



SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY

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SCHOOL OF BIO AND CHEMICAL ENGINEERING

Department of Bioinformatics

1.1.2 Revised courses and newly introduced in 2022 -2023

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Department of Bioinformatics

MINUTES OF MEETING

Subject: Board of Studies- Department of Bioinformatics

Venue: Molecular Modelling Lab

Date: 13/06/2022

Agenda:

- Syllabus Revision
- New curriculum

The following members were present

Chairperson

Dr. Jemmy Christy, HOD, Dept of Bioinformatics, Sathyabama Institute of Science and Technology

Department Members

1. **Dr. D. Alex Anand,** Associate Professor
2. **Dr. Swetha Sunkar,** Associate Professor

Internal Members

1. **Dr.Elizabeth Junious,Assistant Professor, Hindustan Institute of Technology & Science**

A Meeting of the Board of Studies for the Department of Bioinformatics with external member was held on 13-06-22 at 1.30 p.m. to discuss about the revision in B.Sc Bioinformatics and Data science and M.Sc Bioinformatics and Data science curriculum.



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Minutes of the BOS meeting

- The Chairperson Dr. Jemmy Christy, welcomed the External and Internal members for the Board of Studies meeting held on 13 June 2022 at 1.30 PM.
- The curriculum was discussed which was appreciated by the members as the courses incorporated in B.Sc and M.Sc were much needed based on the current trend in research and industry.
- A detailed discussion on the course content was carried out to improvise further.
- Introduction and Review of Course Suggestions:
 - ♦ The meeting began with a brief introduction of the agenda and an overview of the suggested courses.
 - ♦ All attendees were in agreement that the proposed courses were relevant and would enhance the curriculum.
- Research Methodology as an Elective Paper:
 - ♦ It was unanimously agreed to include a course on Research Methodology as an elective paper.
 - ♦ The course will cover experimental design, data collection and analysis, literature review, hypothesis testing, and research ethics.
 - ♦ Emphasis will be placed on developing critical thinking and problem-solving skills in the research process.
- R Programming Lab with Exercises on Statistics in Biology:
 - ♦ The attendees agreed to include a lab-based course on R Programming with a focus on statistics in biology.
 - ♦ The course will cover basic programming concepts, data manipulation, visualization, and statistical analysis techniques using R.
 - ♦ Exercises will be designed to analyze biological datasets, perform statistical tests, and create data visualizations.



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- Incorporating More Student Activities:

- ◆ To increase student engagement and participation, it was decided to include various student activities throughout the courses.
- ◆ Examples of activities include group discussions, case studies, debates, presentations, and student-led projects.
- ◆ The aim is to encourage active learning, critical thinking, and collaboration among students.
- ◆ Recognizing the importance of teamwork and collaboration, it was decided to incorporate team-building activities into the curriculum.
- ◆ These activities will promote communication skills, leadership, and effective collaboration among students.

- Experiments Related to Cell Viability:

- ◆ It was suggested to include experiments related to cell viability, if feasible within the available resources and facilities.
- ◆ The attendees agreed that hands-on experiments in cell viability would provide valuable practical experience for the students.

- Introduction of Concepts Related to Metagenomics:

- ◆ The attendees agreed to introduce concepts related to Metagenomics in the curriculum.
- ◆ This will cover the study of genetic material recovered directly from environmental samples, providing insights into microbial communities and their functions.

- ◆ New elective course introduction - Students may also have the opportunity to explore specific areas of interest within health informatics through elective courses or specializations.
- ◆ Suggested course are Health Informatics, Big data in healthcare



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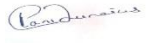
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- The chairperson also informed that complete revision of the syllabus will be carried out and new regulations will be followed from 2023 onwards for which the members were asked to give inputs in framing the syllabus and courses for UG and PG.
- She also suggested that there would be another meeting to discuss the courses for the forthcoming regulation

Meeting ended with vote of thanks.

Minutes approved.

Name of the members	Signature
Dr. C. Elizabeth Rani Juneius	
Dr. Jemmy Christy	
Dr. Alex Anand	
Dr. Swetha Sunkar	



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B.SC BIOINFORMATICS SYLLABUS REVISION

Before revision

SBIA1402	IMMUNOLOGY AND IMMUNOINFORMATICS	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

This course will enable the students to understand the immune system, its components and their functions

Unit I Introduction to immune system

9hrs

Innate and adaptive immune modulatory in vertebrates, Antigen processing and presentation Contemporary challenges to the immune system Infectious diseases Autoimmune diseases Categories of vaccines

Unit II Genetics of immunology

9hrs

Immunoglobulin classes and subclasses DR and LDR regions and sequence numbering, Immunogenetics & immunogenomics, Hybridoma technology: applications, Humanization of antibodies by design, Membrane receptors for antigen

Unit III Immune response

9hrs

The B-cell surface receptor for antigen (BCR), The T-cell surface receptor for antigen (TCR), The major histocompatibility complex (MHC) MHC polymorphism, Causes of MHC polymorphism, MHC supertypes, Epitopes, Affinity Maturation, Recognition of Antigen by B cells, Neutralizing Antibody

Unit IV Databases in immunology

9hrs

Databases in Immunology, Reverse vaccinology, rational vaccine design. Evolution and escape due to variations Immunoinformatics databases & tools IMGT & IEDB BciPep, Epitome, CED, AgAbDb

Unit V Computational immunology

9hrs

Reverse vaccinology and immunoinformatics, MHC- peptide, Specificity characterization, Ag-Ab: Sequential and conformational epitopes, HLA: nomenclature, HLA-peptide interactions & matrices, Epitope prediction algorithms: B-cell epitope predictions using sequence-based approaches, B-cell epitope predictions using structure-based approaches, T-cell epitope prediction methods



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After revision

SBIA1402	IMMUNOLOGY AND IMMUNOINFORMATICS	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

This course will enable the students to understand the immune system, its components and their functions

Unit I Introduction to immune system

9hrs

Innate and adaptive immune modulatory in vertebrates, Antigen processing and presentation
Contemporary challenges to the immune system Infectious diseases Autoimmune diseases Categories of vaccines

Unit II Genetics of immunology

9hrs

Immunoglobulin classes and subclasses, Immunogenetics & immunogenomics, Hybridoma technology: applications, Monoclonal antibodies applications, Membrane receptors for antigens

Unit III Immune response

9hrs

The B-cell surface receptor for antigen (BCR), The T-cell surface receptor for antigen (TCR), The major histocompatibility complex (MHC) MHC polymorphism, Causes of MHC polymorphism, MHC supertypes, Epitopes, Epitope mapping techniques

Unit IV Databases in immunology

9hrs

Databases in Immunology, IMGT resources for epitope mapping, Allergen related databases and IgE epitope mapping

Unit V Computational immunology

9hrs

Reverse vaccinology MHC- peptide, Specificity characterization, Ag-Ab: Sequential and conformational epitopes, HLA: nomenclature, HLA-peptide interactions & matrices, Epitope prediction algorithms: B-cell epitope predictions using sequence-based approaches, B-cell epitope predictions using structure-based approaches, T-cell epitope prediction methods



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Course outcomes

At the end of the course the students will

- C01** – Understand and explore sequence and structural databases relevant in the area of immunology
- C02** – Study informatics-based approaches for prediction of epitopes, design of vaccines and immuno-diagnostic tools
- C03** – Characterize and understand principles of antigen-antibody interactions
- C04** – Understand algorithms and methods for prediction of epitopes
- C05** – Explore and use approaches for vaccine design
- C06** – Implement various computational tools and approaches to understand immunological issues



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Before revision

SBIA1502	DRUG DESIGN AND DEVELOPMENT	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

To understand the basics of drug design and to know the significance of pharmacophores in drug design.

UNIT I Introduction to Drugs

9hrs

Drugs- Classification – Chemical basis of classification, Legal classification of drugs. Soft drugs and Hard drugs, Prodrugs – classification, Application

Unit II Drug Targets and Activity

9hrs

Drug targets - Enzymes, Receptors, Proteins, Nucleic acids, Lipids. Drug solubility - Effect of pH, Effect of polarity and pKa. Drug Metabolism - Absorption, Distribution, Metabolism, Elimination. Pharmacokinetics and Pharmacokinetics of drugs

UNIT III Drug Discovery

9hrs

Introduction to Drug Discovery and Development, stages of drug discovery, Natural sources of drugs, Computers in drug discovery, Rational approaches to lead discovery based on traditional medicine. ADME/T analysis, Oral bioavailability, Drug likeliness, Lipinski's rule.

Unit IV Drug Design

9hrs

Types of drug design- Rational drug design, Structure based – Receptor based and ligand based. Virtual Screening, Hit to Lead identification, Lead optimisation. Pharmacophore analysis and mapping.

Unit V Docking and QSAR

9hrs

Molecular docking – steps, types of docking, Pose identification, applications, software used. QSAR - origin & development, Physicochemical parameters, partition coefficient, Hammett's substitution constant, Taft steric constant, Hansch analysis, Free Wilson analysis, 3D QSAR methods CoMFA & CoMSIA.

Course Outcomes

At the end of the course the students will

CO1 –realize the concept of drugs and their classification

CO2 –explore the various targets of drugs and identify the factors influencing the activity

CO3 –Comprehend the process of drug discovery.

CO4 –Explore the drug design concept and they basics



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C05 –Appreciate the significance of docking and QSAR in drug design.

C06 –Create an approach to design drugs based on the structural knowledge available

Text / Reference Books

- 1) Shayne C. Gad, (2005), Drug Discovery Handbook, 2nd edition, John Wiley & Sons: New York.
- 2) Tudor I. Opera, (2005), Cheminformatics in Drug Discovery, 5th edition, John Wiley & Sons: New York.



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After revision

SBIA1502	DRUG DESIGN AND DEVELOPMENT	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

To understand the basics of drug design and to know the significance of pharmacophores in drug design.

UNIT I Introduction to Drugs

9hrs

Drugs- Classification – Chemical basis of classification, Legal classification of drugs. Soft drugs and Hard drugs, Prodrugs – classification, Application, Prodrug design and clinical application

Unit II Drug Targets and Activity

9hrs

Drug targets - Enzymes, Receptors, Proteins, Nucleic acids, Lipids. Drug solubility - Effect of pH, Effect of polarity and pKa. Drug Metabolism - Absorption, Distribution, Metabolism, Elimination. Pharmacokinetics and Pharmacokinetics of drugs. Tools and databases for PD/PK analysis

UNIT III Drug Discovery

9hrs

Introduction to Drug Discovery and Development, stages of drug discovery, Natural sources of drugs, Computers in drug discovery, Rational approaches to lead discovery based on traditional medicine Fragment based drug design approach

Unit IV Drug Design

9hrs

Types of drug design- Rational drug design, Structure based – Receptor based and ligand based. Virtual Screening, Hit to Lead identification, Lead optimisation. Pharmacophore mapping, softwares used for pharmacophore model generation

Unit V Docking and QSAR

9hrs

Molecular docking – steps, types of docking, Pose identification, applications, software used. QSAR - origin & development, Physicochemical parameters, 3D QSAR methods CoMFA & CoMSIA. Tools for QSAR model generation

Course Outcomes

At the end of the course the students will

CO1 –realize the concept of drugs and their classification

CO2 –explore the various targets of drugs and identify the factors influencing the activity

CO3 –Comprehend the process of drug discovery.

CO4 –Explore the drug design concept and they basics



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C05 –Appreciate the significance of docking and QSAR in drug design.

C06 –Create an approach to design drugs based on the structural knowledge available

Text / Reference Books

- 1) Shayne C. Gad, (2005), Drug Discovery Handbook, 2nd edition, John Wiley & Sons: New York.
- 2) Tudor I. Opera, (2005), Cheminformatics in Drug Discovery, 5th edition, John Wiley & Sons: New York.



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Before revision

SBIA1302	EVOLUTIONARY BIOLOGY	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

The students will be able to understand the basics of evolution and be able to perform evolutionary analyses using molecular data.

UNIT I INTRODUCTION

9hrs

Introduction - What Is Evolution? - The History of Evolutionary Thought - The Evidence for Evolution - From DNA to Phenotypes - Phylogenetics and the History of Life - Interpretation of Phylogenetic Trees - Molecular Clock Dating - Historical Biogeography - Phylogeography - Concepts in Character Macroevolution: Adaptation, Homology, and Evolvability - Using Phylogenies to Study Phenotypic Evolution: Comparative Methods and Tests of Adaptation - Taxonomy in a Phylogenetic Framework - The Fossil Record - Human Evolution

UNIT II Natural Selection and Adaptation

9hrs

Natural Selection and Adaptation, Natural Selection, Adaptation, and Fitness: Overview - Units and Levels of Selection - Theory of Selection in Populations Phenotypic Selection on Quantitative Traits - Responses to Selection: Experimental Populations - Responses to Selection: Natural Populations Evolutionary Limits and Constraints - Evolution of Modifier Genes and Biological Systems - Evolution of Form and Function - Biochemical and Physiological Adaptations

UNIT III Evolutionary Processes

9hrs

Evolutionary Processes - Genetic Drift - Mutation - Geographic Variation, Population Structure, and Migration - Recombination and Sex - Genetic Load - Inbreeding - Selfish Genetic Elements and Genetic Conflict - Evolution of Mating Systems: Outcrossing versus Selfing

UNIT IV Genes, Genomes, Phenotypes

9hrs

Genes, Genomes, Phenotypes, Molecular Evolution - Genome Evolution - Comparative Genomics - Evolution of Sex Chromosomes - Gene Duplication - Evolution of New Genes - Evolution of Gene Expression - Epigenetics - Evolution of Molecular Networks - Evolution and Development: Organisms - Evolution and Development: Molecules - Genetics of Phenotypic Evolution - Dissection of Complex Trait Evolution - Searching for Adaptation in the Genome - Ancient DNA

UNIT V Speciation and Macroevolution

9hrs

Speciation and Macroevolution - Species and Speciation - Speciation Patterns - Geography, Range Evolution, and Speciation - Speciation and Natural Selection - Speciation and Sexual Selection - Gene Flow, Hybridization, and Speciation - Coevolution and Speciation - Genetics of Speciation - Speciation and Genome Evolution - Adaptive Radiation - Macroevolutionary Rates - Macroevolutionary Trends - Causes and Consequences of Extinction - Species Selection - Key Evolutionary Innovations - Evolution of Communities



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Course outcomes

At the end of the course the students will

- C01** – describe the need for phylogenetic studies and understand its significance
- C02** – infer the different methods to infer phylogeny used across history
- C03** – Understand mechanisms of evolution.
- C04** – Understand the fundamentals of macroevolution and coevolution.
- C05** – Understand phylogeography, speciation and extinction.
- C06** – designing a protocol to study phylogenetics with a hypothesis.

TEXT / REFERENCE BOOKS

1. The Princeton Guide to Evolution, edited by David A. Baum, and Douglas J. Futuyma, Princeton University Press, 2013.
2. Davidson, Eric H., and Isabelle Peter. Genomic Control Process: Development and Evolution, Elsevier Science & Technology, 2015.
3. Why does Evolution Matter? The Importance of Understanding Evolution, edited by Gabriel Trueba, CambridgeScholars Publishing, 2014.
4. Martin, Lynn B., et al. Integrative Organismal Biology, John Wiley & Sons, Incorporated, 2014.
5. Wagner, Günter P. Homology, Genes, and Evolutionary Innovation, Princeton University Press, 2014.



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After revision

SBIA1302	EVOLUTIONARY BIOLOGY	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

The students will be able to understand the basics of evolution and be able to perform evolutionary analyses using molecular data.

UNIT I INTRODUCTION

9hrs

Introduction - What Is Evolution? - The History of Evolutionary Thought - The Evidence for Evolution - From DNA to Phenotypes – **origin of Prokaryotes and Eukaryotes** **taxonomy-the science of classification** - Molecular Clock Dating – Concepts in Character Macroevolution: Adaptation, Homology, and Evolvability- Using Phylogenies to Study Phenotypic Evolution: Comparative Methods and Tests of Adaptation - Taxonomy in a Phylogenetic Framework-The Fossil Record-Human Evolution

UNIT II Natural Selection and Adaptation

9hrs

Natural Selection and Adaptation – **Types of Natural selection**, Natural Selection, Adaptation, and Fitness: Overview - Units and Levels of Selection - Theory of Selection in Populations Phenotypic Selection on Quantitative Traits – **Hardy-Weinberg equilibrium and genetic drift**, Evolution of Modifier Genes and Biological Systems- Evolution of Form and Function-Biochemical and Physiological Adaptations

UNIT III Evolutionary Processes

9hrs

Evolutionary Processes-Genetic Drift-Mutation-Geographic Variation, Population Structure, and Migration-Recombination and Sex - Genetic Load - Inbreeding - Selfish Genetic Elements and **Selection of variants by environmental factors**, **Time scale, Convergence and Divergence in related traits**

UNIT IV Genes, Genomes, Phenotypes

9hrs

Evolution of gene families, Genes, Genomes, Phenotypes, **Phenotypic plasticity**- Molecular Evolution - Genome Evolution - Comparative Genomics - Evolution of Sex Chromosomes - Gene Duplication - Evolution of New Genes - Evolution of Gene Expression - Epigenetics – Evolution of Molecular Networks - Evolution and Development: Organisms - Evolution and Development: Molecules - Genetics of Phenotypic Evolution- **Evolution of developmental pathways**.

UNIT V Speciation and Macroevolution

9hrs

Speciation and Macroevolution - Species and Speciation - Speciation Patterns - Geography, Range Evolution, and Speciation-Speciation and Natural Selection-Speciation and Sexual Selection-Gene Flow, Hybridization, and Speciation-Coevolution and Speciation - Genetics of Speciation - Speciation and Genome Evolution - Adaptive Radiation - Macroevolutionary Rates - **Human evolution – a new kind of ape**, **Cancer evolution**

Course outcomes



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At the end of the course the students will

C01 – describe the need for phylogenetic studies and understand its significance

C02 – infer the different methods to infer phylogeny used across history

C03 – Understand mechanisms of evolution.

C04 – Understand the fundamentals of macroevolution and coevolution.

C05 – Understand phylogeography, speciation and extinction.

C06 – designing a protocol to study phylogenetics with a hypothesis.

TEXT / REFERENCE BOOKS

1. The Princeton Guide to Evolution, edited by David A. Baum, and Douglas J. Futuyma, Princeton University Press, 2013.
2. Davidson, Eric H., and Isabelle Peter. Genomic Control Process: Development and Evolution, Elsevier Science & Technology, 2015.
3. Why does Evolution Matter? The Importance of Understanding Evolution, edited by Gabriel Trueba, CambridgeScholars Publishing, 2014.
4. Martin, Lynn B., et al. Integrative Organismal Biology, John Wiley & Sons, Incorporated, 2014.
5. Wagner, Günter P. Homology, Genes, and Evolutionary Innovation, Princeton University Press, 2014.



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SBIA1304	PERL FOR BIOINFORMATICS	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

The student will be able to understand the basics of programming and use the Perl and its strengths for sequence manipulation and analysis.

UNIT I INTRODUCTION

9hrs

Biology and Computer Science - Getting Started with Perl - Perl's Benefits - Installing Perl - Running Perl Programs on various platforms - The Art of Programming - Programming Strategies - The Programming Process - Sequences and Strings - Representing Sequence Data - A Program to Store a DNA Sequence - Control Flow - Comments Revisited - Command Interpretation - Statements - Variables - Strings. **Error Handling in Perl: Techniques for managing and troubleshooting errors in Perl scripts - Perl and Regular Expressions: Advanced usage of regular expressions for complex string matching and manipulation - Debugging Perl Programs: Strategies and tools for debugging Perl code - Perl and JSON: Handling JSON data in Perl for modern data interchange -**

UNIT II STARTING TO CODE AND GETTING HELP

9hrs

Concatenating DNA Fragments - Transcription: DNA to RNA - Using the Perl Documentation - Calculating the Reverse Complement in Perl - Proteins, Files, and Arrays - Reading Proteins in Files - Arrays - scalar and List Context - Motifs and Loops - Flow Control - Conditional Statements - open and unless. **Perl Packages and Namespaces: Organizing code into packages for better code management - Perl and Bioinformatics Libraries: Introduction to other bioinformatics libraries in Perl - Perl Best Practices: Coding standards and best practices for writing efficient and readable Perl scripts**

UNIT III WRITING MORE CODE

9hrs

Finding Motifs - Regular Expressions - Counting Nucleotides - Exploding Strings into Arrays - Operating on Strings - Writing to Files - Subroutines and Bugs - Subroutines - Scoping and Subroutines - Command-Line Arguments and Arrays - Passing Data to Subroutines - Modules and Libraries of Subroutines - Fixing Bugs in Your Code - The Perl Debugger. **Perl and Multithreading: Introduction to multithreading in Perl for performance improvement. Perl and Multithreading: Introduction to multithreading in Perl for performance improvement - Perl and API Integration: Accessing web-based bioinformatics tools and databases via APIs - Perl Script Optimization: Techniques for optimizing Perl code for better performance**

UNIT IV MANIPULATING MACROMOLECULES AND DATABASES

9hrs

Mutations and Randomization - **A Program Using Randomization** - A Program to Simulate DNA Mutation - Generating Random DNA - Analyzing DNA - The Genetic Code - Hashes - **Data Structures and Algorithms for Biology** - A Gene Expression Database - Gene Expression Data Using Unsorted Arrays - Gene Expression Data Using Hashes - **Relational Databases** - Translating Codons to Amino Acids - Translating DNA into Proteins - Reading DNA from Files in FASTA Format - Reading Frames -



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Translating Reading Frames. Data Visualization with Perl: Generating graphs and plots for data visualization - Perl and Cloud Computing: Utilizing cloud resources for bioinformatics computations

UNIT V RESTRICTION MAPS, REGULAR EXPRESSIONS AND MORE

9hrs

Regular Expressions - Logical Operators and the Range Operator - Finding the Restriction Sites - Perl Operations – GenBank - GenBank Files - Libraries - Separating Sequence and Annotation - Parsing Annotations - When to Use Regular Expressions - Protein Data Bank – Recursion - PDB Files - PDB File Format - Parsing PDB Files – BLAST - String Matching and Homology - BLAST Output Files - Parsing BLAST Output - The *printf* Function – Bioperl - Bioperl Tutorial Script. Advanced BLAST Techniques: More in-depth usage of BLAST for sequence analysis - Perl and Metagenomics: Analyzing metagenomic data with Perl - Perl in Evolutionary Biology: Applications of Perl in phylogenetics and evolutionary studies

Course outcomes

- CO1 – Understand and write pseudo and code using Perl.
- CO2 – Write beginner level code in Perl for sequence manipulation.
- CO3 – Understand the deeper aspects of the Perl architecture and use them.
- CO4 – Identify the strengths of Perl and use them in sequence analysis.
- CO5 – Learn the fundamentals of object oriented Perl.
- CO6 – Learn to automate Perl for bioinformatics applications.

TEXT / REFERENCE BOOKS

1. James Tisdall. Beginning Perl for Bioinformatics. O'Reilly Media, Inc. October 2E001. ISBN: 0596000804
2. James Tisdall. Mastering Perl for Bioinformatics. O'Reilly Media. March 2010
3. Michalski, Brent, et al. Beginning Perl, John Wiley & Sons, Incorporated, 2012
4. Dwyer, Rex A. Genomic Perl: From Bioinformatics Basics to Working Code, Cambridge University Press, 2002.
5. Dominus, Mark Jason. Higher-Order Perl: Transforming Programs with Programs, Elsevier Science & Technology, 2005.



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After revision

SBIA1304	PERL FOR BIOINFORMATICS	L	T	P	Credits	Total Marks
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COURSE OBJECTIVES

The student will be able to understand the basics of programming and use the Perl and its strengths for sequence manipulation and analysis.

UNIT I INTRODUCTION

9hrs

Biology and Computer Science - Getting Started with Perl - Perl's Benefits - Installing Perl - Running Perl Programs on various platforms - The Art of Programming - Programming Strategies - The Programming Process - Sequences and Strings - Representing Sequence Data - A Program to Store a DNA Sequence - Control Flow - Comments Revisited - Command Interpretation – Statements – Variables – Strings- **Basic File Handling in Perl: This topic covers how to open, read, write, and close files in Perl. It's essential for handling biological data files, like DNA sequence files, in various formats - Introduction to Perl Libraries for Biology - Simple Data Analysis with Perl**

UNIT II STARTING TO CODE AND GETTING HELP

9hrs

Concatenating DNA Fragments - Transcription: DNA to RNA - Using the Perl Documentation - Calculating the Reverse Complement in Perl - Proteins, Files, and Arrays - Reading Proteins in Files – Arrays - scalar and List Context - Motifs and Loops - Flow Control - Conditional Statements - open and unless. **Basic Sequence Alignment in Perl: Introducing the fundamentals of sequence alignment using Perl. - Counting and Analyzing Amino Acids in Proteins: Focusing on how to use Perl to count the frequency of different amino acids in protein sequences. - reading protein data from files and performing basic statistical analyses - Visualizing Biological Data with Perl:**

UNIT III WRITING MORE CODE

9hrs

Finding Motifs - Regular Expressions - Counting Nucleotides - Exploding Strings into Arrays - Operating on Strings - Writing to Files - Subroutines and Bugs - Subroutines - Scoping and Subroutines - Command-Line Arguments and Arrays - Passing Data to Subroutines - Modules and Libraries of Subroutines - Fixing Bugs in Your Code - The Perl Debugger - **Pattern Matching and String Replacement: - common in bioinformatics for tasks like modifying DNA or protein sequences, or formatting data files - Introduction to BioPerl for Sequence Analysis: - BioPerl for common tasks like sequence alignment, accessing sequence databases, and performing basic genomic and proteomic analyses**



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UNIT IV MANIPULATING MACROMOLECULES AND DATABASES

9hrs

Mutations and Randomization - A Program to Simulate DNA Mutation - Generating Random DNA - Analyzing DNA - The Genetic Code - Hashes - A Gene Expression Database - Gene Expression Data Using Unsorted Arrays - Gene Expression Data Using Hashes - Translating Codons to Amino Acids - Translating DNA into Proteins - Reading DNA from Files in FASTA Format - Reading Frames - Translating Reading Frames - Implementing Genetic Algorithms in Perl - genetic algorithms and how they can be implemented in Perl - Visualizing Genetic Data and Sequences - generating graphical representations of DNA or protein sequences, visualizing mutations and alignments.

UNIT V RESTRICTION MAPS, REGULAR EXPRESSIONS AND MORE

9hrs

Regular Expressions - Logical Operators and the Range Operator - Finding the Restriction Sites - Perl Operations - GenBank - GenBank Files - Libraries - Separating Sequence and Annotation - Parsing Annotations - Protein Data Bank - Recursion - PDB Files - PDB File Format - Parsing PDB Files - BLAST - String Matching and Homology - BLAST Output Files - Parsing BLAST Output - The `printf` Function - Bioperl - Bioperl Tutorial Script - Contributions of Lincoln Stein and Jason Stajich - Integrating Perl with Other Bioinformatics Tools: - integrate and automate workflows involving various bioinformatics tools and databases. - using Perl scripts to interface with tools like RNA-seq data analysis pipelines, genome annotation software, or molecular modeling tools - Advanced Data Filtering and Processing with Perl: Focusing on advanced techniques for data filtering and processing using Perl in bioinformatics.

Course outcomes

- CO1 – Understand and write pseudo and code using Perl.
- CO2 – Write beginner level code in Perl for sequence manipulation.
- CO3 – Understand the deeper aspects of the Perl architecture and use them.
- CO4 – Identify the strengths of Perl and use them in sequence analysis.
- CO5 – Learn the fundamentals of object oriented Perl.
- CO6 – Learn to automate Perl for bioinformatics applications.

TEXT / REFERENCE BOOKS

1. James Tisdall. Beginning Perl for Bioinformatics. O'Reilly Media, Inc. October 2E001. ISBN: 0596000804
2. James Tisdall. Mastering Perl for Bioinformatics. O'Reilly Media. March 2010
3. Michalski, Brent, et al. Beginning Perl, John Wiley & Sons, Incorporated, 2012
4. Dwyer, Rex A. Genomic Perl: From Bioinformatics Basics to Working Code, Cambridge University Press, 2002.
5. Dominus, Mark Jason. Higher-Order Perl: Transforming Programs with Programs, Elsevier Science & Technology, 2005



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Before Revision

SBIA1503	SYSTEMS BIOLOGY	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

To understand the basic concepts in Systems Biology and to apply them to real life problems in biology and medicine.

UNIT I Biological Basis

9hrs

Introduction – systems understanding – what is systems biology? - Reductionism or holism? - Mechanism or emergentism? - Homeostasis or robustness? - What type of systems disease is cancer? - What are the challenges facing systems biology? - **is systems biology a scientific revolution**

UNIT II Integrative Analysis of Omics Data

9hrs

Integrative Analysis of Omics Data - Summary - Introduction - Omics Data and Their Measurement Platforms - Data Processing: Quality Assessment, Quantification, Normalization, and Statistical Analysis - Data Integration: From a List of Genes to Biological Meaning - **Outlook and Perspectives**

UNIT III Flux Analysis

9hrs

Flux Analysis in Biotechnology and Medicine - Introduction - Theoretical Foundations of Emerging Challenges - MFA - Metabolic Flux Analysis in Biotechnology - Metabolic Flux Analysis in Medicine - Metabolic Modelling for Design of Cell Factories - Building and Refining Genome-Scale Metabolic Models - Strain Design Algorithms - Case Studies

UNIT III Genome-Scale Metabolic Modelling

9hrs

Genome-Scale Metabolic Modelling and In silico Strain Design of Escherichia coli - The COBRA Approach - In silico Model-Based Strain Design of E. coli Cell Factories - **Future Directions of Model-Guided Strain Design in E. coli References** - Accelerating the Drug Development Pipeline with Genome-Scale Metabolic Network Reconstructions - Metabolic Reconstructions in the Drug Development Pipeline - The Human Reconstruction - **Community Models - Personalized Medicine**

UNIT IV Computational Modelling of Microbial Communities

9hrs

Computational Modelling of Microbial Communities - Ecological Models - Genome-Scale Metabolic Models - Drug Targeting of the Human Microbiome - The Human Microbiome - Association of the Human Microbiome with Human Diseases - Drug Targeting of the Human Microbiome - Future Perspectives.

UNIT V Modelling Biological Processes

9hrs

Signal Transduction - Toward Genome-Scale Models of Signal Transduction Networks - The Potential of Network Reconstruction - Information Transfer Networks - Approaches to Reconstruction of ITNs – Aging - Systems Biology of Aging - The Biology of Aging - The Mathematics of Aging - Future Challenges – Immune response - Modelling the Dynamics of the Immune Response - **Background - Dynamics of NF- κ B Signalling - JAK/STAT Signalling**

Course outcomes

At the end of the course the students will be able to

CO1 –To understand the basic concepts in Systems Biology

CO2 –To learn to apply systems biology to omics data.

CO3 –To appreciate the importance of flux balance analysis and its importance.

CO4 –To understand and perform genome scale modelling.



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CO5 –To learn model microbial communities and their interactions

CO6 –To model specific biological processes.

Text / Reference books

1. Nielsen, Jens, and Stefan Hohmann. Systems Biology, John Wiley & Sons, Incorporated, 2017.
2. Systems Biology, edited by Robert A. Meyers, John Wiley & Sons, Incorporated, 2012.
3. Systems Biology: Philosophical Foundations, edited by Fred C. Boogerd, et al., Elsevier Science & Technology, 2007.
4. Lodhi, Huma M., and Stephen H. Muggleton. Elements of Computational Systems Biology, John Wiley & Sons, Incorporated, 2010.
5. Ingalls, Brian P. Mathematical Modelling in Systems Biology: An Introduction, MIT Press, 2013.
6. Juan, Hsueh-Fen. Systems Biology: Applications in Cancer-Related Research, edited by Hsuan-Cheng Huang, World Scientific Publishing Co Pte Ltd, 2012.
- Young, Daniel L., and Seth Michelson. Systems Biology in Drug Discovery and Development, John Wiley & Sons, Incorporated, 2011.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks : 100

PART A : 10 questions of 2 marks each - No choice

PART B : 2 questions from each unit of internal choice; each carrying 16 marks

Exam Duration : 3 Hrs.

20 Marks

80 Marks



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After Revision

SBIA1503	SYSTEMS BIOLOGY	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

To understand the basic concepts in Systems Biology and to apply them to real life problems in biology and medicine.

UNIT I Biological Basis

9hrs

Introduction – systems understanding – what is systems biology? - Reductionism or holism? - Mechanism or emergentism? - Homeostasis or robustness? - What type of systems disease is cancer. **Challenges in systems biology studies. Case studies**

UNIT II Integrative Analysis of Omics Data

9hrs

Integrative Analysis of Omics Data - Summary - Introduction - Omics Data and Their Measurement Platforms - Data Processing: Quality Assessment, Quantification, Normalization, and Statistical Analysis - Data Integration: From a List of Genes to Biological Meaning – **Future perspectives of omics data analysis**

UNIT III Flux Analysis

9hrs

Flux Analysis in Biotechnology and Medicine - Introduction - Theoretical Foundations of Emerging Challenges - MFA - Metabolic Flux Analysis in Biotechnology - Metabolic Flux Analysis in Medicine - Metabolic Modelling for Design of Cell Factories - Building and Refining Genome-Scale Metabolic Models - Strain Design Algorithms - Case Studies

UNIT III Genome-Scale Metabolic Modelling

9hrs

Genome-Scale Metabolic Modelling and In silico Strain Design of Escherichia coli - The COBRA Approach - In silico Model-Based Strain Design of E. coli Cell Factories - Future Directions of Model-Guided Strain Design in E. coli References - Accelerating the Drug Development Pipeline with Genome-Scale Metabolic Network Reconstructions - Metabolic Reconstructions in the Drug Development Pipeline - The Human Reconstruction.. **Disease and therapeutic strategies based model generation**

UNIT IV Computational Modelling of Microbial Communities

9hrs

Computational Modelling of Microbial Communities - Ecological Models - Genome-Scale Metabolic Models - Drug Targeting of the Human Microbiome - The Human Microbiome - Association of the Human Microbiome with Human Diseases - Drug Targeting of the Human Microbiome – **Human microbiome and neurodegenerative disorders based case studies and future Perspectives.**

UNIT V Modelling Biological Processes

9hrs

Signal Transduction - Toward Genome-Scale Models of Signal Transduction Networks - The Potential of Network Reconstruction - Information Transfer Networks - Approaches to Reconstruction of ITNs – Aging - Systems Biology of Aging - The Biology of Aging - The Mathematics of Aging - Future Challenges – Immune response - Modelling the Dynamics of the Immune Response – **Diseases and associated pathway modelling and relevant mathematical approaches**

Course outcomes

At the end of the course the students will be able to

CO1 –To understand the basic concepts in Systems Biology

CO2 –To learn to apply systems biology to omics data.



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CO3 –To appreciate the importance of flux balance analysis and its importance.

CO4 –To understand and perform genome scale modelling.

CO5 –To learn model microbial communities and their interactions

CO6 –To model specific biological processes.

Text / Reference books

1. Nielsen, Jens, and Stefan Hohmann. Systems Biology, John Wiley & Sons, Incorporated, 2017.
 2. Systems Biology, edited by Robert A. Meyers, John Wiley & Sons, Incorporated, 2012.
 3. Systems Biology: Philosophical Foundations, edited by Fred C. Boogerd, et al., Elsevier Science & Technology, 2007.
 4. Lodhi, Huma M., and Stephen H. Muggleton. Elements of Computational Systems Biology, John Wiley & Sons, Incorporated, 2010.
 5. Ingalls, Brian P. Mathematical Modelling in Systems Biology: An Introduction, MIT Press, 2013.
 6. Juan, Hsueh-Fen. Systems Biology: Applications in Cancer-Related Research, edited by Hsuan-Cheng Huang, World Scientific Publishing Co Pte Ltd, 2012.
- Young, Daniel L., and Seth Michelson. Systems Biology in Drug Discovery and Development, John Wiley & Sons, Incorporated, 2011.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 questions of 2 marks each - No choice

20 Marks

PART B : 2 questions from each unit of internal choice; each carrying 16 marks

80 Marks



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Newly introduced Elective courses:

SBIA3007	BIGDATA IN HEALTHCARE	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

The course is designed to make the students realize the role and importance of big data in genomics and its implications for research in biology and medicine.

UNIT I Introduction

9hrs

Big Data - Big Data in Medicine? - The Three Vs of Big Data - Can Medicine Learn from Other Industries? - Big Data Framework in Medicine - Fields of Action in Medicine - It is Time for Big Data - The Example of Google Flu Trends - Big Data Adoption Model in Medicine - Big Data in the Context of Health - The Difference to Classic Clinical Analysis (Old Wine in New Bottles?) - Are Hospitals Prepared for Big Data? - Personalized Medicine and Big Data - The (Genetic) Human in Numbers - Big Data, "Personalized Medicine" and IT

UNIT II Data Management and Data Mining Approaches

9hrs

Data Management and Data Mining Approaches - Introduction Challenges of Managing and Mining Big Biomedical Data - Data Management Framework - Data Management Platforms - Data Mining in Translational Medicine - Data Mining Techniques and Methods - Big Data and Data Mining - Applications of Data Mining in Translational Medicine

UNIT III Information Management for Systems Medicine

9hrs

New Data Volumes - The Digitalization of the Knowledge Cycle - Consolidation of the Digital Medical Care and Research Systems - Integration and Differentiation - Good and Bad Data = Digital Expert Systems - Human Beings are More Than the Sum of Their Data - Medicine of the Person is Made More Difficult

UNIT IV Medical Big Data

9hrs

Medical Big Data - Data Protection - - Expectations - Legal Biological Principles - Data Sources - Health-Specific Use of Data - Risks - Data Protection Mechanisms - Data Economy in Particular - Transparency

UNIT V Big Data and Business

9hrs

Big Data in Healthcare from a Business perspective - Data as a Basis for Decisions - Strategy and Data - Big Data as a Part of Digitalization - Consulting as a Decision Support = The Path to an Informed Decision - The Transformation of Big Data to Smart Data - New Technologies in the Area of Big Data – Benefits to the patient.

Course Outcomes

CO1 –To understand the concept and nature of bigdata.

CO2 –To understand the basics of data management and mining approaches of genomic big data.

CO3 –To appreciate the role of bigdata in genomic medicine.

CO4 –Ethical use of medical bigdata.

CO5 –Use of genomic bigdata in entrepreneurship.

CO6 –Appreciate the enormous data available and the means to handle the data



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Text /Reference books

1. Big Data in Medical Science and Healthcare Management : Diagnosis, Therapy, Side Effects, edited by Peter Langkafel, De Gruyter, Inc., 2015.
2. Translational Medicine : Tools and Techniques, edited by Aamir Shahzad, Elsevier Science & Technology, 2015.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 questions of 2 marks each - No choice

20 Marks

PART B : 2 questions from each unit of internal choice; each carrying 16 marks

80 Marks



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SBIA3010	Health Informatics	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

- To Introduce the students the problems and challenges that confront the field of health informatics.
- To Introduce the students about the research avenues and salient features in the practice of health informatics.
- To Provide the students with the basic skills and knowledge in health informatics to apply in a career related to health care.
- To Lead students in the discussion around ethical and diversity issues in health informatics.
- To Provide additional direction to those interested towards the study in the field.

UNIT I Introduction & Overview: Health Information Technology & Health Informatics 9 Hrs.

Define information management, information technology and informatics - Various ways in which HIT has evolved to improve quality or enhance patient safety - Informatics drivers and trends - Standards development organizations: Health Level 7 (HL-7), Healthcare Information Technology Standards Panel (HITSP), and Office of the National Coordinator for Health Information Technology (ONC) Health IT Standards Committee-Health informatics – Needs, objectives and limitations - Medical Terminology for Health Informatics Professionals.

UNIT II Clinical Decision Support Systems (CDSS) And Workflow 9 Hrs.

Fundamental requirements of an effective Clinical Decision Support System-principles of health care data exchange and health care data standards relate to patient care, productivity and data analysis- common controlled vocabularies in use today: ICD, CPT, NDC, RxNorm, LOINC and SNOMED CT-advantages and disadvantages (unintended consequences) of Clinical Decision Support Systems (CDSS) in terms of cognitive support.

UNIT III Healthcare Database Management System 9 Hrs.

Health information systems – design, architecture and interoperability - Electronic health records (EHRs) - Electronic medical record (EMR) with electronic health record (EHR)- emergence of Personal Health Records and their implications for patients, health care providers and Decision Aids and health systems- EHR access agreement.

UNIT IV Computer Applications In Health Care And Biomedicine 9 Hrs.

The language of biomedical informatics: data, information & knowledge; standards and vocabularies - Evidence based practice (EVP) and clinical practice guidelines (CPG) - Evaluation methods for health informatics - Machine learning for extraction of medical knowledge - MATLAB programming for health informatics.

UNIT V Case Studies And Ethical Issues 9 Hrs.

Modelling, simulation and visualisation in health informatics - Ethical Issues in Health Informatics - Fundamentals of data science in medicine - Genomic and Systems Medicine - Advanced data analysis in medicine - Data driven decision making and evaluation in medicine - Legal Aspects of Health Information Systems - E-Healthcare & Ethics - E-Medicine Business Models - Case Studies in Health Information Management.

Max. 45 Hrs.

COURSE OUTCOMES

On completion of the course, student will be able to



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CO1 - Develop knowledge about problems and challenges that health addressed by informatics and apply the knowledge to the research and practice in health informatics.

CO2 - Demonstrate basic skills and knowledge in health informatics for application in future health-related careers.

CO3 - Demonstrate ability to ask, search for information and answer health-related questions.

CO4 - To identify genomic variants associated with a disease phenotype and communicate this association.

CO5 - Perform visualization and simple analysis of a data set to assess difficulty of predicting disease (cardiovascular and other) risk in a synthetic patient dataset.

CO6 - Apply communication skills through an interview with an informatics professional and development of a written summary and analyse ethical and diversity issues in health informatics.

TEXT / REFERENCE BOOKS

1. Hoyt, RE and Yoshihashi, A, Eds. (2014). Health Informatics: Practical Guide for Healthcare and Information Technology Professionals, 6th Edition. Pensacola, FL, Lulu.com.
2. Wager KA, Lee FW, Glaser JP. Health Care Information Systems: A Practical Approach for Health Care Management. San Francisco, California: Jossey-Bass 2009.
3. Shortliffe EH, Cimino JJ. Biomedical Informatics: Computer Applications in Health Care and Biomedicine, 4th Edition. New York, New York: Springer Science +Business Media, LLC 2014.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks : 100

PART A : 10 questions of 2 marks each - No choice

PART B : 2 questions from each unit of internal choice; each carrying 16 marks

Exam Duration : 3 Hrs.

20 Marks

80 Marks



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M.SC BIOINFORMATICS SYLLABUS REVISION

Before revision

SBIA5304	MICROARRAY DATA ANALYSIS	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

Students are allowed to understand the key concepts of class comparison and class discovery of genes.

UNIT I GENE EXPRESSION

Basics of Gene expression- definition , gene expression studies, gene expression patterns- Applications of gene expression studies- Microarrays – definition , discovery, technique, making microarrays, spotted microarrays, In-situ synthesized oligonucleotide arrays, inkjet array synthesis, Affymetrix techniques, DNA CHIP technology, photolithography, spot quality, sample preparation and labelling, washing, image acquisition Sequencing by Hybridization Arrays- DNA MassArray™ Technology- Printing DNA Microarrays-Types of microarrays - **Designing a microarray experiment**

UNIT II IMAGE PROCESSING

Image processing, feature extraction, identifying positions of features- Normalisation – data cleaning and transformation, within array normalization, between array normalization, measuring and quantifying microarray variability **-variability between replicate features on an array-, variability between hybridizations to different arrays** Analysis of differentially expressed genes- significance analysis of microarrays.

UNIT III PREDICTION

Prediction of cross hybridization to related genes, thermodynamics of nucleic acid duplexes, prediction of Tm- probe secondary structure. **Analysis of relationships between genes, tissues or treatments- similarity of gene or sample profiles -dimensionality reduction- principal component analysis, hierarchical clustering, machine learning methods for cluster analysis. Classification of tissues and samples – validation.**

UNIT IV CARBOHYDRATE MICROARRAYS

Carbohydrate microarrays- Carbohydrate sources- **Synthesis of oligosaccharides - Isolation of oligosaccharides from natural sources- Arrays of monosaccharides and disaccharides- Arrays of polysaccharides- Arrays of oligosaccharides- Perspectives- DNA micro array analysis-clustering-immunological applications.**

UNIT V DATABASES AND TOOLS FOR MICROARRAYS



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Bioinformatics in Arrays- Databases and tools for microarrays- Bioconductor, expression profiler, EST databases- Assessing levels of gene expression using EST's, TIGR gene indices, STACK, SAGE, CGAP, Xprofiler, ARRAY DB, cluster, tree view, Scanalyze, gene cluster, informatics aspects of microarray production- MGED and gene-ontology, description of MIAME ((Minimum Information About a Microarray Experiment), Business Aspects of Biochip Technologies- Microarray Technology in Treating Disease.

COURSE OUTCOMES

At the end of the course the students will be able to

- CO 1-** To learn the basics of DNA Microarray and its applications
- CO 2-** To learn how to Analyse of the raw RNA sequence data
- CO 3-** To understand why Statistical computing and Statistical Genetics is required
- CO 4-** To apply data analysis to microarray related concepts
- CO 5-** To apply the finding of the analytics in healthcare
- CO 6-** To develop novel algorithms in the area

TEXT / REFERENCE BOOKS

Dov Stekel - Microarray bioinformatics, Cambridge,

Steen Knudsen - A Biologist's Guide to analysis of DNA microarraydata, second edition, John Wiley & Sons, Inc.,

Andreas D Baxeavanis and BF Francis Ouelette - Bioinformatics: A Practical Guide to the Analysis of Gene and Proteins , Wiley-Interscience,

David W. Mount - Bioinformatics: Sequences and genome analyses, Cold Spring Harbor Laboratory press,



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After revision

SBIA5304	MICROARRAY DATA ANALYSIS	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

Students are allowed to understand the key concepts of class comparison and class discovery of genes.

UNIT I GENE EXPRESSION

Basics of Gene expression- definition , gene expression studies, gene expression patterns- Applications of gene expression studies- Microarrays – definition , discovery, technique, making microarrays, spotted microarrays, In-situ synthesized oligonucleotide arrays, inkjet array synthesis, Affymetrix techniques, DNA CHIP technology, photolithography, spot quality, sample preparation and labelling, washing, image acquisition Sequencing by Hybridization Arrays- DNA MassArray™ Technology- Printing DNA Microarrays-Types of microarrays

UNIT II IMAGE PROCESSING

Image processing, feature extraction, identifying positions of features- Normalisation – data cleaning and transformation, within array normalization, between array normalization, **LIMMA algorithms, R packages for microarray data normalization** measuring and quantifying microarray variability Analysis of differentially expressed genes- significance analysis of microarrays. **Web resources for differential expression analysis**

UNIT III PREDICTION

Prediction of cross hybridization to related genes, thermodynamics of nucleic acid duplexes, prediction of T_m- probe secondary structure. dimensionality reduction- **Feature extraction and algorithms used in feature extraction**, principal component analysis, hierarchical clustering, machine learning methods for cluster analysis. **Case studies in cancer biology**

UNIT IV CARBOHYDRATE MICROARRAYS

Carbohydrate microarrays- Carbohydrate sources- Arrays of polysaccharides- Arrays of oligosaccharides- Perspectives- DNA micro array analysis **Protein microarray role in COVID research, Protein microarray role in cancer biomarker research**

UNIT V DATABASES AND TOOLS FOR MICROARRAYS

Bioinformatics in Arrays- Databases and tools for microarrays- Bioconductor, expression profiler, EST databases- Assessing levels of gene expression using EST's, TIGR gene indices, STACK, SAGE, CGAP, Xprofiler, ARRAY DB, cluster, tree view, Scanalyze, gene cluster, informatics aspects of microarray production- MGED and gene-ontology, description of MIAME



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((Minimum Information About a Microarray Experiment), Business Aspects of Biochip Technologies- Microarray Technology in Treating Disease.

COURSE OUTCOMES

At the end of the course the students will be able to

- CO 1-** To learn the basics of DNA Microarray and its applications
- CO 2-** To learn how to Analyse of the raw RNA sequence data
- CO 3-** To understand why Statistical computing and Statistical Genetics is required
- CO 4-** To apply data analysis to microarray related concepts
- CO 5-** To apply the finding of the analytics in healthcare
- CO 6-** To develop novel algorithms in the area

TEXT / REFERENCE BOOKS

Dov Stekel - Microarray bioinformatics, Cambridge,

Steen Knudsen - A Biologist's Guide to analysis of DNA microarraydata, second edition, John Wiley & Sons, Inc.,

Andreas D Baxeavanis and BF Francis Ouelette - Bioinformatics: A Practical Guide to the Analysis of Gene and Proteins , Wiley-Interscience,

David W. Mount - Bioinformatics: Sequences and genome analyses, Cold Spring Harbor Laboratory press,



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Before – Revision

SBIA5301	SYSTEMS BIOLOGY	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

The course aims to provide an overview of systems biology and the state-of-the-art methods that can be used to study this novel approach.

UNIT I INTRODUCTION

Multiscale Computational Modelling - **Proteomics** - Computational Systems Biology and Aging - Computational Systems Biology in Drug Design - Software Tools for Systems Biology.

UNIT II MODELS IN SYSTEMS BIOLOGY

The Parameter Problem and the Meanings of Robustness - Models as Dynamical Systems - Continuous Models - Discrete Models - The Parameter Problem - **Parameter phobia** - **Measuring and Calculating - Counter Fitting - Beyond Fitting** - The Landscapes of Dynamics - Qualitative Dynamics - Steady State Attractors of ODE Models - **The Meanings of Robustness** - Parameter Biology - Robustness to Initial Conditions - Robustness in Reality - Structural Stability - Classifying Robustness - Rule-Based Modelling and Model Refinement - A Simple Cascade - A (Natural) Computing Perspective on Cellular Processes - **Cell Cycle and Breast Tumor Growth Control**

UNIT III BIOLOGICAL NETWORK INFERENCE

Reconstruction of Biological Networks by Supervised Machine Learning Approaches - Graph Reconstruction as a Pattern Recognition Problem - Problem Formalization - Graph Inference as a Pattern Recognition Problem - Graph Inference with Local Models and Global Models - Examples - Reconstruction of a Metabolic Network - Reconstruction of a PPI Network - **Reconstruction of Gene Regulatory Networks**

UNIT IV GENOMICS AND COMPUTATIONAL SYSTEMS BIOLOGY

From DNA Motifs to Gene Networks: A Review of Physical Interaction Models - Physical Basis of Transcription Regulation and Representation of DNA Patterns - Physical Interaction Algorithms - Genomic Signatures and a Space of Genomes for Genome Comparison - Study of Metabolic Networks Through Sequence Analysis and Transcriptomic Data.

UNIT V SOFTWARE TOOLS FOR SYSTEMS BIOLOGY

ALIBABA: A Text Mining Tool for Systems Biology - Validation Issues in Regulatory Module Discovery - Computational Imaging and Modelling for Systems Biology.

COURSE OUTCOMES

The students will be able to



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CO 1- Learn the basics of computational modelling.

CO 2- Characterise the various models in biology.

CO 3- Relate the role of carbohydrates and lipids in the functioning of the system. CO 4- Understand the basics of network biology and its uses in systems science CO 5- Appraise the right approach to study models in biology

CO 6- Summarize the various tools and databases of relevance.

TEXT / REFERENCE BOOKS

1. Lodhi, Huma M., and Stephen H. Muggleton. Elements of Computational Systems Biology, John Wiley & Sons, Incorporated, 2010.
2. Nielsen, Jens, and Stefan Hohmann. Systems Biology, John Wiley & Sons, Incorporated, 2017.
3. Juan, Hsueh-Fen. Systems Biology: Applications in Cancer-Related Research, edited by Hsuan-Cheng Huang, World Scientific Publishing Co Pte Ltd, 2012.
4. Young, Daniel L., and Seth Michelson. Systems Biology in Drug Discovery and Development, John Wiley & Sons, Incorporated, 2011.



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New Course

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After – Revision

SBIA5301	SYSTEMS BIOLOGY	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

The course aims to provide an overview of systems biology and the state-of-the-art methods that can be used to study this novel approach.

UNIT I INTRODUCTION

Systems biology – Definition and avenues in modern science, Multiscale Computational Modelling - Proteomics - Computational Systems Biology and Aging - Computational Systems Biology in Drug Design - Software Tools for Systems Biology.

UNIT II MODELS IN SYSTEMS BIOLOGY

The Parameter Problem and the Meanings of Robustness - Models as Dynamical Systems - Continuous Models - Discrete Models - The Parameter Problem — Fitting in biology The Landscapes of Dynamics - Qualitative Dynamics - Steady State Attractors of ODE Models - - Parameter Biology - Robustness to Initial Conditions - Robustness in Reality - Structural Stability - Classifying Robustness - Rule-Based Modelling and Model Refinement -A Simple Cascade - A (Natural) Computing Perspective on Cellular Processes -Computational modeling of cell cycle pathways

UNIT III BIOLOGICAL NETWORK INFERENCE

Reconstruction of Biological Networks by Supervised and unsupervised Machine Learning Approaches - Graph Reconstruction as a Pattern Recognition Problem - Problem Formalization - Graph Inference as a Pattern Recognition Problem - Graph Inference with Local Models and Global Models - Examples - Reconstruction of a Metabolic Network - Reconstruction of a PPI Network. Literature studies related to biological network

UNIT IV GENOMICS AND COMPUTATIONAL SYSTEMS BIOLOGY

From DNA Motifs to Gene Networks: A Review of Physical Interaction Models - Physical Basis of Transcription Regulation and Representation of DNA Patterns - Physical Interaction Algorithms - Genomic Signatures and a Space of Genomes for Genome Comparison - Study of Metabolic Networks Through Sequence Analysis and Transcriptomic Data. Tools and databases in genomic regulation related studies

UNIT V SOFTWARE TOOLS FOR SYSTEMS BIOLOGY

ALIBABA: A Text Mining Tool for Systems Biology - Validation Issues in Regulatory Module Discovery - Computational Imaging and Modelling for Systems Biology. Cytoscape modules for systems biology, Cytoscape plug in for network construction

COURSE OUTCOMES



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The students will be able to

CO 1- Learn the basics of computational modelling.

CO 2- Characterise the various models in biology.

CO 3- Relate the role of carbohydrates and lipids in the functioning of the system. CO 4- Understand the basics of network biology and its uses in systems science CO 5- Appraise the right approach to study models in biology

CO 6- Summarize the various tools and databases of relevance.

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3. Juan, Hsueh-Fen. Systems Biology: Applications in Cancer-Related Research, edited by Hsuan-Cheng Huang, World Scientific Publishing Co Pte Ltd, 2012.
4. Young, Daniel L., and Seth Michelson. Systems Biology in Drug Discovery and Development, John Wiley & Sons, Incorporated, 2011.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

PART A: 6 Questions for 5 Marks each –without choice

PART B: 2 Questions from each unit with internal choice, each carrying 14 marks

Exam Duration: 3 Hrs.

30 Marks

70 Marks



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Before – revision

SBIA5303	MACHINE LEARNING FOR BIOINFORMATICS	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

- To enable the student to understand the modelling methods, such as supervised classification and clustering along with the application of probabilistic graphical models for knowledge discovery, as well as deterministic and stochastic heuristics for optimization.

UNIT 1 MACHINE LEARNING

Machine-Learning Foundations: The Probabilistic Framework -Introduction: Bayesian modeling - The Cox Jaynes axioms - Bayesian inference & induction - Model structures: graphical models & other tricks - Probabilistic Modelling & Inference: Examples -The simplest sequence models - Statistical mechanics Machine Learning Algorithms - Introduction -Dynamic programming -Gradient descent -EM/GEM algorithms –Markov chain Monte- Carlo methods - Simulated annealing – Evolutionary & genetic algorithms. Learning algorithms: miscellaneous aspects.

UNIT 2 SUPPORT VECTOR MACHINE (SVM)

SVM: introduction – architecture – kernel - ROC – feature selection – sensitivity – specificity – accuracy – implementation - svm applications in sequence analysis, structure prediction , drug design –svm light - libsvm – weka.

UNIT 3 NEURAL NETWORKS

Neural Networks: The Theory - Introduction - Universal approximation properties – Priors & likelihoods - Learning algorithms: backpropagation - Sequence correlations & neural networks – Prediction of protein secondary structure - Prediction of signal peptides & their cleavage sites - Applications for DNA & RNA nucleotide sequences - Prediction performance evaluation - Different performance measures - Perceptrons and Multilayer Perceptrons - Neural Networks in Drug Design.

UNIT 4 HIDDEN MARKOV MODELS

Hidden Markov Models: The Theory - Introduction -Prior information & initialization -Likelihood & basic algorithms - Learning algorithms -Applications of HMMs: general aspects -Protein applications - DNA & RNA applications

UNIT 5 PROBABILISTIC GRAPHICAL MODELS

Probabilistic Graphical Models in Bioinformatics - Markov models & DNA symmetries - Markov models & gene finders - Hybrid models & neural network parameterization of graphical models -The single-model case – Bi-directional recurrent neural networks for protein secondary structure prediction

TEXT / REFERENCE BOOKS

- Pierre Baldi and Soren Brunak, Bioinformatics: the Machine Learning Approach – Publisher: MIT Press, 1998.
- David W Mount, Bioinformatics: sequence and genome analysis, 2nd edition, CBS publishers, 2004.
- Zupan J., Gasteiger J.- Neural Networks in Chemistry and Drug Design. Wiley-VCH, 2000.



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After – Revision

SBIA5303	MACHINE LEARNING FOR BIOINFORMATICS	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

- To enable the student to understand the modelling methods, such as supervised classification and clustering along with the application of probabilistic graphical models for knowledge discovery, as well as deterministic and stochastic heuristics for optimization.

UNIT 1 MACHINE LEARNING

Machine-Learning Foundations: The Probabilistic Framework -Introduction: Bayesian modeling - Bayesian inference & induction - Model structures: graphical models - Probabilistic Modelling & Inference: Examples -The simplest sequence models - Statistical mechanics Machine Learning Algorithms - Introduction -Dynamic programming -Gradient descent -EM/GEM algorithms –Markov chain Monte- Carlo methods - Simulated annealing – Evolutionary & genetic algorithms.

UNIT 2 SUPPORT VECTOR MACHINE (SVM)

SVM: introduction – architecture – kernel - ROC – feature selection – sensitivity – specificity – accuracy – implementation - svm applications in sequence analysis, structure prediction , drug design –svm light - libsvm – weka. Data mining in bioinformatics using WEKA, methods and validation procedures in WEKA

UNIT 3 NEURAL NETWORKS

Neural Networks: The Theory - Introduction - Universal approximation properties — Learning algorithms: backpropagation - Neural Networks: Applications - Sequence encoding & output interpretation- Sequence correlations & neural networks – Prediction of protein secondary structure - Prediction of signal peptides & their cleavage sites - Applications for DNA & RNA nucleotide sequences - Prediction performance evaluation - Different performance measures - Perceptrons and Multilayer Perceptrons -Neural Networks in Drug Design. multi-layer perceptron to identify origins of replication in eukaryotes

UNIT 4 HIDDEN MARKOV MODELS

Hidden Markov Models: The Theory - Introduction -Prior information & initialization -Likelihood & basic algorithms - Learning algorithms -Applications of HMMs: general aspects -Protein applications - DNA & RNA applications - Advantages & limitations of HMMs – tools – Gene prediction and Profile HMMs

UNIT 5 PROBABILISTIC GRAPHICAL MODELS



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Probabilistic Graphical Models in Bioinformatics - Markov models & DNA symmetries - Markov models & gene finders - Hybrid models & neural network parameterization of graphical models -The single-model case – Bi-directional recurrent neural networks for protein secondary structure prediction ■
GRNs and PPI networks

TEXT / REFERENCE BOOKS

4. Pierre Baldi and Soren Brunak, Bioinformatics: the Machine Learning Approach – Publisher: MIT Press, 1998.
5. David W Mount, Bioinformatics: sequence and genome analysis, 2nd edition, CBS publishers, 2004.
6. Zupan J., Gasteiger J.- Neural Networks in Chemistry and Drug Design. Wiley-VCH, 2000.



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SCHOOL OF BIO AND CHEMICAL ENGINEERING

Department of Bioinformatics

MINUTES OF MEETING

Subject: Board of Studies- Department of Bioinformatics

Venue: Molecular Modelling Lab

Date: 28/01/2023

Agenda:

- New curriculum
- Introduction and review of AICTE and UGC norms for curriculum revision
- Discussion on necessary changes to comply with AICTE and UGC guidelines
- Proposal for revised B.Sc and M.Sc curriculum structure and content
- Assigning responsibilities and timelines for curriculum development

The following members were present

Chairperson

Dr. Jemmy Christy, HOD, Dept of Bioinformatics, Sathyabama Institute of Science and Technology

Department Members

3. **Dr. D. Alex Anand**, Associate Professor
4. **Dr. Swetha Sunkar**, Associate Professor

External Members

2. **Dr.Elizabeth Junious,Assistant Professor, Hindustan Institute of Technology & Science**

A Meeting of the Board of Studies for the Department of Bioinformatics with BOS members was held on 28-01-23 at 1.30 p.m. to discuss about the complete revision in B.Sc Bioinformatics and Data science and M.Sc Bioinformatics and Data science curriculum.



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Minutes of the BOS meeting

- The Chairperson Dr. Jemmy Christy, welcomed the members for the Board of Studies meeting held on 28-01-2023 at 1.30 PM.
- The curriculum was discussed which was appreciated by the members as the courses incorporated in B.Sc and M.Sc were much needed based on the current trend in research and industry.
- Introduction and Review of AICTE and UGC Norms for Curriculum Revision:
 - The meeting commenced with an introduction to the agenda and a thorough review of the AICTE and UGC norms for curriculum revision.
 - Attendees were provided with copies of the guidelines and given time to familiarize themselves with the requirements.
 - An interactive session followed the familiarization period, where attendees shared their initial thoughts, concerns, or suggestions regarding the AICTE and UGC norms.
 - Discussions centered around potential challenges and opportunities in aligning the curriculum with the regulatory requirements.
- Discussion on Necessary Changes to Comply with AICTE and UGC Guidelines:
 - A comprehensive discussion was held regarding the necessary changes to align the B.Sc and M.Sc curricula with the AICTE and UGC guidelines.
 - Attendees identified the key areas that require revision, such as updated industry-oriented topics, skill development, research focus, and interdisciplinary approaches.
 - Emphasis was placed on integrating emerging technologies, including data analytics, artificial intelligence, and Internet of Things, into the curriculum.
- Proposal for Revised B.Sc and M.Sc Curriculum Structure and Content:



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- Based on the discussions, a proposal for the revised B.Sc and M.Sc curriculum structure and content was presented.
- The proposal suggested a modular approach to provide flexibility for students to choose from a variety of electives and specialization tracks.
- It recommended the inclusion of practical training, internships, and industry collaborations to enhance industry readiness and practical skills.
- The importance of research projects and dissertations to foster research aptitude among students was highlighted.
- The credits for PG was set from 75 to 85 while UG course was 120 to 125.
- The members were advised to develop the curriculum inclusive of these categories



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Table 2: Minimum Credit Requirements to Award Degree under Each Category

S. No.	Broad Category of Course	Minimum Credit Requirement	
		3-year UG	4-Year UG
1	Major (Core)	60	80
2	Minor Stream	24	32
3	Multidisciplinary	09	09

University Grants Commission

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4	Ability Enhancement Courses (AEC)	08	08
5	Skill Enhancement Courses (SEC)	09	09
6	Value Added Courses common for all UG	06 - 08	06 – 08
7	Summer Internship	02 - 04	02 – 04
8	Research Project / Dissertation	-	12
	Total	120	160

Note:* Honours students not undertaking research will do 3 courses for 12 credits in lieu of a research project / Dissertation.



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- The members were also informed to prepare the courses based on these points including the latest content that caters to the industry and research needs
- Assigning Responsibilities and Timelines for Curriculum Development:
 - Responsibilities for curriculum development were assigned to respective faculty members and subject experts.
 - Each faculty member was tasked with revising the syllabi for their respective courses to comply with AICTE and UGC guidelines.
 - Timelines were established for syllabi revision, curriculum compilation, and submission for approval.
- The members were informed that there would be a BOS meeting with external members in June 2023 for their approval.

The meeting was adjourned, acknowledging the commitment and active participation of all attendees in revising the B.Sc and M.Sc curriculum to comply with UGC norms and ended with vote of thanks.

Minutes approved.

Name of the members	Signature
Dr. C. Elizabeth Rani Juneius	



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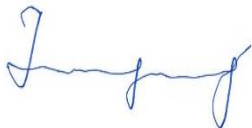
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Dr. Jemmy Christy	
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