

MATHEMATICS DEPARTMENT

M.TECH. COMPUTATIONAL AND SYSTEM BIOLOGY

**Course of Study & Scheme of Examination
2016-17**



**Maulana Azad National Institute of Technology,
Bhopal**

M.TECH - COMPUTATIONAL & SYSTEMS BIOLOGY
(FULL- TIME)

Course No.	Subject	No. of Duration of Theory Paper				Credits		Total Credits
		L	P	No.	Hrs.	L	P	
I SEMESTER								
CSB-501	Foundations of Computational & Systems Biology	3		1	3	3	-	3
CSB -502	Applied Bioinformatics	3		1	3	3	-	3
CSB -503	Mathematical and Computational Biology	3		1	3	3	-	3
CSB - 511 CSB - 512	ELECTIVE-I	3		1	3	3	-	3
CSB - 513 CSB - 514	ELECTIVE-II	3		1	3	3	-	3
CSB - 515 CSB - 516	OPEN ELECTIVE-I	3		1	3	3	-	3
CSB -541	LAB-Practice-I	-	2	-	-	-	2	2
CSB -542	Seminar-I	-	2	-	-	-	2	2
	Total	18	4	-	-	18	04	22
II SEMESTER								
CSB -551	Mathematical Modeling & Simulation of Biological Systems	3	-	1	3	3	-	3
CSB -552	Petri Net Models in Biology	3	-	1	3	3	-	3
CSB -553	Data Warehousing & Data Mining	3	-	1	3	3	-	3

Scheme and Syllabus M.Tech. Computation and System Bioinformatics (BOS dt. 29.09.2016)

CSB -561	ELECTIVE-III	3	-	1	3	3	-	3
CSB -562								
CSB -563	ELECTIVE-IV	3	-	1	3	3	-	3
CSB -564								
CSB -565	OPEN ELECTIVE-II	3	-	1	3	3	-	3
CSB -566								
CSB -591	LAB-Practice-II	-	2	-	-	-	2	2
CSB -592	Seminar-II	-	2	-	-	-	2	2
	Total	18	4	-	-	18	04	22
III SEMESTER								
CSB -648	Major Project Dissertation Phase-I	-	-	-	-	-	23	23
	Total	-	-	-	-	-	23	23
IV (FINAL) SEMESTER								
CSB -698	Major Project Dissertation Phase-II	-	-	-	-	-	23	23
	Total	-	-	-	-	-	23	23

M.TECH - COMPUTATIONAL & SYSTEMS BIOLOGY

List of Electives Semester I

I SEMESTER – ELECTIVE - I

S.No.	Subject	Subject code
1.	Optimization.	CSB -511
2.	Dynamic Systems with Application to Biology & Medicine.	CSB -512

I SEMESTER – ELECTIVE - II

S.No.	Subject	Subject code
1.	Omic Data and Quantitative System Biology.	CSB -513
2.	Algorithmic Bioinformatics.	CSB -514

I SEMESTER – OPEN ELECTIVE - I

S.No.	Subject	Subject code
1.	Biophysics of Molecules and Molecular Mechanics.	CSB -515
2.	Computational Biology & Computational Biochemistry.	CSB -516

SYLLABUS

M.TECH - COMPUTATIONAL & SYSTEMS BIOLOGY FIRST SEMESTER

SUBJECT : **FOUNDATION OF COMPUTATIONAL & SYSTEMS BIOLOGY**

SUBJECT CODE: **CSB-501**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Introduction to Computational Biology & Systems Biology, Biology in time and space. Models and Modeling: purpose, adequateness, advantage of computational modeling, basic notion for computational models, model scope, statements, system state, variables parameters constants, behavior, classification, steady states. Fundamentals of Nucleic acid and protein sequence analysis. Analysis of complex biological systems Sequencing (DNA & amino acid) and Micro array. Protein structure analysis. Genome assembly

Tools and Databases Computational gene hunting (gene predication -HMM) Alignment of bio-molecular sequences (Local, Global, DP, Blast, multiple) their principles and methods. Motif finding. structural modeling and structure prediction Network modeling. Genomic regulation Protein folding Genetic variation RNA world Systems Biology (gene, protein and membrane machine)--Human and Pathogens--Cancer genomics (Tumor complexity)--Gene regulatory network Codon optimization Algorithmic Drug designs. Current and emerging areas in the field of computational and systems biology.

REFERENCES:

1. Systems Biology: A Textbook by Edda Klipp, Wolfram Liebermeister, Wiley BlackWell
2. Pavel A. Pevzner, Computational Molecular Biology, An Algorithmic Approach, The MIT press, 2001
3. Neil C. Jones and Pavel A. Pevzner, An Introduction to Bioinformatics Algorithms, Indian reprint by Ane Books, 2005
4. Nello Cristianini and Matthew W. Hahn, Introduction to Computational Genomics: A Case Studies Approach, 2007, Cambridge University Press

SUBJECT : APPLIED BIOINFORMATICS

SUBJECT CODE: CSB-502

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Overview of Bioinformatics. Data Acquisition, Database Content, Database Structure and Annotation: Biological Data Mining: Introduction to Nucleic Acid and Protein Sequence DataBanks: Database Searching by Similarity: Pair wise sequence alignment: Advance Similarity and Multiple sequence alignments:Patterns, Motifs and Profiles in sequences:

Introduction to Phylogenetics: Introduction to Structural Bioinformatics: Introduction to following: Hidden Markov Model (HMM) & its Application. Microbial Genomics, Metabolic Flux Analysis.

REFERENCES:

- Introduction to Bioinformatics By T. K. Attawood & D.J. Parry-smith
- Bioinformatics By Arthur Lesk.
- Instant notes in Bioinformatics by S. Sundara rajan & R. Balaji
- Bioinformatics – A Practical guide to the analysis of Genes and Proteins, Andreas Baxevanis, Francis Quellerie.
- Introduction to Computational Biology: An evolutionary approach by Bernhard Haubold, Thomas Wiehe, Birkhauser Verlag

SUBJECT : **MATHEMATICAL & COMPUTATIONAL BIOLOGY**

SUBJECT CODE: **CSB-503**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Introduction to Mathematical Modelling and concepts, Modeling process, probabilities and rates, model classes. Discrete Time Models: Scalar Discrete-Time models, Systems of Discrete-Time Equation. Ordinary Differential Equation: Introduction, Scalar equation, systems of equation (reaction kinetics, interaction model for two population, epidemic model, nondimensionalization), Qualitative analysis of 2X2 systems, general system of three or more equation, discrete time model from continuous time model, elementary bifurcations. Partial Differential Equations: Partial Derivative, age structured model, reaction diffusion equation. Stochastic Models: introduction, markov chains, random variables, diffusion process, branching process, linear birth and death process. Cellular Automata and Related Models: Wolframs Classification, theoretical results, Greenberg-Hastings Automata, Generalized cellular automata. Estimating Parameters: Likelihood function, stochastic models without measurement error, deterministic models, Model comparison (Akaike information criterion, likelihood ratio test for nested models, cross validation), Optimization algorithm (algorithms, positivity). Maple Course: constant, functions, data sets, linear regression, discrete dynamical systems (ricker model, procedures in maple, feigenbaun diagram and bifurcation analysis), stochastic models with maple, ODEs (application to epidemic model), PDEs (age structured model), stochastic model (common cold in household) Development of Dynamic System, analytical tools. Initial value problems, boundary value problems and calculus of variations. Mathematics of chemical reaction network. Finite difference methods for parabolic equations in 1D – explicit methods and implicit methods. Von Neumann stability Analysis. Solution of tridiagonal systems

Finite difference methods for parabolic equations in 2D.

REFERENCES:

- A course in Mathematical Biology: Quantitative Modeling with mathematical and Computational by Gerda, Thomas, Mark, Birgitt, CRC.
- Introduction to Computational Biology: An evolutionary approach by Bernhard Haubold, Thomas Wiehe, Birkhauser Verlag
- Finite Difference Schemes and Partial Differential Equations, SIAMS 2004 J.C. Strikwerda.
- Principles of Computational Cell Biology: From Protein Complexes to Cellular networks by Volkhard Helms, Wiley-WCH.

ELECTIVE-I

SUBJECT : **OPTIMIZATION**

SUBJECT CODE: **CSB-511**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

I. Introduction to Optimization and Mathematical Preliminaries.

II. Introduction to Linear Programming and Simplex Method.

III. Assignment and Transportation Model.

IV. Integer programming, Dynamic Programming.

V. Non Linear Programming, Goal Programming, Multiobjective Programming, PERT, CPM.

VI. Games Theory, Sequencing and Replacement.

REFERENCES:

- Engineering Optimization: Theory and practice, 3rd edition by Sinqiresu S. Rao, John Wiley.
- A first course in optimization theory, by Rangarajan K. Sundaram, Cambridge University Press.
- Introduction to Graph Theory by Robin J. Wilson, Prentice Hall.
- Graph Theory Application by Foulds, Springer.
- S.D. Sharma Operations Research, Kedarnath Ramnath & Co. Meerut
- P.K.Gupta & D.S.Hira Operations Research, S.Chand & Co.
- Kantiswaroop Operations Research, S.Chand & Sons.
- Gillet, B.E. Introduction to operations Research - A Computer Algorithm Approach, McGraw Hill.

SUBJECT : DYNAMIC SYSTEMS WITH APPLICATION TO BIOLOGY & MEDICINE

SUBJECT CODE: CSB-512

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Dynamic Models: Descriptive Vs mechanistic, Bathtub models, physical model, optimization model, theoretical vs practical model Matrix Models and Structured Population Dynamics. Membrane Channel and action potential. Cellular dynamics: pathway to gene expression Dynamical system. Differential Equation models for Infectious Disease

Spatial patterns in Biology Agent based other Computational models for Complex Systems.

Building Dynamic Model. One Dimensional Flow, Bifurcation, Flows in Circle Two Dimensional Flow Linear systems, phase plane, limit cycle. One Dimensional Maps

REFERENCES:

- Dynamic Models in Biology by Stephen P Ellner, John Guckenheimer, Princeton University Press
- Non Linear Dynamics and Chaos: with application to Physics, Biology, Chemistry and Engineering.

ELECTIVE-II

SUBJECT : **OMIC DATA & QUANTITATIVE SYSTEMS BIOLOGY**

SUBJECT CODE: **CSB-513**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Omic Technologies, data and Bioinformatics principles. Data standards for omic data: the basis of data sharing and reuse.

Omic data management and annotation. Data and knowledge management in cross omics research projects Statistical analysis principles for omic data. Statistical methods and models for Bridging Omics data levels Analysis of time course omic datasets The use and abuse of Omics Computational analysis of High Throughput Sequencing Data Analysis of SNP in case control studies. Bioinformatics for Copy Number Variation Data Processing ChIP-Chip Data Insights into Global Mechanisms and Disease by Gene Expression Profiling. Bioinformatics for RNomics. Bioinformatics for Qualitative and Quantitative Proteomics Bioinformatics for Mass spectrometry Based Metabolomics. Computational Analysis Workflows for Omics Data Interpretation. Integration, Warehousing, and Analysis Strategies of Omic Data. Integrating Omic Data for signaling pathways, interactome reconstruction and functional analysis. Network Inference from Time Dependent Omics data. Omics and Literature Mining.

Omics-Bioinformatics in the context of clinical data Omics-Based Identification of Pathophysiological Processes. Data Mining Methods in Omics-Based Biomarker Discovery. Integrated Bioinformatics analysis for cancer target identification. Omics-Based molecular target and Biomarker identification. Fundamental Concepts of Quantitative Biology: Free energies, landscapes and fitness in Evolution Dynamics, System design Principles, chance and memory, information theory and adaptation. Quantitative Methods: quantitative in vitro Biochemistry, small angle scattering, subcellular signaling dynamics, single cell behavior. Biophysical models to predict the functions of common genetic parts used in Synthetic Biology, Modeling Cellular Variability.

Molecular & Cellular Systems: PKA: prototype for dynamic signaling in time and space, stochastic simulation of the phage lambda gene regulatory circuitry, chemotaxis.

REFERENCES:

- Bioinformatics for Omics Data Methods and Protocols by Bernd Mayer, Springer
- Quantitative Biology: from molecular to cellular systems by Michael E Wall, Chapman & Hall/CRC.

ELECTIVE-II

SUBJECT : **ALGORITHMIC BIOINFORMATICS** SUBJECT CODE: **CSB-514**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Introduction and Basic Algorithms. String Algorithms. Dynamic Programming Algorithm for Biological Sequence and Structure Comparison. Graph Theoretical Approaches to Delineate Dynamics of Biological Processes. Sorting and FFT-Based Techniques in the Discovery of BioPatterns. Genome and Sequence Analysis. Molecular Structures. Topological Indices in CoCSBnatorial Chemistry. Efficient Algorithms for Structural Recall in Database. Ontology

REFERENCES:

- Bioinformatics Algorithms – Techniques and Applications, Edited by Ion I. Mandoiu and Alexander Zelikovsky, Wiley.
- Algorithmic Aspects of Bioinformatics by Hans Joachim Bockenhauer, Dirk Bongartz, Springer.
- Ontologies for Bioinformatics by Kenneth Baclawski and Tianhua Niu, MIT Press.
 - Anatomy Ontologies for Bioinformatics Principles and Practice by Burger Albert, Davidson Duncan, Springer.

OPEN ELECTIVE-I

SUBJECT : **BIOPHYSICS OF MOLECULES & MOLECULAR MECHANICS** SUBJECT CODE:
CSB-515

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Introduction DNA Proteins Models. Time in Biology. Membrane and membrane transport. Energy and Entropy. Protein-DNA interactions its thermodynamics. Molecular Motors. Ligand receptor binding.

Boltzman distribution, free energy of dilute solutions. Law of Mass action with Cooperativity, Hemoglobin introduction.. Dimoglobin ligand receptor binding and Hemoglobin ligand receptor binding.

Water: Introduction, Life in water (Molecular forces and experiments). Diffusion, First Mean Passage Time, Electrostatic in Salty Solutions.

REFERENCES:

- Physical Biology of the Cell by Phillips, Kondev, Theriot (Garland Science)
- Molecular Biology of Cell by Bruce Alberts.
- Biological Physics by Philip Nelson.
- Random Walks in Biology by Howard Berg.
- Mechanics of Motor Proteins and the Cytoskeleton by Jonathon Howard.

OPEN ELECTIVE-I

SUBJECT : **COMPUTATIONAL BIOLOGY & COMPUTATIONAL BIOCHEMISTRY**

SUBJECT CODE: **CSB-516**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Introduction to Computational Biology and Computational Biochemistry. Analysis and Management of Biological & Biochemical Data. Internet Resources – Biological & Biochemical Exploration. Biochemical Compounds – **Structure and Analysis**. Dynamic Biochemistry. Genomics. Proteomics.

Molecular Modeling. Comparative Features. Structure and Function Assignment and Prediction. Protein Interactions. Molecular Design, Foldamers.

REFERENCES:

- Introduction to Computational Biology by Bernhard Haubold, Thomas Wiehe
- Introduction to Computational Biochemistry by C. Stan Tsai, Wiley
- Structural Bioinformatics by Philip E. Bourne, Wiley.
- Bioinformatics by Andreas Baxevasis.
- Lehninger Principles of Biochemistry, Nelson, Cox.
- Foldamers – Structure, Properties & Applications, Edited by Stefan Hecht & Ivan Huc, Wiley-VCH, 2007.

FIRST SEMESTER

SUBJECT : LAB PRACTICE-I

SUBJECT CODE: CSB-541

CREDITS : 2

PERIOD PER WEEK : Practical - 04

Maximum Marks : End Term –60 , Continuous Evaluation –40

Lab on Computational & Systems Biology. Matlab

SUBJECT : SEMINAR-I

SUBJECT CODE: CSB-542

CREDITS : 2

Maximum Marks : 100

Seminar on Computational & Systems Biology.

SECOND SEMESTER

SUBJECT : **MATHEMATICAL MODELING AND SIMULATION OF BIOLOGICAL SYSTEMS**

SUBJECT CODE: **CSB-551**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Mathematics: Linear Modeling & equation, Gaussian elimination algorithm, systematic solution, matrices, ODE, Difference equation, Graph and network theory Introduction Systems elements and units. Idealization and simplification. First & Second Order Systems, System analogies and equations. Control system. ordinary differential equations, partial differential equations, partial functional differential equations and optimal control theory. steady state and fixed points, stability, numerical solution, creating a mathematical model, modelling and simulating dynamical systems, running simulation. Algorithms for modeling and simulation of biological systems: application to gene regulatory network. continuous, stochastic or Boolean models Mathematical frame work of generalized kinetic theory. Models of system: systems, models modeling, classification, constraint on model structure, misuses of model. Modelling process Qualitative & Quantitative Model Formulation. Numerical Techniques. Parameter Estimation. Model Validation, Analysis. Applications: Photosynthesis & Plant Growth, Hormonal Control, Population and Individual, Chemostat, Diseases, Spatial pattern & processes, scaling models, chaos in biology, cellular automata and recursive growth, evolutionary computation. Modeling of Biochemical Systems, Specific Biochemical Systems. Model Fitting. Analysis of High Throughput Data. Gene Expression model. Stochastic Systems and variability. Optimality and Evolution

Simulation.

Components of Modeling and Simulation System. Modeling and Simulation Processes. Computer Simulation Analysis. Simulation Perspective – Continuous, Discrete, Hybrid discrete/continuous.

Numeric Consideration – Errors, Differential Equations and Integration, Random Numbers. Algorithms – Monte Carlo Method, Metropolis Algorithm. Simulation for conformational analysis, *Ab initio*, DFT and semi-empirical methods, Design of ligands. Foundation of Biomolecular Simulation – classical versus quantum description, statistical mechanics of biomolecules (eg. canonical ensemble, ergodicity), Assumption in biomolecular simulation. Modeling Interactions in Proteins – Bond length & bond angle potential, dihedral angle potential, non bonded interactions. Computation of non bonded energy terms – distance cut-offs, ewald method for electro static interaction, implicit solvent model. Molecular Dynamics Simulation – Idea of MD, structure of MD code (Initialization, force computation, numerical integration of Newton equation of motion(verlet algorithm), constraints in MD (RATTLE, SHAKE)), MD program packages (CHARMM, NAMD, AMBER).

REFERENCES:

- A course in mathematical Biology by Gerda de vries
- D. Frankel and B. Smit "Understanding Molecular Simulations: From Algorithms to Applications"
- Systems Biology: A Textbook by Edda klipp, Willey BalckWell
- D. J. Higham, N. J. Higham: Matlab Guide, SIAM, 2000.
- Matlab & Simulink Guide, The MathWorks, Inc. 2004
- F. Brauer, C. Castillo-Cháves : Mathematical Models in population Biology and Epidemiology, Springer, 2000.
- P. Fishwick: Dynamic Modeling, SCS, 2002
- J. Wu: Theory and applications of partial functional differential equations, Springer, Applied Math. Sciences, 1996
- Mathematical modeling of Complex Biological Systems by Abdelghani Bellouquid and Marcello Delitala, Springer.
- Modelling Biological Systems by James W. Haefner, Springer

SECOND SEMESTER

SUBJECT : **PETRI NET MODELS IN BIOLOGY**

SUBJECT CODE: **CSB-552**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Petri Net Basics: Places, Transitions, Arcs 7 Tokens. Properties of Petri Nets: Sequential Execution, Synchronization, Merging, Concurrency & Conflict. Vector & Matrix Representations of Petri Nets. Mathematical Properties of Petri Nets: Reachability, Liveness & Boundedness. Petri Net Modeling Models of Real Life Systems like Vending Machine, Simple Assembly Lines, Simple Discrete-Event Scenarios. Qualitative and Quantitative Petri Net Analysis.

Static structure of Petri Nets, Dynamic Behavior of Petri Nets, Analysis Techniques, Petri Nets as a modeling techniques for system biology. Modelling Technique: Discrete modeling, modeling regulatory network, hybrid functional Petri Net with extension for Dynamic Pathway Modeling, stochastic modeling, qualitative analysis, Fuzzy modeling Topological analysis of metabolic and regulatory network, Analysis of dynamical models of signaling networks with Petri Nets and Dynamic Graphs, A modular, qualitative modeling of regulatory networks using Petri nets, prediction of network structure.

REFERENCES:

- Petri Net Theory & Modeling of Systems by J.L. Peterson, Prentice Hall.
- Elements of Computational Systems Biology by Huma m Lodhi, Stephen H Muggleton, Wiley
- Modeling in System Biology: The Petri Net Application by Ina Koch, Wolfgang Reisig, Falk, Springer.

SECOND SEMESTER

SUBJECT : DATA WAREHOUSING AND DATA MINING

SUBJECT CODE: CSB-553

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

I. Data Mining.

- Background, Introduction to Data mining in Bioinformatics.
- Data Cleaning, Data Preprocessing, Data Integration and transformation, data reduction, Discretization and concept Hierarchy Generation, Data mining primitives, Data Description for data mining (clustering and link analysis).
- Types of Data Mining, Data Mining query language, Architectures of data mining.
- Exploration of data mining tools for biodata analysis.
- Data mining process model.
- Data generation & Summarization based characterization, Analytical characterization, mining class comparisons, and mining descriptive statistical measures in large data bases.
- Mining Association Rules in large databases: Association rule mining, single dimensional Bookan association rules from Transactional DBS, Multi level association rules from transaction DBS, multidimensional association rules from relational DBS and DWS, Correlation analysis, Constraint based association mining.
- Data Mining Applications.
- Mining BioLiterature: Towards Automatics Annotation of Genes and Proteins.

II. Data Warehousing.

- What's in a Data Warehouse, expectation from data warehouse.
- Need for data warehouse, definition, goals of data warehouse.
- Data Warehouse Architecture, Data extraction, movement and loading process, Data Mart, clean and transform data, star, snowflake and galaxy schemas for multidimensional databases, fact and dimension data, Designing fact tables. Partitioning, partitioning strategy – horizontal partitioning, vertical partitioning.
- Relational Database, Data Warehouse and OLAP technology,
- Multidimensional data models and different OLAP operations,
- OLAP Server: ROLAP, MOLAP and HOLAP.
- Data warehouse implementation, efficient computation of data cubes, processing of OLAP queries, indexing OLAP data.
- Data Privacy in Data Warehouse.

III. Classification and Prediction.

Scheme and Syllabus M.Tech. Computation and System Bioinformatics (BOS dt. 29.09.2016)

- Introduction to classification: Naïve Bayes and Nearest Neighbour.
- Using Decision Trees for Classification, Decision Tree Induction,
- Back Propagation, Bayesian classification, classification based on Association Rules.
- Prediction, classifier accuracy, Estimating the predictive Accuracy of a classifier.
- Cluster analysis, partitioning and hierarchical methods, Density based methods Grid based methods, web mining, Temporal and spatial data mining.

REFERENCES:

- Modeling in System Biology: The Petri Net Application by Ina Koch, Wolfgang Reisig, Falk, Springer.
- Elements of Computational Systems Biology by Huma m Lodhi, Stephen H Muggleton, Wiley.

ELECTIVE-III

SUBJECT: **BIOINFORMATICS FOR SYSTEMS BIOLOGY** SUBJECT CODE: **CSB-561**

PERIOD PER WEEK: Lecture –03; CREDITS: **3**

Maximum Marks: End Term –60, Continuous Evaluation –40

Life of a Cell and its Analysis: Structure and Function of the Nucleus and Cell Organelles.- Transcription and the Control of Gene Expression.- RNA Processing and Translation.- DNA Replication, Recombination, and Repair.- Cell signalling.- Epigenetics of Spermiogenesis: combining in silico and proteomic approaches in the mouse model.- Genomic Tools for Analyzing Transcriptional Regulatory Networks.-

Statistical Tools and Their Application: Probability and Hypothesis Testing.- Stochastic Models for Biological Patterns.- Population Genetics.- Statistical tools for gene expression analysis and system biology and related web resources.-

Transcriptome Analysis: What goes in is what comes out: How to design and implement a successful microarray experiment.- Tools and Approaches for an End-to-End Expression Array Analysis.- Analysis of alternative splicing with microarrays.

Structural and Functional Sequence Analysis: An Introduction to Multiple Sequence Alignment — and the T-Coffee Shop. Beyond just aligning sequences: how good can you make your alignment, and so what?.- A spectrum of phylogenetic-based approaches for predicting protein functional sites.- The role of Transcription Factor Binding Sites in Promoters and Their In Silico Detection.- In silico Discovery of DNA Regulatory Sites and Modules.-

Literature Mining for Association and Meaning: Mining the Research Literature in Systems Biology.- GoPubMed: Exploring PubMed with Ontological Background Knowledge.- BiblioSphere - Hypothesis Generation in Regulatory Network Analysis.- Biological Knowledge Extraction.-

Genomic Databases: Using KEGG in the Transition from Genomics to Chemical Genomics.- Ensembl: Open-Source Software for Large-Scale Genome Analysis.- Management of spatially organised biological data using EMAGE.- Equality of the sexes? Parent-of-origin effects on transcription and de novo mutations.-

Biological Networks: Methods for Structural Inference and Functional Module Identification in Intracellular Networks.- Methods for Dynamical Inference in Intracellular Networks.- ASIAN: Network Inference Web Server.- Bridging the Gap: Bioinformatics for Metabolomics.- Virtual Reality Meets Functional Genomics.- Systems Biology of Personalized Medicine.

REFERENCES:

- Bioinformatics for Systems Biology by Stephen Krawetz, Human Press

ELECTIVE-III

SUBJECT: **COMPUTATIONAL NEUROSCIENCE**

SUBJECT CODE: **CSB-562**

PERIOD PER WEEK: Lecture –03;

CREDITS: **3**

Maximum Marks: End Term –60, Continuous Evaluation –40

Introduction: Structure and functions of Neurons, passive electrical properties of neurons, signal spread, principles of electrical circuits, the cable equation, electrical models of real neurons, ion permeability and membrane potential at equilibrium: the Nernst equation, the Nernst plank equation.

Ion pumps and homeostasis: sodium and potassium, the sodium pumps, the potassium pumps, calcium, anions, the regulation of pH, action potential, Hadgkin Huxley experiments, Hadgkin Huxley model, the mechanism of action potential.

The structure and function of voltage gated channels: structure of sodium and potassium channels, the channel pore, mechanism of activation and inactivation, the diversity of voltage gated channels: sodium channel, potassium channel, calcium channel.

Pre Synaptic mechanism of synaptic transmission, gap junctions, electrical synapses, modulation of electrical synapses, chemical synapses and the calcium hypothesis. Excitatory transmission, Acetyl choline and cholinergic transmission, glutamate and glutametergic transmission, inhibitory transmissions, structure of GABA receptor and Glycine receptor

REFERENCES:

1. Molecular and cellular physiology of neurons by Gordon L. Fain.
2. Brain facts by Candle.

SECOND SEMESTER

ELECTIVE-IV

SUBJECT: **PATTERN RECOGNITION AND MACHINE LEARNING**

SUBJECT CODE: **CSB-563**

PERIOD PER WEEK: Lecture –03;

CREDITS: **3**

Maximum Marks: End Term –60, Continuous Evaluation –40

Introduction to Machine Learning (ML). ML Foundation: the probabilistic framework. Probabilistic Modeling and Inference. ML Algorithms: Dynamic Programming, Gradient Descent, EM. Neural Network theory and application. Hidden Markov Model theory and application.

Probabilistic graphical models in bioinformatics. Probabilistic models of evolution. Stochastic grammars and linguistics. Microarray and gene expression. Feature selection for proteomic and genomic data mining.

REFERENCES:

1. Molecular and cellular physiology of neurons by Gordon L. Fain.
2. Brain facts by Candle.

SECOND SEMESTER

ELECTIVE-IV

**SUBJECT: ARTIFICIAL INTELLIGENCE, SOFT COMPUTING &
NEURAL NETWORK**

SUBJECT CODE: CSB-564

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Introduction to AI various types of production system. Analysis of problem for developing an AI system. Problem characteristics, Production system and its characteristics. BFS, DFS, and Different heuristic search techniques- Hill climbing, Ascent Hill climbing, Constraint satisfaction. A* algorithm AO* Algorithm,

Knowledge Representation: Representation and mappings, Approaches to knowledge representation, Issue in knowledge representation, Knowledge representation using predicate logic resolution, and unification algorithm. Knowledge representation using rules procedural versus declarative knowledge logic programming, Forward and back ward reasoning. Symbolic reasoning under uncertainty monotonic and non monotonic reasoning. Semantic nets, Frames Conceptual dependency.

Natural language processing and study of its different phases, Game planning Minimax Search procedure, Adding Alpha Beta cut-offs, Iterative deepening Planning components of planning system Goal stack planning Nonlinear and Hierarchical planning.

Statistical reasoning Probability and Bayes Theorem Certainty factor and rule base system Bayesian Networks Dempster Shafer Theory Fuzzy Logic. Understanding Parallel and distributed AI Psychological Modeling, Parallelism in reasoning system.

Introduction to learning, various learning techniques Introduction to Expert System. Connectionist Model Hopfield networks learning in Neural Networks Application Common Sense Common Sense ontologies and Memory organizations

REFERENCES:

1. AI by Rich & Knight.
2. AI by Norwing.

SECOND SEMESTER

OPEN ELECTIVE-II

SUBJECT: **STOCHASTIC AND STATISTICAL METHODS IN SYSTEMS
BIOLOGY**

SUBJECT CODE: **CSB-565**

PERIOD PER WEEK: Lecture –03 ;

CREDITS : **3**

Maximum Marks: End Term –60, Continuous Evaluation –40

I. Stochastic

Modelling and Networks. Introduction to Biological modeling: why stochastic modeling necessary, modeling genetic and Biochemical networks, modeling higher level systems. Representation of Biochemical Networks: coupled chemical reaction, graphical representation, stochastic process algebra, System Biology Markup Language (SBML). Probability Models: Probability, discrete probability models, discrete uniform distribution, binomial-geometric-poisson distribution, Continuous probability models, uniform-exponential-normal-gamma distribution., quantifying “noise”. Stochastic Simulation: Introduction, Monte Carlo integration, uniform random number generation, transformation methods, lookup methods, rejection samplers, importance resampling, Poisson process, R statistical programming language, analysis of simulation output. Markov process: finite discrete time markov chains, markov chains with continuous state space, markov chains in continuous time, diffusion process.

Chemical and Biochemical Kinetics: classical continuous deterministic chemical kinetics, molecular approach to kinetics, mass action stochastic kinetics, Gillespie algorithm, stochastic Petri nets, structuring stochastic simulation codes, rate constant conversion, Kolmogorov's equations and other analytic representations, software for simulating stochastic kinetic networks.

Case studies: Dimerisation kinetics, Michaelis Menten enzyme kinetics, auto regulatory genetic network, lac operon. Bayesian inference and MCMC: Likelihood and Bayesian inference, Gibbs sampler, Metropolis-Hastings algorithm, Hybrid MCMC schemes, Bayesian inference for latent variable models. Inference for stochastic kinetic models: inference given complete data, discrete-time observations of the system state, diffusion approximations for inference, Likelihood free methods, network inference and model comparison.

II. Statistical

Introduction to statistical methods for complex systems: class comparison, prediction, discovery. Bayesian Inference and Computation. Data Integration towards understanding biological complexity: storing knowledge, data integration.

Control engineering approached to reverse engineering biomolecular networks: dynamical models for network inference, reconstruction methods based on linear models & non linear models. Algebraic statistics and methods in system biology: computational algebra, algebraic statistical models, parameter inference, model invariants, log linear model, reverse engineering of networks. Transcriptomic technologies and statistical data analysis: genome wide profiling, evaluation and significance of individual genes, grouping of genes to find biological pattern. Statistical data analysis in Matabolomics. Protein interaction networks and their statistical

analysis. Graphical modeling Recovering genetic network from continuous data with dynamic Bayesian networks. Random graph models and their application to protein protein interaction networks. Non linear Dynamics Qualitative inference in dynamical system, stochastic dynamical system, gaussian process inference for differential equation models of transcriptional regulation. Model identification by utilizing likelihood based methods. Bayesian approaches for mass spectrometry based Metabolomics. Systems Biology of microRNAs.

REFERENCES:

- Stochastic Modelling for Systems Biology by Darren James Wilkinson by Chapman & Hall/CRC
- Handbook of Statistical Systems Biology by MPH Stumpf, Wiley.
- Statistical Methods in Bioinformatics, Warren Ewens, Gregory Grant, Springer
- Probabilistic Modeling in Bioinformatics and Medical Informatics, Dirk Husmeier, Richard Dybowski, Stephen Roberts, Springer.

SECOND SEMESTER

OPEN ELECTIVE-II

SUBJECT: **COMPUTATIONAL PHYSICS**

SUBJECT CODE: **CSB-566**

PERIOD PER WEEK : Lecture –03 ;

CREDITS : **3**

Maximum Marks : End Term –60, Continuous Evaluation –40

Differential equation, special functions Bessel's, Hermite's. Laguerre polynomials. Eigen value , Eigen functions. Perturbation theory. Numerical analysis. Idea of visual basic, c++ and c-sharp.

REFERENCES:

1. Mathematical Physics : S.S. Rajput
2. Visual Basic & C ++ : Shyaum Series

FIRST SEMESTER

SUBJECT : LAB PRACTICE-II

SUBJECT CODE: **CSB-591**

CREDITS : **2**

PERIOD PER WEEK : Practical - 04

Maximum Marks : End Term –60 , Continuous Evaluation –40

Lab on Computational & Systems Biology, R.

FIRST SEMESTER

SUBJECT : SEMINAR-II

SUBJECT CODE: CSB-592

CREDITS : 2

Maximum Marks : 100

Seminar on Computational & Systems Biology.

THIRD SEMESTER

SUBJECT : Major Project Dissertation Phase-I

SUBJECT CODE: **CSB-648**

CREDITS : **23**

Maximum Marks : 100 (Continuous evaluation 70 & Viva Voce 30)

Dissertation on Current Trends in Computational & Systems Biology.

Note: Topic is to be selected / finalized in consultation with the concerned guide of the candidate. Accordingly the candidate shall carry out the project work.

FOURTH SEMESTER

SUBJECT : Major Project Dissertation Phase-II

SUBJECT CODE: **CSB-698**

CREDITS : **23**

Maximum Marks : 100 (Continuous evaluation 70 & Viva Voce 30)

Dissertation on Current Trends in Computational & Systems Biology.

Note: Dissertation work is to be carried out and submitted within the stipulated time in consultation with the concerned guide of the candidate. Before submission of Dissertation the student must have one publication in Journal of repute.