	1
CO3	2	3	2	1	1
CO4	3	2	1	1	1
CO5	3	1	1	1	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

LABORATORY: SEM - I

COURSE INFORMATION SHEET

Lab Course: CELL & MOLECULAR BIOLOGY LAB

Course code: BI104
Course title: Cell & Molecular Biology Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:

This course enables the students:

1.	To recapitulate the previous knowledge of cell biology and biochemistry in order to design experiments to analyze some of the established facts about cell biology and biochemistry. To use the techniques, skills, and modern tools necessary for detection of the presence of biomolecules and their estimation collection and analysis of data, and interpretation of results.
2.	To provide quantitative analysis of the macromolecules in the given sample and analyze the results.
3.	To provide students with a deep insight of the various biochemical reactions and cellular processes through quantitative and qualitative analysis of the samples provided.
4.	To inculcate in our students a concrete knowledge of reactions involved in the biological processes and to understand the rationale behind them. Identify, formulate, and solve problems arising due to the inefficient functioning of the systems in life sciences.
5.	Independently execute a laboratory experiment using the standard methods and techniques in molecular biology, with the appropriate analysis and interpretation of results obtained.

Course Outcomes:

At the end of the course, a student should be able:

CO1	To apply knowledge of cell biology and biochemistry in various cellular functions, inculcate a knowledge of various issues related to life processes and the application of research involved in functioning of the different cell organelles and accessories.
CO2	To design and analyze the experiments related with the different molecules involved in cell biology and use of the various techniques in molecular cell biology to study the kinetics and rationale behind each phenomenon.

CO3	To identify, formulate, and solve problems arising due to the inefficient functioning of the various life processes and anatomical aspects of plants and animals.
CO4	o use the techniques, skills, and modern tools necessary for imbalances in various life processes, design a research project, collect and analyze data, and interpret results

SYLLABUS

List of Cytology Experiments

Laboratory Basics - Lab safety, Concept of Aseptic conditions, Preparation of Buffers, Media. Staining technique and working of Compound microscopes.

1. Preparation of slides of mitosis from onion root tip cells.
2. Study of different types of cells in the human blood smear.
3. Identification of Barr bodies in the human cheek cells.
4. To measure the length and breadth of the given cell sample by using a micrometer.
5. To identify the number of cells, present in the given 1 ml sample with the help of a haemocytometer.

List of Molecular Biology Experiments

6. Qualitative Test for Carbohydrates and Amino Acids. Carbohydrate estimation by Anthrone.
7. Protein Estimation by Bradford Method and Lowry Method.
8. Isolation of DNA and RNA. Spectrophotometric estimation of DNA and RNA.
9. Separation of DNA by agarose gel electrophoresis.
10. PCR Amplification, Agarose gel electrophoresis and elution of DNA bands from gel and Estimation of DNA.
11. Electrophoresis of RNA on denaturing gels.
12. Protein precipitation and purification by SDS PAGE.

Books recommended:

1. **Gerczei Fernandez, Timea / Pattison, Scott:** Biochemistry laboratory manual for undergraduates: An inquiry-based approach, SCIENDO, Open Access PDF ISBN 978-3-11-041133-1
2. **Arun Rastogi**: Laboratory Manual in Biochemistry, Anmol Publisher (2011) ISBN 10: 8126144998

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	2	1
CO2	3	2	2	2	1
CO3	3	1	2	2	1
CO4	2	3	3	3	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3
CO3	CD1, CD2, CD3
CO4	CD1, CD2, CD3

COURSE INFORMATION SHEET

Lab Course: Biocomputing with Python, PERL & MySQL

Course code: BI105
Course title: Biocomputing with Python, PERL & MySQL
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students to:

1.	Learn the Basic programming concepts & importance of Linux systems.
2.	Learn and write scientific programmes related to biological data in Python and Perl
3.	Extend comprehensive knowledge of MySQL Databases and its administration.
4.	Create a Database in MySQL and fetch Data using Python and Perl
5.	Grasp the database and programming challenges related to Bioinformatics.

Course Outcomes:

At the end of the course, a student should be able to:

CO1	Write Python and Perl Scripts for the problems related to biological data.
CO2	Analyze and discuss the available databases related to Bioinformatics.
CO3	Collect the proficient knowledge about the database cross-linking and integrated information retrieval system.
CO4	Effectively utilize the developed skills of Python, Perl and MySQL for advanced research in the area of Bioinformatics.
CO5	Develop the key programming skills in Python and Perl and take the challenges of Bioinformatics fundamental problems.

SYLLABUS

List of Exercises and objectives

1. Working with Linux - Architecture, file structure, root, Basics commands, tools and file operations and permission. SCP and SSH. Nano editor.
2. Data handling and presentation with Python and Perl - variables and data types, conditional statements, loops, functions, references, files and libraries & modules.
3. Implementation of regular expression in Biological Data.
4. MySQL - Data types, Tables and Queries, Primary and foreign Key, filtering and sorting, Grouping, Joins, SET operator, Constraints and Indexes, views, functions, Operation - Insert, update, delete. MySQL administrations and control.

Books recommended:

Textbook

- Bioinformatics: a practical guide to the analysis of genes and proteins, Baxevanis A., Ouellette F.B.F., John Wiley and Sons, New York.
- Introduction to Bioinformatics, Arthur Lesk, Oxford University Press ((Indian Edition).
- Downey A.,How to think like a computer scientist: Learning with Python.
- Python for Beginners: Learn Python Programming (Python 3) by Jason Cannon, 2018, O'Reilly
- Learning Perl, 6th Edition by Randal L. Schwartz, brian d foy, Tom Phoenix
- Learning MySQL by Saied M.M. Tahaghoghi, Hugh E. Williams, O'Reilly Media, Inc.

Reference Book

- Bioinformatics: Sequence and Genome Analysis, David W Mount, Cold Spring Harbor Laboratory Press, New York.
- Fundamental Concepts of Bioinformatics, Dan E Krane, Michael L Raymer, Benjamin-Cummings Pub Co (ISBN 0805346333)
- JoseJeeva, Taming Python by Programming, Khanna Publishing House. 2. Jose J. Introduction to Computing and Problem Solving with Python, (ISBN: 978-93- 82609-810).

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through Topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

	PO1	PO2	PO3	PO4	PO5
CO1	3	2	1	1	1
CO2	3	3	1	1	1
CO3	2	3	2	1	1
CO4	3	2	1	1	1
CO5	3	1	1	1	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: DATA STRUCTURES AND ALGORITHMS LAB

Course code: CA406
Course title: Data Structures and Algorithms Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology

Course Objectives
This course enables the students:

1.	To assess how the choice of data structures and algorithm design methods impact the performance of programs.
2.	To choose the appropriate data structure and algorithm design method for a specified application.
3.	To solve problems using data structures such as linear lists, stacks, queues, hash tables, binary trees, heaps, binary search trees, and graphs and writing programs for these solutions.
4.	Analyze and compare the different algorithms

Course Outcomes
After the completion of this course, students will be able to:

CO1	Choose an appropriate data structure given a computational problem
CO2	Design and analyze the time and space efficiency of various data structures
CO3	Analyze run-time execution of previous learned sorting methods, including selection, merge sort, heap sort and quicksort.
CO4	Have practical knowledge on the applications of data structures
CO5	Justify the choice of data structure for a given problem

SYLLABUS

1. Program to Find the Number of Elements in an Array
2. Develop and implement a menu driven program in C for the following Array operations
    a. Creating Array of N Integer elements.
    b. Display of Array elements with suitable headings.
    c. Inserting an element (ELEM) at a given valid position (POS).
    d. Deleting an element at a given valid position (POS).
    e. Exit
3. Programs for Stack, Queues and Circular Queues using Arrays
4. Program to convert an Infix Expression into Postfix and Postfix Evaluation
5. Program to implement stack using arrays and linked list, multiple stack in a single array.
6. Program to convert infix notation to postfix notation using stacks
7. Program to implement a queue using arrays and pointers. Program to reverse elements in a queue and to implement a circular queue using arrays.
8. Program to create add remove & display element from single and double linked list. Program to count number of nodes in linear linked list, to add remove & display element from circular linked list and program to concatenate two linear linked lists.
9. Programs to implement stack & queues using linked representation.
10. Program to accept a singly linked list of integers & sort the list in ascending order. Program to reverse linked list. Program to represent polynomials using linked lists. Program to add two polynomials using a linked list.
11. Program for the creation of binary tree, provide insertion & deletion in c code.
12. Program for pre-order, post-order & in-order traversals of a binary tree using non recursive.
13. Program to count no, of leaves of binary tree. The implementation of B-tree (insertion & deletion). The implementation of multi-way tree in C. The implementation of AVL tree.
14. Program to implement bubble sort program using arrays,merge sort using arrays, selection sort program using arrays, insertion sort program using arrays, topological sort using arrays, heap sort using arrays.
15. Program to implement heap sort using pointers, bubble sort program using pointers , linear search using pointers, binary search using pointers, linear search using arrays, binary search using arrays

Textbook

1. Baluja G S, “Data Structure through C”, Ganpat Rai Publication, New Delhi, 2015.
2. Pai G A V, “Data Structures and Algorithms: Concepts, Techniques and Applications”, 2nd Edn, Tata McGraw-Hill, 2008.
3. Horowitz E., Sahni S., Susan A., “Fundamentals of Data Structures in C”, 2nd Edition, University Press, 2010.

Reference books:

1. Tremblay J. P., Sorenson P. G, “An Introduction to Data Structures with Applications”, 2nd Edn, McGraw-Hill, Inc. New York, NY, USA.
2. Lipschutz Seymour, “Data Structures”, 6th Edn, 9th Reprint 2008, Tata McGraw-Hill.
3. Drozdek Adam, “Data Structures and Algorithms in C++”, Thomson Learning, New Delhi – 2007.

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil

POs met through Gaps in the Syllabus: Nil

Topics beyond syllabus/Advanced topics/Design: Nil

POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO /PO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	3	2	1
CO3	3	2	2	3	1
CO4	3	3	2	1	3
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

PROGRAMME ELECTIVES – I

Program Electives - I with Labs:

1. Molecular Biology & rDNA Technology (BT415)
    - Genomics & rDNA Technology Lab (BT420)
2. Applied Microbiology (BT403)
    - Microbiology LAB (BT406)
3. Object Oriented Programming using JAVA (CA409)
    - Object Oriented Programming using JAVA Lab (CA410)
4. Internet and Web Technology (IT303)
    - Internet and Web Technology Lab (IT340)

COURSE INFORMATION SHEET

Course: MOLECULAR BIOLOGY & rDNA TECHNOLOGY

Course code: BT415
Course title: Molecular Biology & rDNA Technology
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:

This course enables the students to:

1.	Introduce knowledge on basic concepts of molecular biology techniques
2.	Exemplify different types of polymerase chain reactions and their applications
3.	Implement, organize and design different vectors for gene cloning and expression
4.	Generating contextual and conditional knowledge of gene function for various applications

Course Outcomes

After the completion of this course, students will be able to:

CO1	Apply the principles of molecular biology techniques
CO2	Analyze the experimental data to select a suitable PCR for a particular application
CO3	Evaluate selectivity and specificity of vectors for cloning genes and their expressions
CO4	Examine gene function, gene modulation and their effects on improvement of crops and animals.

SYLLABUS

Module I: Genetic Organization: Central dogma of molecular biology, structure of DNA, DNA replication, DNA damage and repair, repetitive DNA, kinetics of DNA renaturation. Discovery and salient features of genetic code, organellar genetic code. RNA synthesis, RNA processing and RNA editing, Protein synthesis and Posttranslational modifications of proteins, collinearity of genes and protein. (8L)

Module II: Gene Regulation: Difference in genetic organization of prokaryote and eukaryote, lac operon, regulation of bacteriophage λ life cycle, nucleic acid binding motifs in regulatory proteins, Small Double stranded RNAs and RNA interference, Epigenetics. (8L)

Module III: Methods in Genetic Engineering: Polymerase Chain Reaction: Thermostable DNA Polymerases, PCR technique and its variants, Quantitative Real-Time PCR, Site directed mutagenesis, Restriction and modifying enzymes. (8L)

Module IV: Creation of Recombinant Molecules and Libraries: Characteristics of plasmid and other cloning vectors, artificial chromosomes, prokaryotic and eukaryotic expression vectors, Recombinant Protein purification by IMAC method. Genomic, cDNA, EST and Large insert genomic libraries, Strategies and approaches to genome sequencing, Overview of Enzymatic DNA sequencing, NGS, Assembly and annotation of DNA sequences. (8L)

Module V: Applications of Recombinant DNA Technology: Transgenic plants and animals, DNA vaccine, Gene therapy, PCR based diagnosis, Golden rice, Terminator technology, Safety guidelines of recombinant DNA research. (8L)

Books recommended:

1. Old and Primrose- Gene Manipulation, Wiley, 2002

Reference Books:

2. Alberts et al, Molecular Biology of the Cell, W. W. Norton & Company
3. Watson, Recombinant DNA., Scientific American Books
4. Lodish et al, Molecular Cell Biology., Freeman and Co., 2013

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD2, CD3
CO2	CD1, CD2, CD3,CD4
CO3	CD1, CD2, CD3,CD4, CD6
CO4	CD1, CD3,CD6

COURSE INFORMATION SHEET

Lab Course: GENOMICS & rDNA TECHNOLOGY LAB

Course code: BT420
Course title: Genomics & rDNA Technology Lab
Pre- requisite(s):
Co- requisite(s): None
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students to:

1.	Introduce knowledge on basic concepts of molecular biology techniques
2.	Exemplify different types of polymerase chain reactions and their applications
3.	Implement, organize and design different vectors for gene cloning and expression
4.	Generating contextual and conditional knowledge of gene function for various applications

Course Outcomes

After the completion of this course, students will be able to:

CO1	Apply the principles of molecular biology techniques
CO2	Analyze the experimental data to select a suitable PCR for a particular application
CO3	Evaluate selectivity and specificity of vectors for cloning genes and their expressions
CO4	Examine gene function, gene modulation and their effects on improvement of crops and animals.

SYLLABUS

List of Experiments

1. Isolation and purification of DNA.
2. Isolation and purification of RNA.
3. Isolation and purification of plasmid DNA.
4. Spectrophotometric estimation of DNA and RNA.
5. Separation of DNA by agarose gel electrophoresis.
6. Electrophoresis of RNA on denaturing gels.
7. PCR Amplification, Agarose gel electrophoresis and elution of DNA bands from gel.
8. T/A cloning of eluted DNA in plasmids.
9. Bacterial transformation and selection of transformants.
10. Validation of transformants using PCR technique.

Books recommended:

Textbook

1. Old and Primrose- Gene Manipulation, Oxford; Seventh edition (2006) 2. Alberts et al, Molecular Biology of the Cell, Garland Science; 5 edition (2008)

Reference Book

1. Watson, Recombinant DNA. W. H. Freeman; Second Edition edition (1992) 2. Lodish et al, Molecular Cell Biology. W. H. Freeman; 6th edition (2007)

Course Evaluation:

Lab (Quiz and End semester) examinations.

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD2, CD3
CO2	CD1, CD2, CD3,CD4
CO3	CD1, CD2, CD3,CD4, CD6
CO4	CD1, CD3,CD6

COURSE INFORMATION SHEET

Course: APPLIED MICROBIOLOGY

Course code: BT403
Course title: Applied Microbiology
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology

Course Objectives:
This course enables the students to:

1.	Establish an understanding of the basic techniques (concept of aseptic work, cultivation and identification) in microbiology
2.	Describe different aspects of microbial nutrition and growth
3.	Describe microbial interactions and their significance in environment
4.	Describe microbial interactions and their significance in agriculture, food and pharmaceuticals
5.	Describe nonspecific body defenses and the immune responses and apply this understanding to the infectious disease process as well as the prevention and control of infectious diseases
6.	Develop and execute oral and writing skills necessary for effective communication of the course, the ability to think critically regarding a topic and the delivery of scientific principles to both scientists and non-scientists community

Course Outcomes:
At the end of the course, a student should be able to:

CO1	Identify microbiological techniques, the defining characteristics of the major groups of microorganisms and apply to study microbial phylogeny
CO2	Classify the nutritional types of microorganisms and measure microbial growth
CO3	Evaluate how microorganisms interact with the environment in beneficial or detrimental ways
CO4	Assess impact of plant- microbe interaction on agriculture in both beneficial and detrimental ways. Identify industrially important microbes
CO5	Determine ways in which microorganisms play an integral role in disease, and the microbial and immunological methodologies are used in disease treatment and prevention
CO6	Apply the scientific method by stating a question; researching the topic; determining appropriate tests; performing tests; collecting, analyzing, and presenting data and effective communicate with both specialist and non-specialist audiences/community

SYLLABUS

Module I:
Techniques in Microbiology & Microbial Diversity: Microscopy, Staining in Microbiology, sterilization, Pure culture Methods, Culture Media and its types, Micrometry, Air Sampling, Waste water analysis, Measurement of Microbial Growth, Types of microorganisms, Methods of identification of microorganisms. (8L)

Module II:
Microbial Nutrition and Growth: Nutritional and Growth Factors requirement of microorganisms, Nutritional Types of Microorganisms, Uptake of Nutrition, Microbial Growth, Influence of Environmental Factors of Growth, Batch Culture, Continuous Culture, Synchronous Growth, Fed-batch Culture. Control of microbial growth by physical and chemical agents. (8L)

Module III:
Environmental Microbiology: Distribution of Microbes in Air and water, Allergic disorders by air microflora, air sampling, Water treatment, Bacteriological analysis of water, Bioleaching, Bioremediation. (8L)

Module IV:
Agricultural Microbiology and Industrial Microbiology: Plant-microbes interactions, Microbial Biodeterioration of agricultural products, control of microbes and safe storage of agricultural products, Biofertilizers, industrially important microorganisms, secondary metabolites from microorganisms, Microbiology of foods, Single cell Protein. (8L)

Module V:
Medical Microbiology: Diseases caused bacteria, virus, fungi, and protozoans; Fungal diseases, Host parasite interaction-recognition and entry process of different pathogens in plants and animals, Toxins produced, Vaccines, Antimicrobial agents, Antibiotics and disinfectants, National Immunization Programme.(8L)

Books recommended:

Textbooks:

1. Willey, Sherwood, Woolverton, Prescott/Harley/Klein's Microbiology, 7th Ed., TMH, 2007
2. Tortora, Microbiology: an Introduction, 12th Ed., Pearson, 2016
3. Frazier and Westhoff, Food Microbiology, 4th Ed., TMH, 1995

Reference books:

1. Pelczar, Chan and Krieg, Microbiology, 5th Ed., McGraw Hill, 1985 2. Stanier, General Microbiology, 1st Ed., MacMillan, 1958

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	1	3	3	1
CO2	1	2	3	3	1
CO3	2	3	3	2	2
CO4	2	3	3	2	2
CO5	2	3	3	2	2
CO6	3	3	3	3	3

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3 and CD6
CO2	CD1, CD2, CD3 and CD6
CO3	CD1, CD2, CD4, and CD6
CO4	CD1, CD2,CD4, CD5 and CD6
CO5	CD1, CD2, CD4, and CD6
CO6	CD1, CD2, CD3, CD4, CD5 and CD6

COURSE INFORMATION SHEET

Lab Course: MICROBIOLOGY LAB

Course code: BT406
Course title: Microbiology Lab
Pre- requisite(s):
Co- requisite(s): BT403
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology

Course Objectives:
This course enables the students to:

1.	To establish an understanding of the basic techniques (concept of aseptic work, cultivation and identification) in microbiology
2.	To describe different aspects of microbial nutrition and growth
3.	To describe microbial interactions and their significance in environment
4.	To describe microbial interactions and their significance in agriculture, food and pharmaceuticals
5.	To develop and execute oral and writing skills necessary for effective communication of the course, the ability to think critically regarding a topic and the delivery of scientific principles to both scientists and non-scientists community

Course Outcomes:
At the end of the course, a student should be able to:

CO1	Identify microbiological techniques, the defining characteristics of the major groups of microorganisms and apply to study microbial phylogeny
CO2	Classify the methods to measure microbial growth
CO3	Evaluate how microorganisms interact with the environment in beneficial or detrimental ways
CO4	Identify industrially important microbes
CO5	Apply the scientific method by stating a question; researching the topic; determining appropriate tests; performing tests; collecting, analyzing, and presenting data and effective communicate with both specialist and non-specialist audiences/community

SYLLABUS

List of Experiments

1. Cleanliness, media preparation, culturing methods, dilution techniques, and isolation of pure cultures by different techniques
2. Staining techniques in microbiology
3. Biochemical tests for identification of unknown microorganisms.
4. Evaluation of disinfectants and antiseptics, evaluation of sterilization methods.
5. Bacterial growth curve.
6. Standard qualitative analysis of water.
7. Micrometry
8. Antibiotic sensitivity test; Isolation of antibiotic resistant bacteria from waste / sewage water.

Book Recommended:

1. James G. Cappuccino and Natalie Sherman: Microbiology: A Laboratory Manual, 7th Edition, Dorling Kindersley (India) Pvt. Ltd., 2005

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	2	1	3	1
CO2	3	2	1	3	1
CO3	3	2	2	3	2
CO4	3	2	2	3	2
CO5	3	3	3	3	3

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD3 and CD6
CO2	CD1, CD3 and CD6
CO3	CD1, CD2, CD3, CD4, CD5 and CD6
CO4	CD1, CD2, CD3, CD4, CD5 and CD6
CO5	CD1, CD2, CD3, CD4 and CD6

COURSE INFORMATION SHEET

Course: OBJECT ORIENTED DESIGN USING JAVA

Course code: CA409
Course title: Object Oriented Design Using Java
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L:3 T:0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	The course shall allow students to understand the basic tenets of OOP.
2.	The course will exemplify the basic syntax and constructs of JAVA
3.	The course will help students understand the application OOP principles and Improve their programming skills in core Java
4.	The course will explain basic JAVA characteristics and their working.
5.	The course aims to expose students to Use the Java packages, applets for software development

Course Outcomes
After the completion of this course, students will be:

CO1	Identify the difference between procedural and OO programming.
CO2	Construct programs using various OOP principles.
CO3	Apply the knowledge gained for their project work as well as to develop some GUI applications using JAVA
CO4	Operate on files and strings in real life scenarios.
CO5	Analyze thread performance and inter thread communication issues

SYLLABUS

Module I:
Procedure-Oriented Programming, Object-Oriented programming, Benefits of OOP, Applications of OOP, Basics, Evolution of Java, Structure of JAVA Program, Simple Java Program, Tokens, Comments, Identifiers, Operators, Literals, Control Structures. Java Environment Setup, Compiling a Java Program, Java Virtual Machine, Philosophy of Java and Benefits**.** (8L)

Module II:
Data types and program statements: Primitive and reference data types, variables and constants, enumerated constants, labelled statement, expression and null statements, compound statement, control statement – decision and loops, jump statement, declaration statement, try-throw-catch-finally statement, declaring and creating arrays, accessing array elements, assigning values to array elements, multidimensional arrays. (8L)

Module III:
Functions, Data Abstraction and classes: Declaration, definition and call, main method arguments, reference variables, method overloading, parameter passing by value for primitive types, object references and arrays, scope of variables, return from methods. Class and object, class members and initialization, access rights of members – public, private and protected access modifiers, constructor and copy constructor, mutability, finalization, dynamic memory management, garbage collection, this keyword, static members, scope of variables, interface – declaration, implementation and extending, package and package visibility. (8L)

Module IV:
Inheritance and Collection classes: multi-level and single inheritance, multiple inheritance of interfaces, Object class, access rights in subclasses and packages, constructor calling sequence, super keyword, dynamic binding of methods, abstract class, overriding, shadowing and hiding, finalize, association, aggregation and composition. String, StringBuffer, Date, Calendar, Math, Object, Class, Exception class. (8L)

Module V:
Input/Output and JAVA Applets: Stream classes – InputStream, OutputStream, Buffered Stream, file classes and handling, pushback streams, reader and writer classes, file reader and writer, serialization. Applet code example, HTML tags for applet, applet life cycle, color, font and basic GUI handling, basic graphics, animation. (8L)

Textbooks:

1. E. Balagurusamy - Programming in Java, 2nd Edition; Tata McGraw Hill Publication; New Delhi.

Reference books:

1. Patrick Naghton & H. Schildt – The Complete Reference Java 2, Tata McGraw Hill Publication, New Delhi.
2. Dietel, Dietel - Java How to program , 7th edition; Pearson Education , New Delhi.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	2	1	3	1
CO2	3	2	1	3	1
CO3	3	2	2	3	2
CO4	3	2	2	3	2
CO5	3	3	3	3	3

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD3 and CD6
CO2	CD1, CD3 and CD6
CO3	CD1, CD2, CD3, CD4, CD5 and CD6
CO4	CD1, CD2, CD3, CD4, CD5 and CD6
CO5	CD1, CD2, CD3, CD4 and CD6

COURSE INFORMATION SHEET

Lab Course: OBJECT ORIENTED DESIGN USING JAVA LAB

Course code: CA410
Course title: Object Oriented Design Using Java Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students to:

1.	Introduce the concepts of object-oriented programming and features of object-oriented programming languages.
2.	To learn advanced features of the JAVA programming language as a continuation of the previous course.
3.	To learn the characteristics of an object-oriented programming language: data abstraction and information hiding, inheritance, and dynamic binding of the messages to the methods
4.	To learn the basic principles of object-oriented design and software engineering in terms of software reuse and managing complexity.
5.	To enhance problem solving and programming skills in JAVA with extensive programming projects

Course Outcomes
After the completion of this course, students will be able to:

CO1	Explain basic concepts of object-oriented programming.
CO2	Use the characteristics of an object-oriented programming language in a program.
CO3	Use the basic object-oriented design principles in computer problem solving
CO4	Develop their own Applications /Projects using JAVA
CO5	Simulate the problem in subjects like Operating systems, Computer networks and real world problems.

SYLLABUS

List of Programs as Assignments:

Objective: To Understand and Implement basic OOP features

1. Write a Program to design a class having a static member function named ShowCount() which has the property of displaying the number of objects created of the class.
2. Write a Program which creates & uses array of object of a class. (For e.g. implementing the list of Managers of a Company having details such as Name, Age, etc..).

Objective: To Understand and Implement special types of functions like friend function

3. Write a Program to swap private data members of classes named as class_1, class_2 using friend function.
4. Write an inline function to find largest of three number

Objective: To Understand and Implement the concept of constructors

5. Write a Program using a copy constructor to copy data of an object to another object.
6. Write a program to perform addition of two complex numbers using constructor overloading. The first constructor which takes no argument is used to create objects which are not initialized, second which takes one argument is used to initialize real and imaginary parts to equal values and third which takes two arguments is used to initialize real and imaginary to two different values.

Objective: To Understand and Implement the concept of Polymorphism

7. Write a program for overloading operator++ and operator—using friend functions
8. Write a program for developing a matrix class which can handle integer matrices of different dimensions. Also overload the operator for addition, multiplication & comparison of matrices.
9. Write a program to compute the area of right angle triangle, equilateral triangle, isosceles triangle using function overloading concept.

Objective: To Understand and Implement the concept of Inheritance

10. Write a Program to design a student class representing student roll no. and a test class (derived class of student) representing the scores of the student in various subjects and sports class representing the score in sports. The sports and test class should be inherited by a result class having the functionality to add the scores and display the final result for a student.
11. Write a Program illustrating how the constructors are implemented and the order in which they are called when the classes are inherited. Use three classes named alpha, beta, gamma such that alpha, beta are base class and gamma is derived class inheriting alpha & beta.

Objective: To Understand and Implement exception handling

12. Write a program to raise an exception if any attempt is made to refer to an element whose

index is beyond the array size.

Objective: To Understand and Implement File Operations

13. Write a program to read the class object of student info such as name, age ,sex ,height and weight from the keyboard and to store them on a specified file using read() and write() functions. Again, the same file is opened for reading and displaying the contents of the file on the screen.
14. Write a program to perform the deletion of white spaces such as horizontal tab, vertical tab, space ,linefeed ,new line and carriage return from a text file and store the contents of the file without the white spaces on another file.

Books recommended:

Textbooks:

1. E. Balagurusamy - Programming in Java, 2nd Edition; Tata McGraw Hill Publication; New Delhi.

Reference books:

2. Patrick Naghton & H. Schildt – The Complete Reference Java 2, Tata McGraw Hill Publication, New Delhi.
3. Dietel, Dietel - Java How to program, 7th edition; Pearson Education , New Delhi.

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	2	1	3	1
CO2	3	2	1	3	1
CO3	3	2	2	3	2
CO4	3	2	2	3	2
CO5	3	3	3	3	3

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD3 and CD6
CO2	CD1, CD3 and CD6
CO3	CD1, CD2, CD3, CD4, CD5 and CD6
CO4	CD1, CD2, CD3, CD4, CD5 and CD6
CO5	CD1, CD2, CD3, CD4 and CD6

COURSE INFORMATION SHEET

Course: INTERNET AND WEB TECHNOLOGY

Course code: IT303
Course title: Internet and web technology
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives

This course enables the students:

1	To provide students with a fundamental understanding as to how an XHTML-compliant web site is developed, implemented, and maintained. XHTML
2	To provide students with a fundamental understanding as to how an Cascading Style Sheets- is developed and implemented.
3	To provide basic understanding of java script to help in designing of web pages.
4	To understand the need of Dom model.
5	To provide the role of xml in web design

Course Outcomes

After the completion of this course, students will be able to do the following:

CO1	Describe the components of the Internet and Web technology
CO2	Analyze common Internet applications such as marketing, collaboration, electronic commerce, and document management
CO3	Explain the basics of Internet technology, such as http and the World Wide Web, HTML, and JavaScripts;
CO4	Create WWW pages to serve as front-end to client/server, Internet applications
CO5	Analyzing and designing Internet applications and testing and documenting the solutions developed.

SYLLABUS

Module I:
Web 2.0: search, content networks, user-generated content, blogging, social networking, social media, tagging, social bookmarking, rich Internet applications, web services, location-based services, Web 2.0 monetization and business models, future of the Web. (8L)

Module II:
Extensible Hypertext Markup Language (XHTML): XHTML syntax, headings, linking, images, special characters and horizontal rules, lists, tables, forms, internal linking, meta elements. (8L)

Module III:
Cascading Style Sheets (CSS): separation of content and presentation, inline styles, embedded style sheets, conflicting styles, linking external style sheets, positioning elements, backgrounds, element dimensions, box model and text flow, media types, building a CSS drop-down menu, user style sheets. (8L)

Module IV:
JavaScript: client-side scripting, control statements, functions, arrays, objects, events.
Document object model: objects and collections. (8L)

Module V:
Extensible Markup Language (XML) and RSS: Advantages and applications, structuring data, XML namespaces, Document Type Definitions (DTDs), XML vocabularies, RSS. (8L)

Books Recommended:

1. Deitel H.M. and P. J. Deitel, Internet & World Wide Web. How to Program, 5/e, Prentice Hall, ISBN 0131752421, 2013.

Reference books:

1. Internet and Web Technologies by Raj kamal, McGraw Hill Education (1 July 2017)

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO /PO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	3	2	1
CO3	3	2	2	3	1
CO4	3	3	2	1	3
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: INTERNET AND WEB TECHNOLOGY LAB

Course code: IT340
Course title: Internet and web technology Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1	To provide students with a fundamental understanding as to how an XHTML-compliant web site is developed, implemented, and maintained. XHTML
2	To provide students with a fundamental understanding as to how a Cascading Style Sheets- is developed and implemented.
3	To provide basic understanding of java script to help in designing of web pages.
4	To understand the need of Dom model.
5	To provide the role of xml in web design

Course Outcomes
After the completion of this course, students will be able to do the following:

CO1	Describe the components of the Internet and Web technology
CO2	Analyze common Internet applications such as marketing, collaboration, electronic commerce, and document management
CO3	Explain the basics of Internet technology, such as http and the World Wide Web, HTML, and JavaScripts;
CO4	Create WWW pages to serve as front-end to client/server, Internet applications
CO5	Analyzing and designing Internet applications and testing and documenting the solutions developed.

SYLLABUS

1. Write an HTML code to display your education details in a tabular format.
2. Write an HTML code to display your CV on a web page.
3. Write an HTML code to create a Home page having three links: About Us, OurServices and Contact Us. Create separate web pages for the three links.
4. Write an HTML code to create a login form. On submitting the form, the user should get navigated to a profile page.
5. Write an HTML code to create a Registration Form. On submitting the form, the user should be asked to login with these new credentials.
6. Write an HTML code to create your Institute website, Department Website and tutorial website for specific subjects.
7. Write an HTML code to illustrate the usage of the following:
   Ordered List , Unordered List , Definition List
8. Write an HTML code to create a frameset having header, navigation and content sections.
9. Write an HTML code to demonstrate the usage of inline CSS.
10. Write an HTML code to demonstrate the usage of internal CSS.
11. Write an HTML code to demonstrate the usage of external CSS.
12. Write a Java script to prompt for the user's name and display it on the screen.
13. Design HTML form for keeping student records and validate it using Java script.
14. Write an HTML program to design an entry form of student details and send it to store at database server like SQL, Oracle or MS Access.
15. Write programs using Java script for Web Page to display browsers information.
16. Create an applet which will have a line, an Oval & a Rectangle
17. Writing a program in XML and create a style sheet in CSS & display the document in internet explorer.
18. Write an XML program to display products
19. Write a program using PHP and HTML to create a form and display the details entered by the user

Textbooks:

1. Deitel H.M. and P. J. Deitel, Internet & World Wide Web. How to Program, 5/e, Prentice Hall, ISBN0131752421, 2013.

Reference books:

1. Internet and Web Technologies by Raj kamal, McGraw Hill Education (1 July 2017)

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO /PO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	3	2	1
CO3	3	2	2	3	1
CO4	3	3	2	1	3
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

Semester - II

Program Core-II:

1. Biological Sequence Analysis & Algorithms (BI201)
2. Computational Structural Biology (BI202)
3. Artificial Intelligence and Machine Learning (BI203)
4. Data Analytics using R (BI204)

Laboratories-II:

1. BioSequence & Structure Analysis Lab (BI205)
2. Data Science Lab (BI206)
3. Communication Skills -2 (MT133)
4. Community Engagement (NP202)

Program Electives-II with Labs:

1. Genomics (BT407)
    - LAB: Genomics Lab (BT408)
2. Database Design Concepts (CA407)
    - LAB: Database Design Concepts Lab (CA408)
3. Systems Biology & Biological Networks (BI207)
    - LAB: Systems Biology & Biological Networks Lab (BI208)

COURSE INFORMATION SHEET

Course: BIOLOGICAL SEQUENCE ANALYSIS & ALGORITHMS

Course code: BI201
Course title: Biological Sequence Analysis & Algorithms
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students to learn:

1.	Various Sequence Comparison and Alignment Methods
2.	Different algorithms used for Multiple Sequence Alignment and Hidden Markov Models used in Bioinformatics
3.	Various aspects of Computational Genomics and Prediction methods for Genes & other Regulatory Site given DNA sequence
4.	Different computational tools for Protein sequence analysis and prediction of different properties given protein sequence
5.	The molecular evolution and different Phylogenetics methods used for tree reconstruction

Course Outcomes
After the completion of this course, students will be able to:

CO1	understand and grasp the rationale behind the computational methods employed for various biological problems related to sequence.
CO2	undertake small research projects dealing with sequence data
CO3	Perform Phylogenetic analysis given DNA or Protein sequence.
CO4	This course may expose them to the latest and challenging computational methods/algorithms currently undertaken by researchers in the domain of sequence data analysis

SYLLABUS

Module I: Sequence Comparison and Alignment Methods – Sequence matching algorithms, Exact matching, Edit distances, Hamming Distances, Dot Matrix. **Pairwise Sequence Alignments** - Local and Global Alignment, Dynamic Programming using Needleman-Wunsch and Smith-waterman Algorithms, Substitution matrices, Construction of PAM and BLOSUM Matrices, Position Specific Scoring Matrices (PSSM). (8L)

Module II: Multiple Sequence Alignment and HMM - Scoring methods of MSA (Sum of Pairs, Entropy based), Dynamic Programming for MSA, Progressive Alignment Methods (ClustalW/X etc.), Genetic Algorithm methods, Iterative Methods and Consensus Methods (M-COFFEE, MergeAlign). MSA constructs (Profiles, PSSM, Patterns, Motifs, Blocks and Fingerprints) and their applications. Sequence Logos. MSA Formats and MSA Editing tool. **Markov & Hidden Markov Models (HMM)** - Introduction to Markov and Hidden Markov models, Viterbi Algorithm, Profile HMM, HMM for CpG Island. HMM Applications in Bioinformatics. HMMER tool. (8L)

Module III: Computational Genomics, Gene & Regulatory Site Prediction: Structure of Genes, Open Reading Frames (ORF), Codon Bias, Pattern Recognition. *Gene Prediction Methods:* Feature based, Homology based, Statistical and HMM based approaches. *Prediction of other Genomic Sites:* Protein Binding Sites, Splice-site, Promoter & Transcription factor bind site, tRNA site prediction. Analysis of Genomic Repeats and tRNA site prediction. Comparative analysis of genomic sequences (Vista). Open-Source packages - Unigene, Emboss, GrailEXP etc. (8L)

Module IV: Protein sequence analysis and prediction: Analysis & Prediction of Physico-chemical properties of proteins - Amino acid composition, Molecular Weight, Isoelectric point, Hydrophobicity & Hydrophilicity. Searching for Conserved Pattern, Block, Motif, Domain in Sequence. Construction of sequence profile, fingerprint, and family signature using MSA. Protein Identification Tools using patterns, profiles, and fingerprints. Protein Analysis Servers (ExPasy, Predict Protein, SAPs etc.). Analysis of Protein Spectra and Peptide Mass Fingerprint (PMF). (8L)

Module V: Phylogenetic Analysis: Phylogenetics basics and numerical taxonomy, Phenetics and Cladistics Approaches, Phenogram, Cladogram and Dendrogram, Tree of Life, Tree structure and topology, Ultrametric Tree, Rooted and Unrooted Tree, Molecular clock hypothesis, Models of DNA sequence evolution, Tree reconstruction methods:- Distance based (UPGMA,NJ), character based methods (Maximum Parsimony) and statistical method (ML), Bootstrapping, Tools of Phylogenetics - ClustalW/X, Mega5, Phylip package etc. (8L)

Recommended Books:

1. Bioinformatics: Sequence and Genome Analysis, David W Mount, Cold Spring Harbor Laboratory Press, New York.
2. Durbin et al (2003). Biological sequence analysis : probabilistic models of Proteins and Nucleic acids. Cambridge University Press (Indian Edition)
3. Handbook of Computational Molecular Biology Ed by Srinivas Aluru. (2005). Indian Edition Chapman & Hall/CRC

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	2	1
CO2	3	2	2	2	1
CO3	3	1	2	2	1
CO4	2	3	3	3	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3, CD4
CO3	CD1, CD2, CD3, CD4, CD7
CO4	CD1, CD2, CD3

COURSE INFORMATION SHEET

Course: COMPUTATIONAL STRUCTURAL BIOLOGY

Course code: BI202
Course title: Computational Structural Biology
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 3
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To cover the necessary introduction about the Computational Structural Biology
2.	To choose the appropriate method for a specified application for Protein Structure Prediction.
3.	To cover a few important Structural Biology algorithms commonly used in the field.
4.	To Analyze and compare different methods and tools that are being used in the field.

Course Outcomes
After the completion of this course, students will be able to:

CO1	understand and grasp the rationale behind the computational methods employed for various problems related to structure biology
CO2	undertake small research projects dealing with Protein structure data
CO3	Perform Molecular Docking and Simulation of a given Protein.
CO4	This course may expose them to the latest and challenging computational methods/algorithms currently undertaken by researchers in the field of Computational Structural Biology

SYLLABUS

Module I: Structure of Biomolecules: Structure of DNA and its different forms(A,B,Z), loops, turns and coils, Secondary Structure Elements (SSEs) and Super Secondary Structures, Motifs and Domains, structure of tRNA, Z-RNA, RNA hairpins and pseudoknots. ***Structure Determination:*** X- Ray Crystallography and NMR Spectroscopy. (8L)

Module II: Protein Structure Analysis, Comparison, and Classification: Protein structure hierarchy, Ramachandran Plot, Contact-Maps analysis, Protein Binding Pockets Prediction. Analysis of Protein Structure Surfaces, Structural Alignment, and Analysis, Protein Structure Folds, Fold libraries, Structural Classification of Protein. (8L)

Module III: Molecular Modeling and Structure Prediction: Protein Folding Problem, Representations of Molecular models, *Protein Secondary Structure Prediction*, *Protein Tertiary Structure Prediction* - Homology Modeling, Protein Threading or Fold recognition method, Ab-initio prediction methods etc. *RNA Structure Prediction methods* - Minimum Free Energy and Machine learning based. (8L)

Module IV: Molecular Docking: Theory of Docking (Sampling Methods, Scoring Functions), Docking methodologies. Application of molecular docking for drug discovery. (8L)

Module V: Molecular Dynamics Simulations
Introduction to Classical Dynamics and Molecular mechanics. Force-fields and Potential Energy Functions, Energy Minimization methods, Ensembles. Solvation, cutoffs, PBC. Results Interpretation and Analysis. (8L)

Textbooks

1. Bioinformatics: Sequence and Genome Analysis, David W. Mount, Cold Spring Harbor Laboratory Press, New York.
2. Guidebook on Molecular Modeling in Drug Design (Illustrated), J. G. Vinter, Mark Gardner (Editor), CRC Press.

Reference Books:

1. Introduction to Protein Structure, Branden & Tooze, Garland Publishing, Inc, New York Structural Bioinformatics, Phil Bourne
2. Molecular Modelling: Principles & Applications, Andrew R. Leach, Prentice Hall The art of Molecular Dynamics Simulations. Rapport, Cambridge University Press

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3,CD4
CO3	CD1, CD2, CD3,CD4, CD6
CO4	CD1, CD3,CD6

COURSE INFORMATION SHEET

Course: ARTIFICIAL INTELLIGENCE & MACHINE LEARNING

Course code: BI203
Course title: Artificial Intelligence & Machine Learning
Pre- requisite(s): BI102, BI103, BI105
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: **MSc**
Semester / Level: III / 5
Branch: **Bioengineering & Biotechnology**
Name of Teacher:

Course Objectives
This course enables the students:

1.	To understand the types and structures of artificial intelligent agents and characteristics of environments. To apply basic informed and uninformed search methods.
2.	To understand various supervised, semi-supervised and unsupervised machine learning algorithms. To formulate machine learning problems corresponding to different applications.
3.	To familiarize various machine learning software libraries and datasets publicly available.
4.	To develop machine learning based systems for various real-world problems.
5.	To assess how the choice of a machine-learning algorithm impacts the accuracy of a system.

Course Outcomes
After the completion of this course, students will be able to:

CO1	Prepare basic design of intelligent agents for a given problem and environment. Formulate machine learning problems corresponding to different applications: data, model selection, model complexity
CO2	To distinguish the given problem as being a case for search method or application of ML methods. Demonstrate understanding of a range of machine learning algorithms along with their strengths and weaknesses
CO3	Implement machine learning solutions to classification, regression, and clustering problems
CO4	Design and implement various machine learning algorithms in a range of real-world applications
CO5	Evaluate and analyze the performance of a machine-learning algorithm or a system based on a machine learning algorithm.

SYLLABUS

Module I: Introduction to Artificial Intelligence and Machine Learning
Basics of artificial intelligence – Agents & Environment, Nature of Environment, Structure of Agents and PEAS specification, Goal Based Agents, Utility Based Agents, Learning Agents, Defining the Problem as State Space Search, Informed and uninformed search methods - Breadth First Search, Depth First Search, Heuristics and A* Search.
Machine Learning – what and why? Basics of Linear Algebra and Statistics (matrices and vectors, Eigenvalue decomposition, principal component analysis), Overview of target function representations; Linear Regression. (8L)

Module II: Supervised Learning
Basics of Feature Selection and Evaluation, Decision Tree, Overfitting and Pruning, Linear Regression, Logistic regression, Support Vector Machine and Kernel; Noise, bias-variance trade-off, under-fitting and over-fitting concepts.(8L)

Module III: Neural Networks
Perceptrons: representational limitation and gradient descent training. Multilayer networks and backpropagation. Hidden layers and constructing intermediate, distributed representations. Overfitting, learning network structure, recurrent networks. (8L)

Module IV: Unsupervised and Semi Supervised Learning
Learning from unclassified data. Clustering. Hierarchical Agglomerative Clustering. K-means partitional clustering. Expectation maximization (EM) for soft clustering. Semi-supervised learning with EM using labeled and unlabeled data. (8L)

Module V: Ensemble
Committees of multiple hypotheses, bagging, boosting, active learning with ensembles. (8L)

Textbook

1. Tom Mitchell, “Machine Learning”, Latest Edition, Mc-Graw Hill.
2. Russel S. and Norvig P. “Artificial Intelligence a Modern Approach”, 3rd Edition, Pearson Education.

Reference Book

1. Shai Shalev-Shwartz, and Shai Ben-David, “Understanding Machine Learning”, Cambridge University Press, 2017.
2. Christopher Bishop, “Pattern Recognition and Machine Learning”, Springer, 2006.
3. Rich E. & Knight K. “Artificial Intelligence”, 2nd Edition, TMH, New Delhi.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations.

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	2	3	1
CO2	3	2	3	3	1
CO3	3	3	3	2	1
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6,CD7
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Course: DATA ANALYTICS USING R

Course code: BI204
Course title: Data Analytics using R
Pre- requisite(s): BI103
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 3
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	Understand the necessity of Data Analytics in Biology.
2.	To grasp methods and techniques used for statistical analysis using R language.
3.	To evaluate and analyze methods used for biological data interpretation and visualization.
4.	Solve biological problems related to Data Analytics using R language
5.	Learn the principles of existing R-tools for Bioinformatics like Bioconductor and be able to make new packages in R.

Course Outcomes
After the completion of this course, students will be able to:

CO1	Describe the fundamentals of data analytical systems using R language for biological data.
CO2	Understand the biological data interpretation and visualization in R.
CO3	Implement and solve statistical problems in R language
CO4	Design and evaluate data analytics models for research and Industrial applications.
CO5	Generate new packages in R language for Bioinformatics domain to solve real life problems, keeping in view social impacts of data analytics.

SYLLABUS

Module I: Basics Programming construct and Data Types: -
Data Types: Numeric, Integer, Complex, Logical, Character, **Vector**: Combining Vectors, Vector, List, Arithmetic, Vector Index, Numeric Index Vector, Logical Index Vector, Named Vector Members, Array Matrix, Data Frame, Factors, **Control Structures -** IF-Else, For loop, While loop, Repeat, Next, Break; Functions.(8L)

Module II: Analysis using Descriptive and Pictorial Statistics:
mean, median, mode, harmonic mean, geometric mean, variance and standard deviation, quantiles, skewness, moments, and kurtosis. Data Visualization: Summary table, Contingency table, Bar plot, Pie chart, Frequency distribution, Relative frequency distribution, Cumulative frequency distribution, Histogram, Frequency polygon, Cumulative frequency graphs, Box plot, Time series plot, Scatter diagram. (8L)

Module III: Data Relationships, Transformation, and Data Cleaning:
Relationships between different types of data: Relationship between two categorical data, Relationship between categorical and quantitative data, Relationship between two quantitative data Transformation: The logarithm transformation, Root and square root transformation Standardization (Z-transformation), Min-max normalization. Data cleaning: missing values, noisy data. (8L)

Module IV: Analysis using Inferential Statistics:
Sampling, Sampling Distribution, and Estimation of Parameters, Sampling distribution of: means, proportions, difference of means, difference of proportions. Hypothesis testing about: population mean, the difference between two means, about a population proportion, difference between two proportions. (8L)

Module V: Packages & Bioinformatics Applications:
Designing Packages, Popular Packages for Bioinformatics applications, Introduction to Bioconductor, R packages for Microarray/NGS Data analysis, Protein Structure visualization.(8L)

Textbooks:

1. Gupta and Gupta, “Business Statistics”, Sultan Chand and Sons, 2014.
2. Maheshwari Anil, “Data Analytics”, Mc Graw hill publication, 2017

Reference Books:

1. Bishnu and Bhattacherjee, Data Analysis: Using Statistics and Probability with R Language, PHI Learning, 2019.
2. Han J and Kamber M, “Data Mining: Concepts and techniques”, Morgan Kaufmann
3. TanPang-Ning, SteinbachMichael, and KumarVipin, “Introduction to Data Mining, Pearson Education”, New Delhi.Dunham
4. H.M. & Sridhar S., “Data Mining”, Pearson Education, New Delhi, 2006.
5. Norman Matloff, The Art of R Programming, A Tour of Statistical Software Design 1st Edition.
6. Hadley Wickham, Garrett Grolemund, R for Data Science: Import, Tidy, Transform, Visualize, and Model Data, O'reilly, 1st Edition.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	2	2	2	2	-
CO2	1	-	1	3	1
CO3	3	2	2	3	2
CO4	2	3	3	2	3

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3, CD6
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6, CD7

LABORATORY: SEM - II

COURSE INFORMATION SHEET

Lab Course: BIOSEQUENCE & STRUCTURE ANALYSIS LAB

Course code: BI205
Course title: Biosequence & Structure Analysis Lab
Pre- requisite(s):
Co- requisite(s): None
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To cover the necessary aspects of Biological Sequence Analysis and Computational Structural Biology
2.	To choose the appropriate method for Biological Sequence Analysis and Protein Structure Prediction.
3.	To cover a few important algorithms commonly used for genome analysis and protein structure prediction.
4.	To Analyze and compare different methods and tools that are being used in the Sequence Analysis, Structure Prediction and Simulation.

Course Outcomes
After the completion of this course, students will be able to:

CO1	understand and grasp the rationale behind the computational methods used for various problems related to structure biology and Sequence Analysis.
CO2	undertake small research projects dealing with Protein structure data and Biological Sequence of Protein or DNA.
CO3	Able to perform Molecular Docking and Simulation of a given Protein.
CO4	This course may expose them to the latest methods/algorithms currently undertaken by researchers in the domain of Structural Biology & Sequence Analysis.

SYLLABUS

Sequence Analysis Coding Exercises:

1. Dot Plot
2. Pairwise Alignment
3. ORF Identification
4. Protein Sequence Analysis
5. DNA Sequence Analysis
6. Phylogenetic Tree Construction

Biomolecular Structure Coding Exercises

7. PDB file parsing
8. Aromaticity, Hydrophobicity
9. Protein-ligand Interactions
10. SASA - Solvent accessible surface area calculations

Open-Source Packages

11. Open-source Packages for Sequence analysis
12. Open-source Packages for Modeling, Docking and Simulations

Textbook:

1. Bioinformatics: Sequence and Genome Analysis, David W Mount, Cold Spring Harbor Laboratory Press, New York.
2. Introduction to Bioinformatics, Arthur Lesk, Oxford University Press ((Indian Edition).
3. Durbin et al (2003). Biological sequence analysis: probabilistic models of Proteins and Nucleic acids. Cambridge University Press (Indian Edition)
4. Handbook of Computational Molecular Biology Ed by Srinivas Aluru. (2005). Indian Edition Chapman & Hall/CRC

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	2	2	2	2	-
CO2	1	-	1	3	1
CO3	3	2	2	3	2
CO4	2	3	3	2	3

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3, CD6
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6

COURSE INFORMATION SHEET

Lab Course: DATA SCIENCE LAB

Course code: BI206
Course title: Data Science Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives

This course enables the students

1.	To learn Various Packages for data processing, machine learning, data visualization and data analytics tools in python and R.
2.	To implement linear regression and compute relevant statistics.
3.	To learn basics of Clustering and classification using commonly used algorithms
4.	To evaluate and analyze methods used for biological data interpretation and visualization.
5.	Learn the principles of existing R-tools for Bioinformatics like Bioconductor and also be able to make new packages in R.

Course Outcomes

After the completion of this course, students will be able to:

CO1	The student should be able to manipulate large datasets and perform data preprocessing and Perform attribute reduction using PCA
CO2	Implement common techniques for performing Linear Regression and measure its performance. Able to cluster and classify data and measure performance.
CO3	Describe the fundamentals of data analytical systems for biological data and understand the biological data interpretation and visualization in R.
CO4	Implement and solve statistical problems in R language. Design and evaluate data analytics models for research and Industrial applications.
CO5	Generate new packages in R language for Bioinformatics domain to solve real life problems, keeping in view social impacts of data analytics.

SYLLABUS

A) Machine Learning Exercise using Python

1. Exercises to learn data types, operators, and mathematical functions of python.
2. Exercises to learn ndarray operations using numpy.
3. Explore a dataset using Pandas. Compute attribute statistics, correlation, covariance, and other inferential statistics.
4. Perform PCA on a dataset to reduce attributes. Compare performance with available PCA modules in python.
5. Perform Linear regression on a dataset and compute the relevant parameters. Compute the error in the interpolation. Compare your results with implementations in Standard modules.
6. Classify a dataset with binary class distribution using logistic regression. Compute the values for accuracy, precision and recall and present the confusion matrix. Perform all necessary data preprocessing of the attributes involved.
7. Use logistic regression to perform classification on a multi label dataset.
8. Classify a dataset using the K-NN algorithm. Perform a grid search to decide on the optimal value of K. Report the statistics of the results obtained.
9. Use the K-NN algorithm developed in Question 6 to perform K -fold cross validation. Compare your results with the basic implementation of the algorithm.
10. Perform binary K-Means on a dataset and compare its performance with the basic implementation of the K-Means.
11. Classify a dataset using the Naïve Bayes algorithm. Extend your algorithm to incorporate numerical attributes.
12. Cluster a dataset using the K-Means algorithm. Compute a suitable value of K using the grid search mechanism. Report the performance metrics of your algorithm e.g. homogeneity score, silhouette coefficient etc.
13. Write a program in python to cluster a dataset using the DBSCAN algorithm. The inputs to the algorithm would include epsilon and “p”.
14. Perform agglomerative clustering of a dataset in python. The number of clusters would be an input to the algorithm and your algorithm should provide options to choose the distance metrics e.g. distance between centers, distance between nearest neighbors, distance between farthest points etc.
15. Write a program to train a single hidden layer neural network to classify a binary dataset.
16. Write a program using Information Gain to decide the splitting attribute for a dataset and classify a dataset using a Decision tree.

B) Bioinformatics Problem solving using Machine Learning - any application such as Sequence Analysis and modeling, microarray data, medical imaging data etc.

C) List of Exercises for Data Analytics using R Language

1. Lab Assignment No: 1 Objective: To Understand and Implement Data Types;
Data Types - R Objects and Attributes, Vectors and Lists, Matrices, Factors, Data Frames, Named Attribute, Summary.
2. Lab Assignment No: 2 - Objective: To Understand and Implement Control Structures

If-else, For loops, While loops, Repeat, Next, Break,

3. Lab Assignment No: 3 Objective: To Understand and Implement Data Analysis
Reading Tabular Data, Reading Large Tables, Textual Data Formats, Subsetting - Basics, Lists, Matrices, Partial Matching, Removing Missing Values, Vectorized Operations, lapply, apply, split

4. Lab Assignment No: 4 Objective: To Understand and Implement Functions - Functions Symbol Binding, R Scoping Rules,

5. Lab Assignment No: 5 Objective: To Understand and Implement Descriptive Statistics and visualization using R

- Get the central tendency measures, range, and summary statistics of iris data.
- For iris data- Draw boxplot, scatterplot, barplot, piechart, histogram for suitable variables
- Write R script to determine skewness, kurtosis
- Create following table and use suitable functions and plots to describe statistical properties with different specifications given:

	rain	month
1	3	Jan
2	5	Feb
3	7	Mar
4	5	Apr
5	3	May
6	2	Jun
7	6	Jul
8	8	Aug
9	5	Sep
10	6	Oct
11	9	Nov
12	8	Dec

Textbooks for Machine Learning:

1. Geron A., "Hands on Machine Learning with Scikit Learn and Tensorflow", 2nd edition, O' Reilly Press, 2020
2. Muller A. C., Guido S., "Hands Machine Learning with Python", O'Reilly Press, 2016

Textbooks for Data Analytics using R language:

1. Lander: R for Everyone: Advanced Analytics and Graphics. Pearson Education India
2. Sandip Rakshit: R Programming for Beginners. McGraw Hill Education

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	2	3	3
CO3	3	3	3	3	3
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

PROGRAMME ELECTIVES – II

Program Electives - II with Labs:

1. Genomics (BT407)
    - Genomics LAB (BT408)
2. Database Design Concepts (CA407)
    - Database Design Concepts Lab (CA408)
3. Systems Biology & Biological Networks (BI207)
    - Systems Biology & Biological Networks Lab (BI208)

COURSE INFORMATION SHEET

Course: GENOMICS

Course code: BT407
Course title: Genomics
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:

This course enables the students to:

1.	To understand differences between prokaryotic and eukaryotic genomes as well as forward and reverse genetics.
2.	To learn about techniques used in genomics, genome sequencing, annotation, database development as well as their applications.
3.	To impart knowledge about the advances in structural and functional aspect of newly sequenced genome
4.	To understand the use of genomics in crop improvement, drug discovery, value added crops as well as development of recombinant protein.

Course Outcomes:

At the end of the course, a student should be able to:

CO1	Explain the detailed characteristics of prokaryotes and eukaryotes genome as well as application of forward and reverse genetics.
CO2	Get knowledge and design the experiments using various techniques of genome sequencing as well proper organization of generated biological data
CO3	Apply structural and functional genomics approaches on newly sequenced genomes for functional characterization of genes.
CO4	Develop capacity to pin point the strategies used for crop improvement and development of drug, recombinant proteins or value added crop.

SYLLABUS

Module I: Genomic Evolution & Organization: RNA world hypothesis, Genetics to Genomics, Forward and reverse genetics. Eukaryotic and prokaryotic genomes, Chromosome structure and function, Chromatin remodeling/organization, DNA as genetic material, Central dogma of molecular biology.(8L)

Module II: Genome Sequencing: Overview of conventional and new sequencing technologies, Strategies used in whole genome sequencing, NGS technologies, RNAseq, Genome annotation, Candidate gene discover and data mining, Transcription factor, Development of databases and their uses, Genome mapping by genetic and physical technique, Comparative genomics and SNP analysis.(8L)

Module III: Techniques for Genomics: Restriction and modifying enzymes, Various blotting techniques, PCR techniques, RT-PCR, qPCR, Digital PCR, Site directed mutagenesis, Genomic and cDNA libraries, Screening of libraries, DNA microarray, Antisense RNA, RNA interference, TALEN, CRISPR-Cas9. (8L)

Module IV: Genome Initiatives: Structural and functional genomics, Advances in human genome, Advances in buffalo genome, Advances in Arabidopsis genome, Advances in rice genome, Advances in wheat genome, Advances in tomato genome, Advances in sorghum genome, Advances in peanut genome etc. (8L)

Module V:
Application of Genomics: Genomics in gene function analysis, Genomics in plant and animal breeding and improvement, Genomics in drug discovery, Genomics in valued added crops, Genomics in recombinant protein etc.(8L)

Book Recommended:

Textbooks

1. Principles of Genome analysis and Genomics, 3rd Edition, By S. B. Primrose and R. L. Twyman, Blackwell publishing (2003), ISBN: 1405101202
2. Bioinformatics and Functional Genomics, 3rd Edition, By Jonathan Pevsner, Wiley Blackwell (2015), ISBN: 978-1-118-58178-0.

Reference Book

1. Principles and Practices of Plant Genomics (Volume 3), By Chittaranjan Kole and Albert G. Abbott. CRC Press (2017): ISBN 9781138116498
2. Genome Analysis: Current Procedures and Applications by Maria S. Poptsova. Caister Academic Press (2014) ISBN: 978-1-908230-29-4.

Course Evaluation:

Individual assignment, Presentations, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	2	2	2	2	-
CO2	1	-	1	3	1
CO3	3	2	2	3	2
CO4	2	3	3	2	3

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3, CD6
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6

COURSE INFORMATION SHEET

Lab Course: GENOMICS LAB

Course code: BT408
Course title: Genomics Lab
Pre- requisite(s): NIL
Co- requisite(s):BT 407
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students:

1.	To recapitulate the previous knowledge of Molecular Biology and biochemistry to design experiments.
2.	To use the techniques and skills necessary for estimation and quantification of DNA and their further analysis.
3.	To use the techniques and skills necessary for estimation and quantification of RNA and their further analysis.
4.	Use of modern tools for analysis of Nucleic acids and their further analysis.
5.	Independently execute a laboratory experiment using the standard methods and techniques in molecular biology, with the appropriate analysis and interpretation of results obtained.

Course Outcomes:
At the end of the course, a student should be able:

CO1	To handle DNA and its manipulation
CO2	To handle RNA and its manipulation
CO3	Hands on and gain expertise in handling routine laboratory equipment used in Genomics lab
CO4	To use modern tools for analysis of Nucleic acids and their further analysis. Independently execute a laboratory experiment using the standard methods and techniques in molecular biology, with the appropriate analysis and interpretation of results obtained.

SYLLABUS

List of Experiments

1. Isolation and purification of DNA.
2. Separation of DNA by agarose gel electrophoresis.
3. Isolation and purification of RNA.
4. Electrophoresis of RNA on denaturing gels.
5. Spectrophotometric estimation of DNA and RNA.
6. Preparation cDNA.
7. PCR amplification of genes of interest.
8. Real Time PCR/ PCR based comparative gene expression analysis of different tissue samples.
9. Visualization/analysis of data.

Textbooks

1. 3rd Edition, By S. B. Primrose and R. L. Twyman, Blackwell publishing (2003), ISBN: 1405101202
2. Bioinformatics and Functional Genomics, 3rd Edition, By Jonathan Pevsner, Wiley-Blackwell (2015), ISBN: 978-1-118-58178-0.

Reference book

1. Principles and Practices of Plant Genomics (Volume 3), By Chittaranjan Kole and Albert G. Abbott. CRC Press (2017): ISBN 9781138116498
2. Genome Analysis: Current Procedures and Applications by Maria S. Poptsova. Caister Academic Press (2014) ISBN: 978-1-908230-29-4.

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	2	1
CO2	3	2	2	2	1
CO3	3	1	2	2	1
CO4	2	3	3	3	1

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3
CO3	CD1, CD2, CD3
CO4	CD1, CD2, CD3

COURSE INFORMATION SHEET

Course: DATABASE DESIGN CONCEPTS

Course code: CA407
Course title: Database Design Concepts
Pre- requisite(s):
Co-requisite(s):
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students to:

1.	Observe that how the real world data is stored, retrieved, and communicate under the DBMS environment
2.	Design a logical model which has the unique relation between the Data.
3.	Apply the query for the modification of the system.
4.	Develop a conceptual design which allows us to avoid anomalies in superior's data.
5.	Discuss a system which allows to restrict the uncontrolled exaction and provide rigorous variation of the task.

Course Outcomes
After the completion of this course, students will be able to:

CO1	Describe various data models and schemas used in database management systems.
CO2	Explain the fundamental concepts, data definitions and query processing tasks in relational query languages.
CO3	Recognize database design theory and evaluate functional dependencies and normal forms in databases.
CO4	Formulate the operations of transaction and concurrent query processing tasks to obtain the correct results even under strict time constraints.
CO5	Interpret the foundational concepts of distributed databases. Illustrate several techniques related to transaction management and query processing in distributed database management systems.

SYLLABUS

Module I: Introduction and Conceptual Modelling: Purpose of Database Systems, Data Models, Schemas and Instances, Three-Schema Architecture and Data Independence, Database languages, Database Architecture, Classification of DBMS, relational database, Database users and Administrators, Advantages of DBMS. Entities and Entity Sets, Relationships and Relationship Sets, Keys, Mapping, Constraints, ER Diagram, Reducing ER Diagram to tables, Generalization and Specialization, Aggregation**.** (8L)

Module II: Relational Model: Concepts, Constraints, Languages, Design and Programming: Relational database Schemas, Relational Algebra, Relational Calculus (Tuple Relational calculus and Domain Relational calculus), Update operations, Transactions, Dealing with constraint violations. Binary Relational operation: JOIN and DIVISION, SQL, more complex SQL Queries, Security & Integrity violations, authorization and views, integrity constants, encryption, Statistical databases. (8L)

Module III: Database Design Theory and Methodology: Pitfalls in relational database design, Functional Dependencies, Decomposition Using Functional Dependencies. Normalization using functional Dependencies, General Definition of First, Second, Third and Fourth Normal Form. Boyce-Codd Normal Form (BCNF), Multivalued and join dependencies, DKNF**.** (8L)

Module IV: Transaction Processing Concepts and Concurrency Control Techniques: Transaction Processing, Desirable Properties of Transactions, Transaction State, Characterizing Schedules based on Recoverability and Serializability. Lock-Based Protocols, Timestamp-Based Protocols, Validation-Based Protocols, Multiple Granularity, Deadlock Handling, Recovery and Atomicity, Log-Based Recovery**.** (8L)

Module V: Distributed Databases and Client-Server Architectures: Concepts and Types of Distributed databases, data fragmentation, Replication and Allocation Techniques for Distributed Database Design, Query Processing in Distributed Databases, Overview of Concurrency Control and Recovery in Distributed Databases, An Overview of 3-Tier Client-Server Architecture. (8L)

Textbook:

1. Elmasri Ramez, & Navathe S.B., "Fundamentals of Database Systems", 5th Edition, Pearson Education, 2006.

Reference Book:

1. Silberschatz A., &Korth H., "Database Systems Concepts", 5th Edition, McGraw Hill Higher Education, 2005.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO /PO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	3	2	1
CO3	3	2	2	3	1
CO4	3	3	2	1	3
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6, CD7
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: DATABASE DESIGN CONCEPTS LAB

Course code: CA408
Course title: Database Design Concepts Lab
Pre- requisite(s):
Co-requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester/Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To observe that how the real world data is stored, retrieved, and communicate under the DBMS environment
2.	To design a logical model which has the unique relation between the Data.
3.	To apply the query for the modification of the system.
4.	To develop a conceptual design which allows us to avoid anomalies in superior's data.
5.	To discuss a system which allows to restrict the uncontrolled exaction and provide rigorous variation of the task.

Course Outcomes
After the completion of this course, students will be able to:

CO1	Describe various data models and schemas used in database management systems.
CO2	Explain the fundamental concepts, data definitions and query processing tasks in relational query languages.
CO3	Recognize database design theory, and evaluate functional dependencies and normal forms in databases.
CO4	Formulate the operations of transaction and concurrent query processing tasks to obtain the correct results even under strict time constraints.
CO5	Interpret the foundational concepts of distributed databases. Illustrate several techniques related to transaction management and query processing in distributed database management systems.

SYLLABUS

For the Tables given below: emp(empno,ename,job,mgr,hiredate,sal,comm,deptno,gr), dept(deptno,dname,loc)

Write the following queries:

1. List all information about all departments from the emp table.
2. List all employee names along with their salaries from the emp table.
3. List all department numbers, employee numbers and their managers numbers in descending order of deptno from emp table.
4. List department names and locations from the dept table.
5. List the employees belonging to the department 20.
6. List the name and salary of the employees whose salary is more than 1000.
7. List the names of the clerks working in department 20.
8. List the names of analysts and salesmen.
9. List the details of the employees who have joined before the end of September 81.
10. List the names of employees who are not managers.
11. List the names of employees whose employee numbers are 7369, 7521, 7839, 7934, 7788.
12. List the employee details not belonging to the department 10, 30, and 40.
13. List the employee name and salary, whose salary is between 1000 and 2000.
14. List the employee names, who are not eligible for commission.(salary having >15,000 eligible for commission)
15. List the employees who are eligible for commission.
16. List the details of employees, whose salary is greater than 2000 and commission is NULL.
17. List the employees whose names start with an “S” (not”s”).
18. List the name, salary and PF amount of all the employees(PF is calculated as 10% of salary).
19. List the empno, ename, sal in ascending order of salary.
20. List the employee name, salary, job and Department no descending order of Department No and salary.
21. List the employee details in ascending order of salary.
22. List the employee details in descending order of salary
23. Display name, and sal and commission of all employees whose monthly salary is greater than their commission.
24. Select SMITH HAS WORKED IN THE POSITION OF CLERK IN DEPT 20. Display result in this format.
25. Generate a statement which prompts the user at runtime. The intention is to display employees hired between 2 given dates.
26. Define a variable representing an expression used to calculate total annual remuneration. Use the variable in a statement which finds all employees who earn $30000 a year or more.
27. List all the employees' names and salaries increased by 15% and expressed as a whole number of dollars.
28. Produce the following

    EMPLOYEE AND JOB
    SMITH CLERK
    ALLEN SALESMAN

29. Produce the following output:

    SMITH (Clerk)
    ALLEN (Salesman)

30. Do a case sensitive search for a list of employees with a job that the user enters.
31. It has been discovered that the sales people in dept. 30 are not all male. Please produce the following output.

    ENAME DEPTNO JOB

ALLEN 30 Sales Person

32. Display each employees name and hire date of dept 20.
33. Display each employees name, hiredate and salary review date. Assume the salary review date is one year from hire date. Output should be in ascending review date.
34. Print list of employees displaying just salary, if more than 1500. If exactly 1500 display " On Target". If less than 1500 display " Below 1500".
35. Write a query which returns DAY of the week (i.e. MONDAY) for any date entered in the format DD/MM/YY.
36. Write a query to calculate the length of service of each employee.
37. Find the minimum salary of all employees.
38. Find the maximum, minimum, and average salaries of all employees.
39. List the maximum and minimum salary of each job type.
40. Find how many managers are in each dept.
41. Find the average salary and average total remuneration of each job type. Remember salesmen earn commission.
42. Find out the difference between highest and lowest salary.
43. Find all departments which have more than three employees.
44. Check whether all employee nos are unique. (No Duplicate)
45. List lowest paid employee working for each Manager. Exclude any groups where the minimum salary is less than 1000. Sort the output by salary.
46. Produce a list showing employees 'salary grade'.(> 10000 A, >10000 &<20000 B, >20000 C)
47. Show only employee on Grade C.
48. Show all employee in Dallas.
49. List the employees name, job, salary, grade and department for everyone in the company except clerks. Sort on salary, displaying the highest first.
50. List the following details of employees who earn $36000 a year or who are clerks.

Ename Job Annual Sal Dept no Dname Grade

51. Display all employees who earn less than their managers.
52. Display all employees by name and eno along with their managers name and number.
53. Modify above spoliation to display KING who has no MANAGER.
54. Find the job that was filed in the first half of 1983 and the name job that was filled in the same period in 1984.
55. Find all employees who have joined before their manager.

EMPLOYEE HIREDATE MANAGER HIREDATE

56. Find the employees who earn the highest salary in each job, type, sort in descending order of salary.
57. Find the employees who earn the minimum salary for their job, Display the result in descending order of salary
58. Find the most recently hired employees in the department. Order by hiredate.
59. Show the details of any employee who earns a salary greater than the average for their department. Sort in department number order.
60. List all departments where there are no employees.

Textbook:

1. SQL, PL/SQL the programming Language of Oracle, Ivan Bayross, 4th edition

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO /PO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	3	2	1
CO3	3	2	2	3	1
CO4	3	3	2	1	3
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6, CD7
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Course: SYSTEMS BIOLOGY & BIOLOGICAL NETWORKS

Course code: BI207
Course title: Systems Biology & Biological Networks
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L: 3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	use publicly available biological data to create a computer model;
2.	create a computer model of a biological system;
3.	apply computational systems biology methods to perform model analysis;
4.	derive hypotheses about the modeled biological system based on the analysis of the model

Course Outcomes
After the completion of this course, students will be able to:

CO1	understand *in-silico* model, basic techniques of modeling and analysis of biological systems
CO2	assess and discuss the advantages and disadvantages of methods from the field of computational systems biology
CO3	interpret the systems biology paradigm and defend thoughts and opinions
CO4	create and modify a qualitative model of a biological network.
CO5	analyze selected types of experimental data and apply software tools to selected data processing problems.

SYLLABUS

Module I: Systems Biology:

System-level-Understanding of Biological Systems, Introduction, Measurement Technologies and experimental methods, Comprehensive Measurements, Measurement for Systems Biology, Next-generation Experimental Systems. System structure identification, Bottom-up-approach, Top-down-approach. Application areas of Systems Biology. (8L)

Module II: Epigenetics:

Introduction to epigenetics, The biochemistry of DNA Methylation and the role of Transcription Factors. Basic concepts on identification of disease genes, role of bioinformatics, reference genome sequence, integrated genomic maps, gene expression profiling; identification of SNPs, SNP database (DbSNP). Role of SNP in Pharmacogenomics, SNP arrays. (8L)

Module III: Modeling Genetic Networks:

Why Modeling is necessary, What type of Modeling is appropriate, Modeling the activity of a single gene, Gene Regulatory Network (GRN) Understanding gene regulation, Understanding the Biology, Biochemical Processes; transcription, exons & introns, splicing, translation, post translational modification. Overview of Models; Boolean, Differential equation, stochastic Models, Kinetic Logic Model. (8L)

Module IV: Biological Network Reconstruction

Computational approaches for the reconstruction of gene regulatory networks with DNA pattern scanning (Information Theory, Position weight matrices), gene expression compendia (CLR and similar), and integration of ChIP-Seq data. (8L)

Module V: Metabolomics and Epigenomics:

Metabolomics Basics (Introduction; Metabolites; Fingerprinting and footprinting of metabolites; Profiling of metabolites; Targeted analysis of metabolites), The role of metabolomics in systems biology (Microbial metabolomics; Plant metabolomics; Human metabolomics), Data analysis. **Epigenomics:** Epigenomics using ChiP-Seq Method (Transcription Factors, histone modifications and chromatin states, DAP-Seq). Case studies examples (ChIP-Seq analysis with identification of transcription factor binding sites, CLR on a gene expression compendium of E. coli). (8L)

Books recommended:

1. Hiroaki Kitano: Foundations of Systems Biology, MIT Press
2. Bower & Bolouri: Computational Modeling of Genetic & Biochemical Networks, MIT Press
3. Alon: Introduction to Systems Biology of Biological Circuits, Chapman & Hall/CRC.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	2	2	2	2	-
CO2	1	-	1	3	1
CO3	3	2	2	3	2
CO4	2	3	3	2	3

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3, CD6
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6

COURSE INFORMATION SHEET

Lab Course: SYSTEMS BIOLOGY & BIOLOGICAL NETWORKS LAB

Course code: BI208
Course title: Systems Biology & Biological Networks Lab
Pre- requisite(s): NIL
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: II / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives

This course enables the students:

1.	use publicly available biological data to create a computer model;
2.	create a computer model of a biological system;
3.	apply computational systems biology methods to perform model analysis;
4.	derive hypotheses about the modeled biological system based on the analysis of the model

Course Outcomes
After the completion of this course, students will be able to:

CO1	understand *in-silico* model, basic techniques of modeling and analysis of biological systems
CO2	assess and discuss the advantages and disadvantages of methods from the field of computational systems biology
CO3	interpret the systems biology paradigm and defend thoughts and opinions
CO4	create and modify a qualitative model of a biological network.
CO5	analyze selected types of experimental data and apply software tools to selected data processing problems.

SYLLABUS

List of Exercises

1. Database Searching KEGG, PATHWAY, BRENDA, Gene Ontology etc.
2. Construction of Biological network in Cytoscape. online tools.
3. Analysis Gene-gene network in Cytoscape.
4. Designed multiple other models and computational techniques to analyze the experimental data.
5. Analyzing Epigenomics using ChiP-Seq Method (Transcription Factors, histone modifications and chromatin states, DAP-Seq).
6. ChIP-Seq analysis with identification of transcription factor binding sites, CLR on a gene expression compendium of E. coli).

Books recommended:

4. Hiroaki Kitano: Foundations of Systems Biology, MIT Press
5. Bower & Bolouri: Computational Modeling of Genetic & Biochemical Networks, MIT Press
6. Alon: Introduction to Systems Biology of Biological Circuits, Chapman & Hall/CRC.

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	2	2	2	2	-
CO2	1	-	1	3	1
CO3	3	2	2	3	2
CO4	2	3	3	2	3

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3
CO2	CD1, CD2, CD3, CD6
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6

Semester - III

Program Core-III:

1. Proteomics, Metabolomics and Biomarker Design (BI301)
2. Cheminformatics and Drug Design (BI302)
3. NGS Data Analysis (BI303)
4. Image Processing (CA439)

Laboratories-III:

1. Cheminformatics and Drug Design Lab (BI304)
2. NGS Data Analysis Lab (BI305)
3. Image Processing Lab (BI306)

Mini Project - Dissertation Part-1 (BI307)

Program Electives-III with Labs:

1. Medical Genomics (BI308)
    - LAB: Medical Genomics LAB (BI309)
2. Biocomputing with Perl & BioPerl (BI310)
    - LAB: Biocomputing with Perl & BioPerl LAB (BI311)
3. Immuno-Informatics and Vaccine Design (BI312)
    - LAB: Immuno-Informatics and Vaccine Design LAB (BI313)

COURSE INFORMATION SHEET

Course: PROTEOMICS, METABOLOMICS & BIOMARKER DESIGN

Course code: BI301
Course title: Proteomics, Metabolomics & Biomarker Design
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology

Course Objectives:
This course enables the students to:

1.	Understand protein structure hierarchy, protein folding, post translational modifications and spectroscopic methods used for proteins.
2.	Understand different separation techniques used for protein extraction and purifications, SDS Page, 2D Gel electrophoresis etc.
3.	Learn the spectroscopic and spectrometry techniques used in proteomics.
4.	Grasp the underlying concepts of metabolomics and Pathway modeling.
5	Gain knowledge about the Biomarker Designing along with their use and importance in clinical diagnostics.

Course Outcomes:
At the end of the course, a student should be able to:

CO1	Handle a protein and its characterization. Know the principles of proteome quantification.
CO2	Demonstrate how various types of mass spectrometers can be used for proteome quantification and for post translational modifications.
CO3	Use software tools to analyze various quantitative proteomic data types and how this data can be applied in biology, clinical research and drug discovery and designing novel proteins.
CO4	Demonstrate metabolomics and able to explain protein-protein interactions and protein complexes
CO5	Demonstrate and implement the techniques for Biomarkers design

SYLLABUS

Module I: Proteomics basics: Forces that determine protein structure and physicochemical properties, Mechanisms of protein folding. Protein isolation and profiling: Method for protein isolation and purification, Profiling by Native-PAGE, SDS-PAGE, 2-D/IEF SDS-PAGE, staining and destaining, imaging and analysis of 1-D and 2-D gels. Proteomics tools and databases. (8L)

Module II: Protein Spectroscopy: Background and basic principles of various spectroscopic techniques used for protein structure determination, Absorption and fluorescence, Circular dichroism, FT-Raman, FT-IR. Application of DSC, Protein denaturation, aggregation and gelation. (8L)

Module III: Protein characterization & mass Spectrometry: Protein sequencing using various methods, Site directed mutagenesis for specific protein function, Protein identification by mass spectrometry, MALDI-TOF, ESI-MS-MS, Q-TOF. Peptide Mass Fingerprinting. Peptide Sequence Analysis by Tandem Mass Spectrometry. Determination of post translational modification. Identifying Protein-Protein Interactions and Protein Complexes(8L)

Module IV: Metabolomics: Metabolites, Primary and Secondary metabolic pathways, KEGG, MetaCyc, Human Metabolome database, Interactions with biological systems, inborn dysbiosis and diseases. Techniques of metabolomic analysis, metabolomics, and precision medicines. (8L)

Module V: Biomarker Design: Types of Biomarkers, Features of Biomarkers, Omics based Biomarker design, Measurement of Biomarkers, Potential uses and limitations. Biomarker based clinical trial design, statistical approaches to model building. (8L)

Textbook

1. Carl, Branden and Tooze, John. Introduction to Protein Structure, Garland Publishing (Taylor and Francis Group). New York.
2. Yada, R. Y.; Jackman, R. L.; Smith, J. L. Protein Structure-Function Relationships Blakie Academic and Professional: London

Reference Books:

1. Clark, R. J. H and Hester, R. E. Spectroscopy of Biological Systems, John Wiley and Sons, New York
2. Nakai, S. and Modler, H. W. Food Proteins: Properties and Characterization, VCH Publishers, New York.

Course Evaluation

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	1	3	3	1
CO2	1	1	3	3	1
CO3	2	1	3	2	1
CO4	2	2	3	2	2
CO5	2	2	3	2	1

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3,CD4
CO2	CD1, CD2, CD3,
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2, CD3, CD4, CD6

COURSE INFORMATION SHEET

Course: CHEMINFORMATICS AND DRUG DESIGN

Course code: BI302
Course title: Cheminformatics and Drug Design
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 3
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To grasp the fundamental concepts of computational chemistry and cheminformatics
2.	To explain the behavior and mechanism of drug-human interaction through the basics of Pharmacology: Pharmacokinetics and Pharmacodynamics.
3.	To efficiently utilize the available databases and tools that are being used in Computer Aided Drug Discovery today.
4.	To identify drug targets and perform QSAR, Virtual Screening of compounds, Lead Identification, Lead Optimization and ADME/Toxicity analysis.

Course Outcomes
After the completion of this course, students will be able to:

CO1	Design small molecules and compounds that can be used as Lead which possess the required pharmacological properties to be developed as a drug.
CO2	Design & screen the chemical libraries of compounds using combinatorics & virtual screening techniques.
CO3	Perform the QSAR, ADME/T, Modeling, Docking & Simulation.
CO4	Attempt the modern drug discovery challenge using current approaches based upon Rational or Structure based method, Analog or Ligand based method and the Pharmacophore based method.
CO5	Use the existing known drug for Drug-Repurposing and implement scaffold hopping technique for alternate applications.

SYLLABUS

Module I: Basics of Cheminformatics and Molecular Visualization: Introduction to Cheminformatics, Computer representation and Manipulation of Chemical Structures (2D, 3D), SMILES, Chemical Structure & Substructure searching. Chemical Structure sketching, building and optimization. 2D to 3D structure conversion, Structure Electrostatics Analysis, File **formats in CADD -** pdb, pdbqt, mol2, sdf, dlg etc. Open Source/ Free Tools for Sketching. (8L)

Module II: Basics of Pharmacology: Pharmacokinetics and Pharmacodynamics: Introduction to Drug, Physicochemical properties (LogP, LogD, and Topological Polar Surface Area), Lipinski's rule of Five, QSAR (2D, 3D) and its applications (QSAR for predicting biological property, QSAR for Virtual Screening), Chemistry of drug-metabolism, drug deactivation and elimination. Drug-receptor interactions, receptor theories and drug action; Theories of enzyme inhibition and inactivation. ADME and toxicity properties of drugs. (8L)

Module III: CADD Databases and tools of Drug Discovery: PDB, PubChem, UniProt, KEGG, Zinc, DrugBank, Chembl, MMsINC, STITCH, STRING, GENECARD, MALACARDS, SuperTarget, Therapeutic target DB, Disgenet, BindingDB, DataWarrie. **CADD-Tools** - Prediction of Physico-chemical properties (VCCLAB,ChEMBL, Chemaxon), Prediction of ADME/T properties (admetSAR, ADMETlab etc). Drug dose Response (EC50, IC50, ED50, TD50, LD50) and Therapeutic index, Lipophilicity (ALOGPS 2.1), Toxicity Analysis and Prediction (protox_II, lazar,ToxiM). (8L)

Module IV: Drug Discovery Process and CADD: Introduction to drug and drug discovery pipeline, Overview of conventional and rational drug design, High-throughput screening (HTS) in Drug Discovery. ***In-Silico Drug designing approaches:*** Structure based (Rational), Ligand based, Pharmacophore based methods. Pre-Clinical and Clinical Trials. Bioethics and Drug Regulatory Procedures. Drug Repurposing, Scaffold Hopping Multitarget Analysis. (8L)

Module V: Drug Targets, Lead Identification & Optimization: Druggable Genome and Known Drug Targets, Pathway Analysis. Target Identification and characterization, Validation of Target against known drugs for other diseases, Binding Pockets and Surface Analysis, Pharmacophore and Molecular Descriptor Analysis. Combinatorial Library Designing. Random Screening, Generation of hits/leads by structure-based virtual screening against target. QSAR-based VS in drug discovery. High-throughput Virtual Screening. Docking and Simulation Analysis for Drug-Receptor interactions (Autodock, Gromacs). Lead Optimization. (8L)

Textbooks:

1. Pharmacoinformatics and Drug Discovery Technologies: Theories and Applications Tagelsir Mohamed Gasmelseid Publisher: Idea Group, 2012. (ISBN: 978-1466603097
2. Molecular Modeling and Simulation: An Interdisciplinary Guide - Tamar Schlic, Publisher: Springer-Verlag New York, 2002. ISBN: 978-1441963505

Reference Books:

1. A.R. Leach, Molecular Modelling Principles and Application, Longman, 2001.
2. J.M. Haile, Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons, 1997.

Course Evaluation

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	1	3	3	1
CO2	1	1	3	3	1
CO3	2	1	3	2	1
CO4	2	2	3	2	2
CO5	2	2	3	2	1

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD2, CD3,CD4
CO2	CD1, CD2, CD3,
CO3	CD1, CD2, CD3, CD4, CD6
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2, CD3, CD4, CD6

COURSE INFORMATION SHEET

Course: NGS DATA ANALYSIS

Course code: BI303
Course title: NGS Data Analysis
Prerequisite(s):
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students to learn:

1.	To learn the current DNA sequencing technologies and NGS data resources and data conversion.
2.	To get an exposure of NGS Data Analysis and Pipeline Development.
3.	To perform and evaluate Transcriptomics by RNA-Seq
4.	To learn Genotyping and Genomic Variation Discovery
5.	To learn *De novo* Genome Assembly & ChIP-Seq Analysis:

Course Outcomes
After the completion of this course, students will be able to:

CO1	To handle the NGS data and their adaptor libraries and explain the theoretical and experimental aspects of NGS data from different sequencing platforms.
CO2	Perform NGS data analysis - quality checking, indexing & sorting, alignment & mapping and variant calling.
CO3	Perform Deno Genome assembly, annotations & CHIP-Seq Analysis. NGS Pipeline Development.
CO4	Explain Genotyping and Genomic Variation Discovery.
CO5	Undertake small project related to NGS data analysis of Genomics and Transcriptomics experiments.

SYLLABUS

Module I: Introduction to NGS: Generation to DNA sequencing technologies, A Typical NGS Experimental Workflow, Different NGS Platforms – Illumina, Ion Torrent Semiconductor Sequencing, Pacific Biosciences SMRT, ONT Nanopore; Major Applications of NGS. (8L)

Module II: Base Calling, Quality Control & Read Mapping: Base Calling, FASTQ File Format, Base Quality Score, NGS Data Quality Control and Preprocessing; Reads Mapping – Mapping Approaches and Algorithms, Selection of Mapping Algorithms and Reference Genome Sequences, SAM/BAM as the Standard Mapping File Format, Mapping File Examination and Operation, Tertiary Analysis, NGS Data Storage, Transfer, and Sharing, Computing Power Required for NGS Data Analysis, Bioinformatics Skills & Software Required for NGS Data Analysis. (8L)

Module III: Transcriptomics by RNA-Seq: Principle of RNA-Seq; Experimental Design: Factorial Design, Replication and Randomization, Sample Preparation, Sequencing Strategy; *RNA-Seq Data Analysis:* Data Quality Control and Reads Mapping, RNA-Seq Data Normalization, Identification of Differentially Expressed Genes, Differential Splicing Analysis, Visualization of RNA-Seq Data, Functional Analysis of Identified Genes; RNA-Seq as a Discovery Tool. *Small RNA Sequencing:* Data Generation, Preprocessing, Mapping, Identification of Known and Putative Small RNA Species, Normalization, Identification of Differentially Expressed Small RNAs, Functional Analysis of Identified Small RNAs. (8L)

Module IV: Genotyping and Genomic Variation Discovery: Data Preprocessing, Mapping, Realignment, and Recalibration; Single Nucleotide Variant (SNV) and Indel Calling: SNV Calling, Identification of de novo Mutations, Indel Calling, Variant Calling from RNA-Seq Data, Variant Call Format (VCF) File, Evaluating VCF Results. Structural Variant (SV) Calling: Read-Pair-Based SV Calling, Breakpoint Determination, De novo Assembly-Based SV Detection, CNV Detection, Integrated SV Analysis; Annotation of Called Variants, Testing of Variant Association with Diseases or Traits. (8L)

Module V: De novo Genome Assembly & ChIP-Seq Analysis: Genomic Factors and Sequencing Strategies for de novo Assembly, Genomic Factors That Affect de novo Assembly, Sequencing Strategies for de novo Assembly; Assembly of Contigs, Sequence Data Preprocessing, Error Correction, and Assessment of Genome Characteristics, Contig Assembly Algorithms; Scaffolding, Assembly Quality Evaluation, Gap Closure, Limitations and Future Development. Principle of ChIP-Seq, Experimental Design: Experimental Control, Sequencing Depth, Replication; Read Mapping, Peak Calling, and Peak Visualization, Differential Binding Analysis, Functional Analysis, Motif Analysis, Integrated ChIP Seq Data Analysis. (8L)

Textbooks

1. Big Data Analysis for Bioinformatics and Biomedical Discoveries, Edited By Shui Qing Ye, CRC Press, Chapman & Hall Book.

Reference Book

1. Next-Generation Sequencing Data Analysis by Wang. CRC Press.
2. Bioinformatics: A Practical Handbook of Next Generation Sequencing and Its Applications, by Lloyd Low, Martti Tammi. World Scientific Publishing Co.
3. Statistical Analysis of Next Generation Sequencing Data. Data & Nettleton. Springer.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	2	3	1
CO2	3	2	3	3	1
CO3	3	3	3	2	1
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6, CD7
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Course: IMAGE PROCESSING

Course code: CA439
Course title: Image Processing
Pre- requisite(s):
Co-requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 4
Branch: Bioengineering & Biotechnology

Course Objective:
This course enables the students:

1	Understand the fundamentals of digital image processing. Apply the definitions of the image classification and analysis problem to common problems in computer vision
2	Develop a Broad knowledge of Spatial and Frequency image transforms used for enhancing an image
3	Learn Image restoration techniques and noise models used for restoring an image.
4	Understand Lossless and lossy image compression techniques.
5	Know Morphological processing algorithms for various operations on an image.

Course Outcomes
After the completion of this course, students will be able to:

CO1	Understand the concept of image formation, digitization and the role human visual system plays in perception of image data.
CO2	Synthesize a solution to image compression using the concept of information theory and lossless and lossy compression techniques.
CO3	Acquire an appreciation for spatial and frequency based techniques for enhancing the appearance of an image duly applying them in different applications.
CO4	Discern the difference between noise models, gain an insight into assessing the degradation function and realize different spatial and frequency based filtering techniques for reduction and removal of noise.
CO5	Design and execute an implementation of an image processing system using tools such as PyTorch or TensorFlow

SYLLABUS

Module I
What Is Digital Image Processing, Fundamental Steps in Digital Image Processing, Components of an Image Processing System, Elements of Visual Perception, Light and the Electromagnetic Spectrum, Image Sensing and Acquisition, Image Sampling and Quantization, Some Basic Relationships Between Pixels, Linear and Nonlinear Operations. **(8L)**

Module II
Enhancements in Spatial Domain: Some Basic Gray Level Transformations, Histogram Processing, Enhancement Using Arithmetic/Logic Operations, Basics of Spatial Filtering, Smoothing Spatial Filters, Sharpening Spatial Filters, Combining Spatial Enhancement Methods. **Enhancements in Frequency Domain**: Introduction to the Fourier Transform and the Frequency Domain, Smoothing Frequency-Domain Filters, Sharpening Frequency Domain Filters, Homomorphism Filtering **(8L)**

Module III
Image Restoration: A Model of the Image Degradation/Restoration Process, Noise Models. Restoration in the Presence of Noise Only-Spatial Filtering, Periodic Noise Reduction by Frequency Domain Filtering, Linear, Position-Invariant Degradations, Estimating the Degradation Function, Inverse Filtering, Mean Square Error (Wiener) Filtering, Constrained Least Squares Filtering, Geometric Mean Filter, Geometric Transformations. **(8L)**

Module IV
Image Compression: Fundamentals, Image Compression Models, Elements of Information Theory, Error-Free Compression, Lossy Compression. **(8L)**

Module V
Morphological Image Processing and Segmentation: Preliminaries, Dilation and Erosion, Opening and Closing, The Hit-or-Miss Transformation. Some Basic Morphological Algorithms, Detection of Discontinuities, Edge Linking and Boundary Detection, Thresholding, Region Based Segmentation. **(8L)**

Textbooks:

1. Rafael. C. & Woods Richard E. “Digital Image Processing”, 3rd Edition, Pearson Education, New Delhi, 2009.

Reference books:

1. Pratt W.K. “Digital Image Processing”, 4th Edition, John Wiley & sons Inc., 2006. 2. Sonka M., Hlavac Vaclav, Boyle Roger “Image Processing, Analysis and Machine Vision”, 2nd Edition, Thomson Learning, India Edition, 2007.
2. Jayaraman “Digital Image Processing”, Tata McGraw. Hill Education, 2011.

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	2	3	1
CO2	3	2	3	3	1
CO3	3	3	3	2	1
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6,CD7
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2, CD3, CD4,CD5,CD7

LABORATORY: SEM - III

COURSE INFORMATION SHEET

Lab Course: CHEMINFORMATICS AND DRUG DESIGN LAB

Course code: BI304
Course title: Cheminformatics and Drug Design Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives

This course enables the students to learn:

1.	Basics of CADD and Various file formats and their conversion. Latest tools & trends of the technologies.
2.	Specialized Databases and tools related to CADD
3.	ADMET & QSAR Analysis.
4.	Combinatorial Library and Virtual Screening of compounds.
5.	Various approaches of Drug Design - Rational, Ligand based, Pharmacophore based methods.

Course Outcomes

After the completion of this course, students will be able to:

CO1	Explain the theoretical and experimental aspects of CADD
CO2	Perform the combinatorial library design, ADME/T analysis, Virtual Screening of compounds
CO3	Perform SBDD, LBDD and Pharmacophore based drug design.
CO4	Understand Ligand Receptor Interactions. Scaffold hopping and drug repurposing.
CO5	Undertake small project related to CADD

SYLLABUS

List of Exercises for CADD

1. **2D to 3D structure sketching and Visualization:** ChemSketch, BIOVIA Draw, Molinspiration, Marvin Draw and Marvin Sketch etc., SMILES . **File formats in CADD -** pdb, pdbqt, mol2, sdf, dlg etc. Visualization - DS Visualizer, Pymol, Chimera etc.
2. **Physicochemical properties and Toxicity Analysis**: LogP, LogD, and Topological Polar Surface Area. **Tools** - VCCLAB, ChEMBL, Chemaxon. Therapeutic index, Lipophilicity (ALOGPS 2.1), Toxicity Analysis and Prediction (protox_II, lazar,ToxiM). ADME/T and QSAR Analysis - admetSAR, SwissADME, ADMETlab etc.
3. **CADD Databases-** PubChem, UniProt, KEGG, Zinc, DrugBank, Chembl, MMsINC, STITCH, STRING, GENECARD, MALACARDS, SuperTarget, Therapeutic target DB, Disgenet, BindingDB, DataWarrier etc.
4. Pharmacophore Searching and Modeling using Pharmit tool.
5. Combinatorial Library Designing & Virtual Screening. - SMILIB, Autodock-Vina etc.
6. Protein Modeling tools: Modeller, Swiss-Model,Chimera etc.
7. Docking (Protein-Ligand & Protein-Protein): Autodock, Swiss-Dock, Hex, Haddock, Cluspro etc.
8. Molecular Simulation & Analysis for Drug-Receptor interactions: Gromacs, NAMD, VMD
9. Case Studies of Drug Designing: LBDD and SBDD. Drug Repurposing and Scaffold Hopping.

CADD Books:

1. A.R. Leach, Molecular Modelling Principles and Application, Longman, 2001.
2. J.M. Haile, Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons.
3. Gupta, S.P. QSAR and Molecular Modeling, Springer - Anamaya Publishers, 2008.
4. Satya Prakash Gupta, QSAR and Molecular Modeling, Springer – Anamaya Publishers.
5. Guidebook on Molecular Modeling In Drug Design, J. G. Vinter, Mark Gardner (Editor), J. G. Vinter (Editor), CRC Press (May 1994) ISBN: 0849377722

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	2	3	3
CO3	3	3	3	3	3
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6,CD7
CO4	CD1, CD3, CD6, CD7
CO5	CD1, CD2, CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: NGS DATA ANALYSIS LAB

Course code: BI305
Course title: NGS Data Analysis Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives

This course enables the students to learn:

1.	To learn the current DNA sequencing technologies and NGS data resources and data conversion.
2.	To get an exposure of NGS Data Analysis and Pipeline Development.
3.	To perform and evaluate Transcriptomics by RNA-Seq
4.	To learn Genotyping and Genomic Variation Discovery
5.	To learn *De novo* Genome Assembly & ChIP-Seq Analysis:

Course Outcomes

After the completion of this course, students will be able to:

CO1	Explain the theoretical and experimental aspects of NGS Technology and data analysis.
CO2	Perform NGS data analysis - quality checking, indexing & sorting, alignment & mapping and variant calling.
CO3	Develop pipelines of NGS data analysis
CO4	Design experiments and analyze the NGS Data effectively coming from various experiments using different libraries.
CO5	Undertake small project related to NGS data analysis

SYLLABUS

List of Exercises for NGS

Tools - Unigene, GATK Tools, Galaxy, Google Colab

1. Basic Linux Commands and nano editor.
2. Data manipulation & Parsing with One liner in Perl, awk, sed
3. Working with NGS databases (NCBI-SRA, etc.), NGS file formats, File format conversion.
4. NGS Tools & Commands basics - FastQC, GATK, BWA or Bowtie, SAM, IGV etc.
5. Quality control checks and filtering raw sequences (FastQC, GATK Tools)
6. Indexing and Sorting Reference Genome (GATK Tools)
7. Read Alignment & Mapping - Interpretation & Visualization. (BWA/Bowtie, SAM, IGV)
8. Downstream Processing and Variant Calling (VCF)
9. SNP Mining using GATK Pipeline.
10. RNA-Seq and Chip-seq data analysis
11. Functional Annotations of Common Differentially Expressed Genes (DAVID, ClueGo)

NGS Books

1. Big Data Analysis for Bioinformatics and Biomedical Discoveries, Edited By Shui Qing Ye, CRC Press, Chapman & Hall Book.
2. Bioinformatics: A Practical Handbook of Next Generation Sequencing and Its Applications, by Lloyd Low (Author, Editor), Martti Tammi (Editor), Publisher-World Scientific Publishing Co.

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	3	3	2
CO2	3	3	2	3	3
CO3	3	3	3	3	3
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6, CD7
CO4	CD1, CD3, CD6, CD7
CO5	CD1, CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: IMAGE PROCESSING LAB

Course code: BI306
Course title: Image Processing Lab
Pre- requisite(s): Python Programming
Co-requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 4
Branch: Bioengineering & Biotechnology

Course Objective:

This course enables the students:

1	Understand the fundamentals of digital image processing.
2	Develop a Broad knowledge of Spatial and Frequency image transforms used for enhancing an image.
3	Learn Image restoration techniques and noise models used for restoring an image.
4	Understand Lossless and lossy image compression techniques.
5	Know Morphological processing algorithms for various operations on an image.

Course Outcomes

After the completion of this course, students will be able to:

CO1	Apply the definitions of the image classification and analysis problem to common problems in computer vision.
CO2	Explain the basics of object recognition and image search, object detection techniques, motion estimation, object tracking in video using convolutional filters.
CO3	Apply convolutional neural networks to image data for object recognition and detection
CO4	Select different network architectures for the appropriate image processing problems.
CO5	Design and execute an implementation of an image processing system using tools such as PyTorch or TensorFlow

SYLLABUS

List of Exercises:

Image Processing Tools: PyTorch, NumPy, Scikit-image, OpenCV, PIL/pillow

A) Basic Image Processing Operations
   - Extract data, transform and analyze images using NumPy and Scikit-image.
   - Convert RGB images to grayscale.
   - Get data from images and obtain histograms containing information, and separate objects from the background.

B) Working on Filters, Contrast, Transformation and Morphology
   - To detect object shapes using edge detection filters, improve medical images with contrast enhancement and even enlarge pictures to five times its original size.
   - To apply morphology to make thresholding more accurate when segmenting images

C) Working on Image restoration, Noise, Segmentation and Contours
   - To apply image restoration to remove texts, logos, objects, and to restore corrupted images.
   - To apply noise, use segmentation to speed up processing and find elements in images by their contours.

D) Advanced Operations, Detecting Faces and Features
   - To detect edges, corners, and faces in the image.
   - To detect front faces, face profiles, animals (cat, dogs etc).

E) Image Processing application in Bioinformatics
   - To apply machine learning based image processing to complex real-world applications in Bioinformatics. Eg. Microarray and Medical Imaging data

Textbooks:

1. Geron A., "Hands on Machine Learning with Scikit Learn and Tensorflow", 2nd edition, O' Reilly Press, 2020
2. Rafael. C. & Woods Richard E. "Digital Image Processing", 3rd Edition, Pearson Education, New Delhi, 2009.

Reference books:

1. Pratt W.K. "Digital Image Processing", 4th Edition, John Wiley & sons Inc., 2006. 2. Sonka M., Hlavac Vaclav, Boyle Roger "Image Processing, Analysis and Machine Vision", 2nd Edition, Thomson Learning, India Edition, 2007.
2. Jayaraman "Digital Image Processing", Tata McGraw. Hill Education, 2011.
3. Computer Vision: Algorithms and Applications, Richard Szeliski, Springer, 2010 (draft available online)

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	3	3	2	3	1
CO2	3	2	3	3	1
CO3	3	3	3	2	1
CO4	3	3	3	3	2
CO5	3	3	3	2	2

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1, CD6
CO2	CD1, CD6, CD7
CO3	CD1, CD2, CD3, CD6, CD7
CO4	CD1, CD3, CD6,CD7
CO5	CD1, CD2,CD3,CD4,CD5,CD7

PROGRAMME ELECTIVES - III

Program Electives - III with Labs:

1. Medical Genomics (BI308)
    - Medical Genomics Lab (BI309)
2. Biocomputing with Perl & BioPerl (BI310)
    - Biocomputing with Perl & BioPerl Lab (BI311)
3. Immuno-Informatics and Vaccine Design (BI312)
    - Immuno-Informatics and Vaccine Design Lab (BI313)

COURSE INFORMATION SHEET

Course: Medical Genomics

Course code: BI308
Course title: Medical Genomics
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To appreciate the role of genetics and genomics in health and disease.
2.	The course will facilitate the understanding of human molecular genetics, by contrasting and comparing 'normal' and 'diseased' states.
3.	To learn genetic diagnostic analysis techniques and interpretation of results
4.	To appreciate the role of microbiome in health and disease

Course Outcomes
After the completion of this course, students will be able to:

CO1	To acquire basic and specialized knowledge and understand the aspects of genetics and genomics.
CO2	Familiarize themselves with the common genetic disorders
CO3	To understand the complexity of the human genome and the molecular mechanism at the system level and how the body functions in health and illness.
CO4	Knowledge and use of important databases such as OMIM and ACMG, Clinvar
CO5	Appreciate the Interactions between Genetic factors, Environmental factors and Lifestyle in health and disease

SYLLABUS

Module I: Fundamentals, Molecular basis of Genetics, Eukaryotic gene structure, Regulatory architecture of the human genome, Mitochondrial genome, DNA amplification (PCR), DNA libraries, NGS, DNA variation, Important advances that contributed to the development of genetics and genomics. **(8L)**

Module II: Mendalian traits, Genetic recombination, Genetic linkage and association analysis, Quantitative difference in genetic traits, Hardy-Weinberg Equilibrium principle, inbreeding, Regulation of Gene function, Targeted gene disruption, Non-coding RNAs, Epigenetic modifications, DNA methylation, Changes in chromatin structure, Genomic imprinting, Signaling pathways**. (8L)**

Module III: Genetic diagnosis, Genome analysis with microarrays, GWAS, Array CGH, Genetics in medicine, Genetic classification of diseases, OMIM, Homeostasis and its imbalance, Metabolic disorders, Immune system disorders, Impaired Cell and tissue structure, dysregulated signaling pathways**. (8L)**

Module IV: Genomic disorders, Telomere defects, cancer prognosis and diagnosis, Haemoglobin disorders, Mitochondrial diseases Chromosomal translocations, Chromosomal aberrations, ACMG guidelines, Pharmacogenetics, Pharmacogenomics, gene and stem cell therapy, Ethical and societal issues, patient education and counseling**. (8L)**

Module V: Human Microbiome, Microbiome in health and disease, Methods of microbiome analysis, 16s rDNA metagenomics, Shotgun metagenomics, Functional analysis of metagenomic data, Network analysis of metagenomic data, modulation of human microbiome, Microbiome as drug candidate. **(8L)**

Textbook

1. Human Molecular Genetics 3rd edition by Tom Strachan and Andrew Read, 2003
2. Emery's Elements of Medical Genetics and Genomics 16th Edition by Peter Turnpenny, Sian Ellard, Ruth Cleaver. 2020

Reference Book

3. Big Data Analysis for Bioinformatics and Biomedical Discoveries, Edited By Shui Qing Ye, CRC Press, Chapman & Hall Book.
4. Application of Clinical Bioinformatics. Editors: Xiangdong Wang, Christian Baumgartner, Denis C. Shields, Hong-Wen Deng, Jacques S. Beckmann. Series: Translational Bioinformatics 11. Publisher Springer
5. ACMG web site
6. ASHG web site

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: MEDICAL GENOMICS LAB

Course code: BI309
Course title: Medical Genomics Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To appreciate the role of genetics and genomics in health and disease.
2.	The course will facilitate the understanding of human molecular genetics, by contrasting and comparing 'normal' and 'diseased' states.
3.	To learn genetic diagnostic analysis techniques and interpretation of results
4.	To appreciate the role of microbiome in health and disease

Course Outcomes
After the completion of this course, students will be able to:

CO1	To acquire basic and specialized knowledge and understand the aspects of genetics and genomics.
CO2	Familiarize themselves with the common genetic disorders
CO3	To understand the complexity of the human genome and the molecular mechanism at the system level and how the body functions in health and illness.
CO4	Knowledge and use of important databases such as OMIM and ACMG, Clinvar
CO5	Appreciate the Interactions between Genetic factors, Environmental factors and Lifestyle in health and disease

SYLLABUS

List of Exercises

Hands-on-Session with Open-Source tools - GATK, Galaxy, Unigene etc.

1. Database Searching - KEGG, Gene ontology (GO), OMIM, Medline, ACMG, Clinvar, STRING, other pathway and network Databases
2. Browsing Human Genome through Genome Browsers
3. UCSC Genome Browser - downloading
4. Experimental Design - Data Collection and Processing
5. Genome Assembly and Annotation
6. NGS Data Analysis - Exploring and Developing Pipelines
7. SNP Discovery - Variant Calling & Analysis, Result Interpretation
8. Metagenomics studies using 16s rDNA method
9. Functional analysis of metagenomic data
10. Network analysis of metagenomic data

Books Recommended

1. Big Data Analysis for Bioinformatics and Biomedical Discoveries, Edited By Shui Qing Ye, CRC Press, Chapman & Hall Book.
2. Bioinformatics: A Practical Handbook of Next Generation Sequencing and Its Applications, by Lloyd Low (Author, Editor), Martti Tammi (Editor), Publisher-World Scientific Publishing Co.
3. Application of Clinical Bioinformatics. Editors: Xiangdong Wang, Christian Baumgartner, Denis C. Shields, Hong-Wen Deng ,Jacques S. Beckmann. Series: Translational Bioinformatics 11. Publisher Springer

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): NIL
POs met through Gaps in the Syllabus: NIL
Topics beyond syllabus/Advanced topics/Design: NIL
POs met through Topics beyond syllabus/Advanced topics: NIL

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2
CO5	2	3	3	1	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Course: BIOCOMPUTING WITH PERL & BioPerl

Course code: BI310
Course title: Biocomputing with Perl & BioPerl
Pre- requisite(s): Basic Programming
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To learn the basic and advanced concepts of Perl language to be used for the analysis of biological data.
2.	To implement the anonymous data types and Regular Expressions
3.	To create objects using Object-Oriented Perl and to use Perl-CGI for web interface development and server-side request handling.
4.	To develop perl modules for the application in Bioinformatics field
5.	To use and apply the BioPerl package for sequence and structure analysis

Course Outcomes
After the completion of this course, students will be able to:

CO1	Use Perl language to solve different algorithms used in bioinformatics
CO2	Construct & explore regular expressions for different patterns that are present in biological sequences of DNA, RNA and Protein
CO3	Develop online tools using Perl-CGI programming.
CO4	Develop understanding of the language so that new modules can be efficiently developed in the thrust areas like NGS and CADD.
CO5	Utilize the BioPerl package for addressing various bioinformatics applications related to Genomics and Proteomics

SYLLABUS

Module I: Introduction: History of Perl, Availability, Support, Versions, Installation. Significance of Perl in Bioinformatics. **Basic Concepts:** Scalar Data, Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Operators and Functions. Arrays and List Data: Literal Representation, Variables, Array Operators and Functions, Scalar and List Context. Hashes: Hash Variables, Literal Representation of a Hash, Hash Functions, Hash Slices. Control Statement blocks, Loops and Conditions. Basic Input/Output. (8L)

Module II: Advance Constructs and Features: Regular Expressions: Concepts of Regular Expressions, Simple Usage of Regular Expressions, Patterns, Matching Operators, Substitutions, Split and Join functions, Subroutines: System and User Functions, Local Operator, Length, Parameter Lists, Lexical Variables, File Handles and File Tests: Opening and Closing a File handle.(8L)

Module III: Object-Oriented Perl and Perl-CGI: Introduction to Modules, Creating Objects and References. Anonymous Data types, CGI Programming: The CGI.pm Module, CGI Program in Context, Simple CGI Programs, Passing Parameters via CGI, Perl and the Web. (8L)

Module IV: Perl Programming Constructs for Bioinformatics: Representing String and Sequenced Data in Perl, Manipulation of Biological Sequences, Concatenating DNA Fragments, DNA to RNA Transcription, Translation, Reading Genes & Proteins from File, Finding Motifs, Counting Nucleotides and Composition Analysis. Reading FASTA files. Finding Open Reading Frame, Generating random DNA, RNA & Protein sequences. Parsing Genbank and PDB Files, Parsing BLAST Output. (8L)

Module V: BioPerl: BioPerl Overview, Installation Procedures; Fundamental Constructs and Special Features; BioPerl Modules, Creating BioPerl Objects. (8L)

BOOKS RECOMMENDED

Textbook

1. Learning Perl, Tom Phoenix, Randal L. Schwartz, Wiley Publications

Reference Books

2. Perl Cookbook, Tom Christiansen, Nathan Torkington, O'Reilly Publications
3. Programming Perl, Tom Christiansen, brian d foy, Larry Wall, Jon Orwant, O'Reilly
4. Mastering Perl for Bioinformatics by James Tisdall, Publisher(s): O'Reilly

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements): Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined: **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Lab Course: BIOCOMPUTING WITH PERL & BioPerl Lab

Course code: BI311
Course title: Biocomputing with Perl & BioPerl Lab
Pre- requisite(s): Basic Bioinformatics
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To learn the basic and advanced concepts of Perl language to be used for the analysis of biological data.
2.	To implement the anonymous data types and Regular Expressions
3.	To create objects using Object-Oriented Perl and to use Perl-CGI for web interface development and server-side request handling.
4.	To develop Perl modules for the application in Bioinformatics field
5.	To use and apply the BioPerl package for sequence and structure analysis

Course Outcomes
After the completion of this course, students will be able to:

CO1	Use Perl language to solve different algorithms used in bioinformatics
CO2	Construct & explore regular expressions for different patterns that are present in biological sequences of DNA, RNA and Protein
CO3	Develop online tools using Perl-CGI programming.
CO4	Develop understanding of the language so that new modules can be efficiently developed in the thrust areas like NGS and CADD.
CO5	Utilize the Bioperl package for addressing various bioinformatics applications related to Genomics and Proteomics

SYLLABUS

Module I: Introduction & Basic Concepts:

1. Writing Programs for understanding basic data types of Perl includes Scalar Data, Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Operators and Functions.
2. Writing Programs for Arrays and List Data: Literal Representation, Variables, Array Operators and Functions, Scalar and List Context.
3. Writing Programs for Hashes: Hash Variables, Literal Representation of a Hash, Hash Functions, Hash Slices.
4. Writing Programs for Control Statement blocks, Loops and Conditions.
5. Writing Programs for Basic Input/Output. Standard Input by Keyboard.

Module II: Advance Constructs and Features:

6. Writing Programs for Regular Expressions for understanding Quantifier, Qualifier, Classes of pattern, Pattern Searching Operators for Matching, Substitutions and transliteration.
7. Writing Programs for Split & Join functions, Map and Grep functions.
8. Writing Programs for Subroutines: System and User Functions, Local Operator, Length, Parameter Lists, Lexical Variables.
9. Writing Programs for File Handles and File Tests: Opening, Closing and appending a File.
10. Writing Programs for References - Scalar, Array and Hash referencing and dereferencing.

Module III: Object-Oriented Perl and Perl-CGI:

11. Writing programs for Anonymous Data types and referencing and dereferencing.
12. Writing programs for packages in Perl, making Perl Modules, Creating Objects and References. Accessing packages. Implementing Inheritance, Polymorphism etc.
13. Writing programs for CGI Programming: The CGI.pm Module. Embedding HTML in CGI Program for web development.
14. Create CGI based web pages using Apache server including CSS.
15. Writing programs for Passing Parameters via CGI (scalar & array data). Use of GET and POST methods. Form data parsing and result display.

Module IV: Perl Programming Constructs for Bioinformatics:

16. Writing programs for Representing String and Sequenced Data in Perl,
17. Writing programs for Manipulation of Biological Sequence Data, Concatenating DNA Fragments, DNA to RNA Transcription, Translation, Reading Genes & Proteins from Fasta File, Finding Motifs, Counting Nucleotides and Composition Analysis.
18. Writing programs for Reading multiple FASTA files. Finding Open Reading Frame, Generating random DNA, RNA & Protein sequences.
19. Writing programs for Parsing PDB Files and displaying various file attributes.

Module V: BioPerl Modules:

20. BioPerl - Installation Procedures; BioPerl Objects - Bio::Seq, Bio::SeqIO
21. Writing programs to Parse BLAST Reports with Bioperl (Bio::SearchIO)
22. Writing programs for Alignment (Bio::SimpleAlign, Bio::AlignIO)
23. BioPerl Modules - Accessing Databases, Parsing Genbank File, etc.

BOOKS

1. Learning Perl , Tom Phoenix, Randal L. Schwartz, Wiley Publications
2. Mastering Perl for Bioinformatics by James Tisdall, Publisher(s): O'Reilly

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2
CO5	2	1	2	2	1

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD6,CD7
CO5	CD1,CD2,CD3,CD4,CD5,CD7

COURSE INFORMATION SHEET

Course: IMMUNO-INFORMATICS AND VACCINE DESIGN

Course code: BI312
Course title: Immuno-Informatics and Vaccine Design
Pre- requisite(s): Basic Immunology
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To grasp the basic understanding of Immune System and its response
2.	To get an exposure of various specialized Immuno-informatics Databases and tools that are being used in the field
3.	To Analyze the Epitopes and to predict the Antigenicity of a molecule to activate the immune response.
4.	To learn the Bioinformatics based approach towards designing vaccine candidate molecules through case studies.
5.	To learn various structural analyses methods for selected Vaccine Lead molecule

Course Outcomes
After the completion of this course, students will be able to:

CO1	Understand the concepts of Vaccine Design using Computational methods
CO2	Identify the target protein or other molecules to be used as lead for vaccine
CO3	Perform modeling, docking and simulation studies required for vaccine development.
CO4	To take the challenge of vaccine design for any established disease caused by an infectious agent

SYLLABUS

Module I: Immunity Basics

Introduction to Immunity and Immune response, Antigens and Antibody Structure, B-Cell and T-Cell Epitopes, MHC, Immune-Receptors,Vaccines, Types of Vaccines, Concepts of Vaccine Design and Reverse vaccinology. (8L)

Module II: Immuno-informatics Databases & Tools:

Specialized Databases for Vaccine Design - Signal 1.4 database - Single Peptide Cleavage site; IEBD database - Epitope prediction:MHC-I, MHC-II, B-Cell,T-cell); Pep-Fold database - Peptide and mini-protein structure prediction. Prediction of immunogenic regions in antigenic protein.(8L)

Module III: Analysis of Epitopes and Antigenicity Prediction:

Functional Analysis of Antigenic Proteins - physico-chemical characteristics, antigenicity, allergic nature; CTL Prediction (NETCTL1.2), B-Cell/T-cell Prediction (BCP/FBC/AAP Method), Antigenicity Epitope Prediction (VAXIJEN), Allergenicity & Antigenicity Prediction(ALG-PRED).(8L)

Module IV: Bioinformatics Based Vaccine Design: Case Studies (Malaria)

Biochemistry of disease, identification of antigenic targets for vaccine (KEGG-Pathway analysis), Prediction and analysis of Antigenic Target Protein for Epitopes, Antigenicity & Antiallergicity, Screening of Minimal Epitope Set, Screening of Epitopes assembled and Prediction Population Coverage (PPC) analysis, Use of Adjuvants and Linkers for Epitope binding and formation of vaccine lead. (8L)

Module V: Structure Analysis of Vaccine Lead:-

Antigen-Antibody Modelling (Automated and Alignment based) and Docking, Secondary and Tertiary structure prediction of Lead (PSI-PRED), Ramachandran Plot Analysis, Molecular Docking of Vaccine lead with Immune Receptors, Molecular Dynamics Simulation of Target-Receptor complex. Interpretation of Results. Experimental Validation - Preclinical and Clinical Testing. (8L)

Textbooks

1. Rajat K. De, Namrata Tomar , Immunoinformatics, Springer, 2014, Volume 1184, ISBN : 978-1-4939-1114-1
2. Immunoinformatics by Christian Schönbach, Shoba Ranganathan, Vladimir Brusic, 2014, Springer, ISBN-13: 9781489997838

Reference Books

3. Immunoinformatics by Namrata Tomar , Humana New York, NY, ISBN, 978-1-0716-0391-8, Published: 12 March 2021, Series - Methods in Molecular Biology (MIMB, volume 2131).
4. Bioinformatics for immunomics (series: immunomics reviews:), Coordinators: Flower Darren D.R., Davies Matthew, Ranganathan Shoba, Publisher - Springer (Vol 1- 2009, Vol 2- 2010,Vol 3 - 2012)
5. Making and Using Antibodies: A Practical Handbook, Second Edition, ISBN 10: 1439869081 ISBN 13: 9781439869086, Publisher: CRC Press, 2013

Course Evaluation:

Individual assignment, Presentation, Theory (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
CD4	Industrial/guest lectures
CD5	Industrial visits/in-plant training
CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD4, CD5, CD6,CD7

COURSE INFORMATION SHEET

Lab Course: IMMUNO-INFORMATICS AND VACCINE DESIGN LAB

Course code: BI313
Course title: Immuno-Informatics and Vaccine Design Lab
Pre- requisite(s):
Co- requisite(s):
Credits: 1.5 L: 0 T: 0 P: 3
Class schedule per week: 03
Class: MSc
Semester / Level: III / 5
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To grasp the basic understanding of Immune System and its response
2.	To get an exposure of various specialized Immuno-informatics Databases and tools that are being used in the field
3.	To Analyze the Epitopes and to predict the Antigenicity of a molecule to activate the immune response.
4.	To learn the Bioinformatics based approach towards designing vaccine candidate molecules through case studies.
5.	To learn various structural analyses methods for selected Vaccine Lead molecule

Course Outcomes
After the completion of this course, students will be able to:

CO1	Understand the concepts of Vaccine Design using Computational methods
CO2	Identify the target protein or other molecules to be used as lead for vaccine
CO3	Perform modeling, docking and simulation studies required for vaccine development.
CO4	To take the challenge of vaccine design for any established disease caused by an infectious agent

SYLLABUS

List of Exercises

1. Database searching for antigenic protein - Literature and specialized databases
    - KEGG Pathway
    - Signal 1.4 database - Single Peptide Cleavage site.
    - IEBD database - Epitope prediction:MHC-I, MHC-II, B-Cell,T-cell);
    - Pep-Fold database - Peptide and mini-protein structure prediction.
2. Prediction of immunogenic regions in antigenic protein
3. Functional Analysis of Antigenic Proteins -
    - physico-chemical characteristics,
    - antigenicity, allergic nature.
    - CTL Prediction (NETCTL1.2),
    - B-Cell/T-cell Prediction (BCP/FBC/AAP Method).
4. Prediction of Epitope, Antigenicity, Allergenicity in antigenic protein-
    - Antigenicity Epitope Prediction (VAXIJEN),
    - Allergenicity & Antigenicity Prediction (ALG-PRED).
5. Vaccine lead Construction:
    - Use of Adjuvants and Linkers for Epitope binding and
    - Construction of Vaccine lead.
6. Structure Analysis of Vaccine Lead:
    - Antigen-Antibody Modelling (Automated and Alignment based)
    - Secondary and Tertiary structure prediction of Lead (PSI-PRED),
    - Ramachandran Plot Analysis,
    - Molecular Docking of Vaccine lead with Immune Receptors,
    - Molecular Dynamics Simulation of Target-Receptor complex
7. CASE STUDY: Malaria and Other Diseases
    - Biochemistry of disease, identification of antigenic targets for vaccine (KEGG-Pathway analysis),
    - Prediction and analysis of Antigenic Target Protein for Epitopes, Antigenicity & Antiallergics,
    - Screening of Minimal Epitope Set, Screening of Epitopes assembled and
    - Prediction Population Coverage (PPC) analysis,
    - Use of Adjuvants and Linkers for Epitope binding and
    - formation of vaccine lead.

Recommended Books

1. Rajat K. De, Namrata Tomar , Immunoinformatics, Springer, 2014, Volume 1184, ISBN : 978-1-4939-1114-1
2. Immunoinformatics by Christian Schönbach, Shoba Ranganathan, Vladimir Brusic, 2014, Springer, ISBN-13: 9781489997838
3. Making and Using Antibodies: A Practical Handbook, Second Edition, ISBN 10: 1439869081 ISBN 13: 9781439869086, Publisher: CRC Press, 2013

Course Evaluation:

Lab (Quiz and End semester) examinations

Gaps in the syllabus (to meet Industry/Profession requirements) : Nil
POs met through Gaps in the Syllabus: Nil
Topics beyond syllabus/Advanced topics/Design: Nil
POs met through topics beyond syllabus/Advanced topics/Design: Nil

COURSE DELIVERY METHODS

CD1	Lecture by use of boards/LCD projectors/OHP projectors
CD2	Assignments/Seminars
CD3	Laboratory experiments/teaching aids
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CD6	Self- learning such as use of NPTEL materials and internets
CD7	Simulation

MAPPING BETWEEN COURSE OUTCOMES AND PROGRAM OUTCOMES

CO	PO1	PO2	PO3	PO4	PO5
CO1	1	-	3	3	1
CO2	1	-	3	3	1
CO3	2	1	3	2	-
CO4	2	2	3	2	2

Correlation Levels 1, 2 or 3 as defined : **< 34% = 1(L), 34-66% = 2(M), > 66% = 3(H)**

MAPPING BETWEEN COURSE OUTCOMES AND COURSE DELIVERY METHOD

Course Outcomes	Course Delivery Method
CO1	CD1,CD6
CO2	CD1, CD6,CD7
CO3	CD1, CD2, CD3,CD6,CD7
CO4	CD1, CD3,CD4, CD5, CD6,CD7

OPEN ELECTIVES

Open Electives - I (MO Session)

1. Biological Databases and MySQL (BI102)
2. Biosafety, Bioethics and IPR (BT503)

Open Electives - II (SP Session)

1. Biocomputing with Perl & BioPerl (BI310)
2. Analytical Techniques (BT418)

COURSE INFORMATION SHEET

Course: BIOLOGICAL DATABASES AND MYSQL

Course code: BI102
Course title: Biological Databases and MySQL
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: I / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students to:

1.	Learn the fundamental concepts & importance of international repositories and also explain the theoretical knowledge of database systems and algorithms.
2.	Extend comprehensive knowledge about Major Databases including Primary and Secondary Databases
3.	Gain knowledge about the techniques for database crosslinking and information retrieval systems.
4.	Demonstrate concept about various specialized & Genome databases in Bioinformatics
5.	Grasp the current fundamental problems of Bioinformatics and challenges of the subject.

Course Outcomes:

At the end of the course, a student should be able to:

CO1	Access various Bioinformatics resources and molecular databases and explain their collaborative effects in the field of Bioinformatics.
CO2	Analyze and discuss the similarity search results of BLAST & FASTA algorithms
CO3	Collect the proficient knowledge about the database cross-linking and integrated information retrieval system.
CO4	Effectively utilize the specialized and genome databases for advanced research.
CO5	Develop the key skills of Bioinformatics fundamental problems related to databases, crosslinking and mechanism of information retrieval.

SYLLABUS

Module I: Major Information Resources: Biological Data types, Biological Literature Information access, storage and retrieval systems. Primary and secondary databases of genomics, transcriptomics, proteomics, metabolomics and structural. Major file formats and their conversion tools. Human Genome Project, ENCODE project (8L).

Module II: Database Searching and Sequence Retrieval Methods: Sequence Similarity, Identity, and Homology; Sequence Similarity Searching Tools: BLAST, FASTA, PSI & PHI BLAST etc. Query Filtering and Limits, Algorithms of BLAST & FASTA and their statistical significance (E value and other parameters), Various flavors of BLAST & FASTA (8L).

Module III: Database Systems: Characteristics of Database, Database Concepts, Schemas & Instances, Database users and Administrators, DBMS architecture. (8L).

Module IV: Database Management using MySQL - Data types, Tables and Queries, Primary and foreign Key, filtering and sorting, Grouping, Joins, SET operator, Constraints and Indexes, views, functions, Operation - Insert, update, delete. MySQL administrations and control. (8L).

Module V: Specialized Databases and Current Challenges: Databases of Genomic Sequences (EST,STS etc), Chemical Structure database. Gene expression and Microarray Databases. Pathway Databases. Gene Ontology (GO) database, Protein-Interaction Databases (STRING, IntAct etc.), Database of Genetic Variations (dbSNP, dbVar etc.). Current Challenges - NGS data generation and handling. (8L).

Textbook

- Bioinformatics: a practical guide to the analysis of genes and proteins, Baxevanis A., Ouellette F.B.F., John Wiley and Sons, New York.
- Introduction to Bioinformatics, Arthur Lesk, Oxford University Press ((Indian Edition).
- Learning MySQL by Saied M.M. Tahaghoghi, Hugh E. Williams, O'Reilly Media, Inc.

Reference Book

- Bioinformatics: Sequence and Genome Analysis, David W Mount, Cold Spring Harbor Laboratory Press, New York.
- Fundamental Concepts of Bioinformatics, Dan E Krane, Michael L Raymer, Benjamin-Cummings Pub Co (ISBN 0805346333)

COURSE INFORMATION SHEET

Course: BIOSAFETY, BIOETHICS AND IPR

Course code: BT503
Course title: Biosafety, Bioethics & IPR
Pre- requisite(s):
Co- requisite(s):
Credits: L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: III/05
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:
This course enables the students to:

1.	To create awareness on IPR issues and need for knowledge in patents in biotechnology
2.	To understand the biosafety regulations and ethical practices in biotechnology
3.	To become familiarize with the ethical practices in biotechnology

Course Outcomes:
At the end of the course, a student should be able to:

CO1	To understand and follow the regulatory framework important for the product safety and benefit for the society.
CO2	To devise business strategies by taking account of IPRs
CO3	To acquire adequate knowledge in the use of genetically modified organisms and its effect on human health
CO4	To gain more insights into the regulatory affairs.

SYLLABUS

Module I: Intellectual Property: Patents, Trademarks, Copyright, Related Rights, Industrial Design, Traditional Knowledge, Geographical Indications, Protection of GMOs,IPs of relevance to Biotechnology and Case Studies; Agreements and Treaties, Indian Patent Act 1970 & recent amendments. (8L)

Module II: Patents and Concept of Prior Art: Types of patent applications, Ordinary, PCT, Conventional, Divisional and Patent of Addition; Specifications: Provisional and complete; Forms and fees, Invention in context of "prior art". (8L)

Module III: Patent Filing Procedures: National & PCT filing procedure; Time frame and cost; Status of the patent applications filed; Precautions while patenting–disclosure/non-disclosure; Patent licensing and agreement Patent infringement. (8L)

Module IV: Biosafety: Introduction to Biological Safety Cabinets; Biosafety Levels of Specific Microorganisms; Biosafety guidelines:Definition of GMOs & LMOs; Roles of Institutional Biosafety Committee, applications in food and agriculture; Environmental release of GMOs; Risk Analysis, Risk management and communication; National Regulations and relevant International Agreements, Cartagena Protocol.(8L)

Module V: Bioethics: Ethical implications of biotechnological products and techniques, Social and ethical implications of biological weapons. (8L)

Text books:

1. Deepa Goel & Shomini Parashar IPR, Biosafety and Bioethics, Pearson Education India, (2013)
2. Anupam Singh Intellectual Property Rights and Bio-Technology Biosafety and Bioethics, Narendra Publishing House, (2012)

Reference books:

1. BAREACT, Indian Patent Act 1970 Acts & Rules, Universal Law Publishing Co. Pvt. Ltd., (2007)
2. Kankanala C., Genetic Patent Law & Strategy, 1st Edition, Manupatra Information Solution Pvt. Ltd., (2007)

COURSE INFORMATION SHEET

Course: BIOCOMPUTING WITH PERL & BioPerl

Course code: BI310
Course title: Biocomputing with Perl & BioPerl
Pre- requisite(s):
Co- requisite(s):
Credits: 3 L: 3 T: 0 P: 0
Class schedule per week: 03
Class: MSc
Semester / Level: III / 4
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives
This course enables the students:

1.	To learn the basic and advanced concepts of Perl language to be used for the analysis of biological data.
2.	To implement the anonymous data types and Regular Expressions
3.	To create objects using Object-Oriented Perl and to use Perl-CGI for web interface development and server side request handling.
4.	To develop Perl modules for the application in Bioinformatics field
5.	To use and apply the BioPerl package for sequence and structure analysis

Course Outcomes
After the completion of this course, students will be able to:

CO1	Use Perl language to solve different algorithms used in bioinformatics
CO2	Construct & explore regular expressions for different patterns that are present in biological sequences of DNA, RNA and Protein
CO3	Develop online tools using Perl-CGI programming.
CO4	Develop understanding of the language so that new modules can be efficiently developed in the thrust areas like NGS and CADD.
CO5	Utilize the BioPerl package for addressing various bioinformatics applications related to Genomics and Proteomics

SYLLABUS

Module I: Introduction: History of Perl, Availability, Support, Versions, Installation. Significance of Perl in Bioinformatics. **Basic Concepts:** Scalar Data, Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Operators and Functions. Arrays and List Data: Literal Representation, Variables, Array Operators and Functions, Scalar and List Context. Hashes: Hash Variables, Literal Representation of a Hash, Hash Functions, Hash Slices. Control Statement blocks, Loops and Conditions. Basic Input/Output. (8L)

Module II: Advance Constructs and Features: Regular Expressions: Concepts of Regular Expressions, Simple Usage of Regular Expressions, Patterns, Matching Operators, Substitutions, Split and Join functions, Subroutines: System and User Functions, Local Operator, Length, Parameter Lists, Lexical Variables, File Handles and File Tests: Opening and Closing a File handle.(8L)

Module III: Object-Oriented Perl and Perl-CGI: Introduction to Modules, Creating Objects and References. Anonymous Data types, CGI Programming: The CGI.pm Module, CGI Program in Context, Simple CGI Programs, Passing Parameters via CGI, Perl and the Web. (8L)

Module IV: Perl Programming Constructs for Bioinformatics: Representing String and Sequenced Data in Perl, Manipulation of Biological Sequences, Concatenating DNA Fragments, DNA to RNA Transcription, Translation, Reading Genes & Proteins from File, Finding Motifs, Counting Nucleotides and Composition Analysis. Reading FASTA files. Finding Open Reading Frame, Generating random DNA, RNA & Protein sequences. Parsing Genbank and PDB Files, Parsing BLAST Output. (8L)

Module V: BioPerl: BioPerl Overview, Installation Procedures; Fundamental Constructs and Special Features; BioPerl Modules, Creating BioPerl Objects. (8L)

Books

1. Learning Perl , Tom Phoenix, Randal L. Schwartz, Wiley Publications
2. Programming Perl , Tom Christiansen, brian d foy, Larry Wall, Jon Orwant, O'Reilly Publications
3. Perl Cookbook , Tom Christiansen, Nathan Torkington, O'Reilly Publications

COURSE INFORMATION SHEET

Course: ANALYTICAL TECHNIQUE IN BIOTECHNOLOGY

Course code: BT418
Course title: Analytical Techniques in Biotechnology
Pre- requisite(s):
Co- requisite(s): None
Credits: 3 L:3 T:0 P:0
Class schedule per week: 03
Class: MSc
Semester / Level: II/04
Branch: Bioengineering & Biotechnology
Name of Teacher:

Course Objectives:

This course enables the students to:

1.	The primary objectives of this course are to develop the skills to understand the theory and practice of bioanalytical techniques
2.	Additionally, an overview of the instruments used in isolation and separation of molecules will also be provided.
3.	To provide scientific understanding of analytical techniques and detail interpretation of results.
4.	This will enable the students to understand all subjects of Biotechnology as these tools and techniques will be used therein.

Course Outcomes:

At the end of the course, a student should be able to:

CO1	Familiarity with working principles, tools and techniques of analytical techniques.
CO2	Apprehend the functioning, maintenance and safety aspects of the apparatus used in a Biotechnology lab.
CO3	Assimilate the principles and applications of centrifuge, electrophoresis, chromatography and spectroscopy in research and related experiments.
CO4	To understand the strengths, limitations and creative use of techniques for problem solving.

SYLLABUS

Module I: Centrifugation Techniques and Imaging: Principle, instrument and application of steady state sedimentation, density gradient centrifugation, ultracentrifugation, Atomic Force Microscopy, Scanning & Transmission Electron Microscopy. **(8L)**

Module II: Electro-kinetics: Electro-osmosis and electrophoresis, Helmholtz-Smoluchowski equation, Zeta potential, Principle, Design & application of Gel electrophoresis; SDS PAGE, gradient gels, Two-dimensional gels, isoelectric focusing**. (8L)**

Module III: Chromatographic Techniques: Principles, design and application of column chromatography, partition and adsorption chromatography, Affinity Chromatography; Ion Exchange Chromatography, Gas Chromatography, HPLC. **(8L)**

Module IV: Spectroscopy -I**:** Beer's-Lambert's law, Principles, Instrumentation, and applications of Visible and UV Spectrophotometry; Spectrofluorimetry (FRET); FTIR, NMR spectroscopy.

Module V: Spectroscopy – II and Thermal Analysis: Principles, Instrumentation & applications for flame emission / atomic absorption spectrophotometry and their comparative study; ICP (b) Mass spectrometry; Principles, Instrumentation, and applications. Instrumentation and application of Differential scanning calorimetry and Thermogravimetry**. (8L)**

Textbook

1. K. Wilson & K.H. Goulding, A biologist's guide to Principles and Techniques of Practical Biochemistry. Cambridge University Press, 1994

Reference Book

1. Willard and Merrit, Instrumental Methods and Analysis, CBS Publishers & Distributors; 7th edition (December 1, 2004)
2. Ewing GW, Instrumental Methods of Chemical analysis. "McGraw-Hill Inc.