R-927
13.8.2026

UNIVERSITY OF CALCUTTA

Notification No. CSR/98/2026

It is notified for information of all concerned that in terms of the provisions of Section 54 of the Calcutta University Act, 1979, (as amended), and, in the exercise of his powers under 9(6) of the said Act, the Vice-Chancellor has, by an order dated 05.08.2026, approved the syllabus of 2-year (Four Semester) M.Sc. Course of Study in Biophysics, Molecular Biology & Bioinformatics, under NEP guidelines, as laid down in the accompanying pamphlet.

The above syllabus shall take effect from the academic session 2026-2027 and onwards.

12.08.2026

Prof.(Dr.) Debasis Das
Registrar

SENATE HOUSE
Kolkata-700073
12.08.2026

UNIVERSITY OF CALCUTTA

DEPARTMENT OF BIOPHYSICS, MOLECULAR BIOLOGY and BIOINFORMATICS

POSTGRADUATE CURRICULUM

Master of Science
in
Biophysics and Molecular Biology

Formulated under the National Education Policy (NEP 2020) Framework

2026

OBJECTIVES OF THE PROGRAM

The primary objective of the M.Sc in Biophysics and Molecular Biology program is to provide a rigorous, interdisciplinary education at the interface of physics, chemistry, mathematics, and biology. The curriculum is designed to equip students with a deep quantitative understanding of biological phenomena, transitioning from static descriptive models to predictive, molecular-level insights.

The program focuses on achieving the following core objectives:

- Interdisciplinary Training and Quantitative Excellence: To impart foundational and advanced training across the physical and life sciences, enabling graduates to seamlessly apply the mathematical, physical, and computational frameworks of exact sciences to solve complex biological problems.
- Structural Biology and Molecular Insight: To build a robust conceptual and practical understanding of how biomolecular structure dictates biological function. Students are trained to critically analyze, model, and simulate macromolecular assemblies, preparing them to evaluate and contribute to global structural databases.
- Advanced Methodological and Instrumentation Proficiency: To provide hands-on expertise in state-of-the-art analytical tools, spectroscopy, microscopy, and physical characterization techniques. The curriculum balances theoretical knowledge with intensive laboratory training so that students can independently isolate, purify, and determine the three-dimensional structures of both small drug molecules and large biomacromolecules.
- Computational Frameworks and Systems Modeling: To foster technical competency in scientific programming, algorithms, data analytics, and computational modeling. Students learn to harness data science tools to navigate the multi-omics landscape and build complex simulations of biological circuits and network kinetics.
- Research Literacy, Ethics and Global Competitiveness: To cultivate critical thinking and problem-solving capabilities through independent research projects, dissertations, and journal clubs. The program formally nurtures professional soft skills, emphasizing literature appraisal, rigorous data interpretation, research integrity, and an awareness of Intellectual Property Rights (IPR).

Ultimately, the program establishes a solid scientific foundation for students planning to pursue advanced doctoral studies, succeed in national-level competitive fellowship examinations, or build professional careers in cutting-edge academic, pharmaceutical, biotechnology, and clinical environments.

Master of Science (M.Sc.) in Biophysics and Molecular Biology

Curriculum Framework and Course Orientation

Total Marks: 1000 | **Total Credits:** 80

Course Structure: 600 (Theoretical Marks) + 400 (Practical Marks)

Semester-wise course distribution

1st Year. First Semester

Code	Title	Marks	Credits
BMB411	Molecular biology I	50	4
BMB412	Cell biology I	25	2
BMB413	Biomolecules I	50	4
BMB414	Bioenergetics and enzymology	25	2
BMB415	Mathematical biology I	25	2
BMB416	Computer programming (Practical)	25	2
BMB417	Biological data analysis (Practical)	25	2
BMB418	Experiments in molecular biology (Practical)	25	2
		175 (Theoretical) + 75(Practical) = 250	14 (Theoretical) + 6 (Practical) = 20

1st Year Second Semester

BMB421	Molecular biology II	25	2
BMB422	Cell biology II	25	2
BMB423	Biomolecules II	25	2
BMB424	Physico-chemical techniques	50	4
BMB425	Mathematical biology II	25	2
BMB426	Experiments in cell biology (Practical)	25	2
BMB427	Physico-chemical techniques (Practical)	25	2
BMB428	Bioinformatic tools and techniques (Practical)	25	2
		175 (Theoretical) + 75 (Practical) = 250	14 (Theoretical) + 6 (Practical) = 20

2nd Year First Semester

BMB511	Cell biology III	25	2
BMB512	Developmental biology	25	2
BMB513	Evolution and ecology	25	2
BMB514	Cellular basis of immunity and host pathogen interaction	25	2
BMB515	Biomolecules III	25	2
BMB516	Genetics and genomics	50	4
BMB517	Systems and integrated biology	50	4
BMB518	Molecular and cell biology techniques (Practical)	25	2
		225(Theoretical) + 25 (Practical) = 250	18(Theoretical) + 2 (Practical) = 20

2nd Year Second Semester

BMB521	M.Sc. thesis (Research)	150	12
BMB522	Research methodology and project writing	50	4
BMB523	Grand viva	50	4
		250 (Practical)	20 (Practical)

Detailed Course Syllabus

BMB411: Molecular biology I (Credits: 4 | Marks: 50)

Course Objectives

1. To provide an in-depth understanding of the fundamental mechanics governing DNA replication, mutation profiles, structural repair pathways, and recombination events across both prokaryotic and eukaryotic systems.
2. To establish a rigorous conceptual framework for prokaryotic gene expression, exploring the structural components of transcription and translation, genetic code degeneracy, and the biophysical control of operon systems.
3. To examine the chemical and environmental causes of DNA mutations, the specific biochemical pathways executing structural correction, and the physiological consequences of defects within these repair networks.
4. To equip students with the theoretical and practical knowledge of macromolecular separation techniques, including multi-dimensional electrophoresis, high-resolution chromatography, and autoradiography.
5. To train students to select, analyze, and interpret modern experimental assays used to quantify transcripts, determine in vivo transcription rates, map DNA-protein promoter footprints, and execute translational proteomic profiling.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Compare and contrast replication and recombination topologies across distinct systems.
- **CO-2:** Classify mutations and predict metabolic repair pathway recruitment based on DNA structural distortions.
- **CO-3:** Evaluate transposition mechanics across insertion sequences, composite/non-composite transposons, and retrotransposons.
- **CO-4:** Dissect prokaryotic transcriptional and translational kinetics, factoring in wobble mechanics and operon controls.
- **CO-5:** Synthesize experimental multi-step strategies to isolate, map, and analyze macromolecular nucleic acid targets.

- **CO-6:** Interpret promoter dynamics and translational outputs using quantitative transcriptomic and proteomic assay parameters.

Course Modules

- **Module 1: DNA Replication:** Overview of DNA replication: Different models and modes of DNA replication; Enzymes and accessory factors involved in DNA replication and their roles; Replication process: DNA replication in prokaryotes and eukaryotes; end replication problem in eukaryotes.
- **Module 2: DNA Mutation:** Causes and effects of mutation; Types of mutation: Transition, Transversion, Missense, Nonsense, Insertion or Deletion, Duplication, Frameshift mutations.
- **Module 3: DNA Repair:** Direct, Excision, Mismatch, Non-homologous end-joining, Homologous end-joining; SOS response; DNA repair errors: Defects in DNA repair and its consequences.
- **Module 4: DNA Recombination and Transposition:** Homologous DNA recombination - Holiday models, molecular events. Site specific DNA recombination. Transposable elements: Structure: Insertion Sequences, Composite and Non-composite transposons, mechanism of transposition: replicative and non replicative mechanisms. Retrotransposons.
- **Module 5: Prokaryotic Gene Expression:** Overview of transcriptional machinery:The transcription unit, Enzymes and transcription factors, Process of transcription: initiation, elongation and termination. Fine control of bacterial transcription: lac operon as a model. Components of translational machinery and their roles, mRNA, Ribosomes and rRNA, tRNA and tRNA aminoacylation. Process of translation: initiation, elongation and termination. Genetic code and significance of wobble and degeneracy in genetic code.
- **Module 6: Methods to Study Replication, Recombination, and Repair:** Basic knowledge about electrophoresis: Agarose gel, PAGE, Isoelectric focusing, 2-D gel electrophoresis; Chromatography: TLC, Paper, Size exclusion, Ion exchange, Affinity. Radioactive and nonradioactive Tracers, Autoradiography, Southern Blots, DNA Fingerprinting and DNA Typing, In Situ Hybridization, DNA Sequencing and Physical Mapping.
- **Module 7: Analysis of Gene Expression:** Quantifying Transcripts (Northern Blots, Primer Extension, Run-Off Transcription); Measuring Transcription Rates *in vivo* (Nuclear Run-On, Ribonuclease Protection Assay), methods to study promoter: assaying DNA–Protein interactions (Filter Binding, Gel Mobility Shift, DNase Footprinting, Chromatin Immunoprecipitation, *etc*.), Translational analysis – Western Blot, ICC, 2D gel and proteomics.

Recommended Reading

- Krebs, J. E., Goldstein, E. S., and Kilpatrick, S. T. (2018) *Lewin's GENES XII*.
- Watson, J. D. et al. (2017) *Molecular Biology of the Gene*, 7th ed., Pearson.
- Weaver, R. (2011) *Molecular Biology*, 5th ed., McGraw-Hill Education.

BMB412: Cell biology I (Credits: 2 | Marks: 25)

Course Objectives

1. Provide a deep evolutionary context on how primitive cells transitioned into highly specialized prokaryotic and eukaryotic architectures.
2. Analyze the biophysical, chemical, and structural organization of biological membranes, emphasizing the relationship between structure, microdomains, and cellular signaling.
3. Understand the mechanisms governing passive, facilitated, and active molecular transport across lipid bilayers.
4. Explain the electrical properties of excitable membranes, focusing on the mathematical and molecular basis of resting membrane potentials and action potential propagation.
5. Elucidate the structure and function of the nucleus, semi-autonomous organelles, and peroxisomes, alongside the molecular mechanisms driving targeted protein sorting and nucleocytoplasmic transport.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Differentiate and analyze the structural, genetic, and architectural complexities of prokaryotic and eukaryotic systems to explain how compartmentalization drives functional efficiency.
- **CO-2:** Critically evaluate the fluid mosaic model, modeling how the composition of lipid bilayers, transmembrane proteins, and specialized microdomains (lipid rafts, caveolae) regulate structural integrity and signaling.
- **CO-3:** Apply principles of membrane energetics to explain the initiation, regulation, and directional propagation of action potentials, and predict how specific ion channel or pump mutations affect cellular excitability.
- **CO-4:** Categorize and map diverse membrane transport pathways (diffusion, active transport, symport/antiport).
- **CO-5:** Develop an understanding on Nucleocytoplasmic and Organellar Trafficking Mechanics.

Course Modules

- **Module 1: Evolution of Cells:** Evolution of cells, evolution of organelles (Endo-symbiotic theory); cellular architecture; differences between prokaryotes and eukaryotes.

- **Module 2: Membrane Structure and Excitability:** Structure of model membrane, lipid bilayer and membrane proteins, fluid mosaic model, structure and function of lipid rafts and caveolae; ion channels and ion pumps. Electrical properties of membranes. Initiation and propagation of action potential in electrically excitable membranes.
- **Module 3: Membrane Transport Systems:** Membrane transport - Passive diffusion, osmosis, facilitated diffusion, primary and secondary active transport, uniport, symport and antiport. Patch clamp technique.
- **Module 4: Structure and Function of the Nucleus:** Structure and function of the nucleus and molecular mechanisms underlying transport of molecules between nucleus and cytosol.
- **Module 5: Mitochondria and Chloroplasts:** Structure and function of mitochondria and chloroplasts, their genetic systems and protein sorting into these organelles.
- **Module 6: Peroxisomes:** Structure, function and protein transport into peroxisomes.

Recommended Reading

- Alberts, B. et al. (2014) *Molecular Biology of the Cell*, 6th ed., W. W. Norton and Co.
- Cooper, G. M. and Hausman, R. E. (2015) *The Cell: A Molecular Approach*, 7th ed., Sinauer Associates.
- Lodish, H. et al. (2016) *Molecular Cell Biology*, 8th ed., W. H. Freeman.

BMB413: Biomolecules I (Credits: 4 | Marks: 50)

Course Objectives

1. To enable students to conceptualize biological macromolecules and the Central Dogma through an information-theoretic lens, understanding how evolutionary forces shape sequence variations.
2. To establish a rigorous mathematical and physical understanding of the weak, non-covalent interactions that dictate macromolecular stability, hydration, and molecular recognition.
3. To provide a deep understanding of the stereochemical and geometric constraints that govern the structural folds of proteins and the polymorphic states of nucleic acids.
4. To equip students with the ability to manually execute and computationally evaluate foundational sequence alignment algorithms.
5. To train students to model molecular evolution using probabilistic substitution matrices (PAM, BLOSUM) and mathematically reconstruct phylogenetic relationships using character- and distance-based methodologies.
6. To teach students how to mathematically analyze three-dimensional structural data, including the extraction of backbone dihedral angles, parsing the furanose pseudorotation cycle, and calculating helical parameters from coordinate datasets.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Evaluate the statistical significance of database search results and choose appropriate substitution matrices based on evolutionary distance.
- **CO-2:** Calculate the potential energy profiles of varied non-covalent interactions as a function of distance and local dielectric properties.
- **CO-3:** Predict allowed and disallowed steric regions for a given peptide backbone using the fundamental principles of the Ramachandran plot.
- **CO-4:** Differentiate between the structural parameters, sugar puckering preferences,and glycosidic torsion angles of A-, B-, and Z-DNA.
- **CO-5:** Correlate the physical packing parameters of amphiphilic lipids with their spontaneous self-assembled topologies (micelles vs. bilayers).

Course Modules

- **Module 1: Quantitative Sequence Analysis and Molecular Evolution:** The Biological Information Framework: The Central Dogma as an information-processing system; information and entropy; nature of sequence variations (transitions, transversions, indels) in biomolecules. Substitution Models and Scoring Metrics: Statistical Molecular evolution; Jukes-Cantor 1-Parameter and Kimura 2-Parameter models; Derivation and probabilistic rationale of PAM and BLOSUM matrices. Pair-wise alignments: Needleman Wunsch and Smith Waterman algorithms. Multiple sequence alignments. Phylogenetic Tree.

- **Module 2: Biomolecular Conformations**
    - *Peptides and Proteins:* Chemical constituents of proteins; primary structure; geometry of the peptide bond and protein backbone; backbone rotations in proteins; secondary structure - alpha helix, beta-sheets, polyproline helix and other structures.
    - *Nucleic Acids:* Chemical constituents of nucleic acids; primary structure - base, sugar, phosphodiester bond, Tautomeric equilibria of nucleic acid bases; Glycosidic torsion configurations; The furanose ring pseudorotation cycle: Envelope and Twist forms, C2'-endo vs. C3'-endo conformational preferences; The Watson-Crick paradigm (canonical geometry) vs. Hoogsteen/Wobble base-pairing; Base-stacking physics (dipole-induced dipole and London dispersion dominance); Conformational profiles of A-, B-, and Z-DNA.
    - *Carbohydrates and Polysaccharides:* Monosaccharides and disaccharides: linear and cyclic forms, The Anomeric Effect, importance of oligosaccharides in the living system. Polysaccharides: Structural organization of glycogen, starch and cellulose.
    - *Lipids and Self-Assembly:* Chemical Structure and Classification of Lipids: Glycerophospholipids: Major structural categories including phosphatidylcholine (PC), phosphatidylethanolamine (PE), and phosphatidylserine (PS). Sphingolipids and Glycolipids, Sterols.
    - Thermodynamics of Self-Assembly: Critical Micelle Concentration (CMC), shape-factor rules, micelles, and inverted micelles.

- **Module 3: Intermolecular Forces:**

  Electrostatic and Polar Potentials: Coulombic interactions; screening effects; Dipole moments of amino acids and peptide bonds; Charge-dipole and dipole-dipole interactions; Polarizability and

induced dipoles (Debye, Keesom and London dispersions). Short-range steric repulsion and the Lennard-Jones potential.

The Hydrogen Bond and Aqueous Solvation: Quantum-chemical and electrostatic character of the H-bond; directional geometry and network cooperative properties of water. The Hydrophobic Effect: Entropic origin of hydrophobic driving forces; Quantifying hydrophobic free energy changes via Solvent Accessible Surface Area (SASA).

Recommended Reading

- Tinoco, I. et al. (2014) *Physical Chemistry: Principles and Applications in Biological Sciences*, Pearson.
- Atkins, P. and de Paula, J. (2010) *Physical Chemistry for the Life Sciences*, 2nd ed., Oxford University Press.
- Jackson, M. B. (2006) *Molecular and Cellular Biophysics*, Cambridge University Press.
- Finkelstein, A. V. and Ptitsyn, O. B. (2016) *Protein Physics: A Course of Lectures*, 2nd ed., Academic Press.
- Calladine, C. and Drew, H. (2004) *Understanding DNA*, Academic Press.
- Mount, D. W. (2004) *Bioinformatics: Sequence and Genome Analysis*, 2nd ed., CSHL Press.
- Solomons (2017) Organic Chemistry, Global Edition
- Schlick, T. (2010) Molecular modelling and simulation: an interdisciplinary guide. 2nd edition. Springer
- Gu, J. and Bourne, P.E. (2009) Structural bioinformatics. 2nd edition. Wiley-Blackwell

BMB 414: Bioenergetics and enzymology (Credits: 2 | Marks: 25)

Course Objectives

1. To provide a rigorous physical chemistry framework for viewing the living cell as an open, non-equilibrium thermodynamic system, evaluating the distinction between the homeostatic "living" state and thermodynamic equilibrium ("dead").
2. To establish a clear mathematical understanding of standard and actual Gibbs free energy changes and the thermodynamic and kinetic mechanisms governing high-energy biomolecules and coupled reactions.
3. To examine the transport of ions and molecules across semipermeable barriers from both thermodynamic (chemical and electrochemical potentials) and kinetic (transporter saturation) perspectives, including the mathematical treatment of osmotic pressure and the Donnan membrane equilibrium.
4. To explore the physical chemistry of catalysis, the structural and kinetic properties that define "kinetically perfect" enzymes, the unique roles of water as an active solvent, and the precise molecular mechanisms of model enzymes.
5. To provide a comprehensive, systemic view of the classical metabolic pathways, exploring how individual enzymatic steps are orchestrated, thermodynamically driven, and kinetically regulated to maintain homeostatic flux.
6. To contrast the carbon assimilation and metabolic networks of photo-autotrophs with heterotrophic pathways, focusing on their unique thermodynamic challenges and regulatory checkpoints.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Calculate the actual Gibbs free energy changes for non-equilibrium cellular reactions and mathematically model how endergonic biochemical processes are driven forward through chemical coupling with high-energy intermediate hydrolysis (e.g., ATP).
- **CO-2:** Formulate and solve quantitative problems involving electrochemical gradients, calculate osmotic pressure deviations, and apply the Gibbs-Donnan equilibrium equation to predict steady-state ion distributions across selective biological boundaries.

- **CO-3:** Determine the order of chemical and biochemical reactions from experimental data, derive integrated rate laws, compute respective half-lives, and evaluate the mathematical parameters of enzymatic systems.
- **CO-4:** Critically analyze the environmental factors (temperature, pH, ionic strength, inhibitors) that modulate enzyme properties, identify the physical criteria that define a kinetically perfect enzyme, and dissect the multi-step molecular mechanisms (e.g., transition state stabilization, acid-base catalysis) of model enzymes.
- **CO-5:** Differentiate and explain the explicit physical roles played by water as an active solvent during enzymatic catalysis, including its contributions to hydrophobic collapse, hydrogen-bonded networks, proton wires, and reactant desolvation energetics.
- **CO-6:** Map the interconnected networks of intermediary metabolism, identify rate-limiting enzymatic checkpoints based on kinetic and thermodynamic parameters, and critique the distinct regulatory mechanisms (allosteric feedback, covalent modification, genetic control) that govern heterotrophic *vs.* photo-autotrophic carbon pathways.

Course Modules

- **Module 1: Cellular Thermodynamics:** Cellular Thermodynamics: Cell as a system as living and dead, High-Energy Biomolecules: Thermodynamic and Kinetic features, Gibbs Free Energy Changes in Biochemical reactions, Thermodynamically Coupled reactions.
- **Module 2: Enzyme Catalysis and Water Solvation:** Importance of Catalysis in Cellular reactions, Unique aspect of Enzymes as Catalysts, Roles of Water as a solvent in Enzymatic reactions.
- **Module 3: Reaction and Enzyme Kinetics:** Kinetics of reactions, their orders and respective half-lives, Kinetic characteristics of Enzymatic reactions, Kinetically Perfect Enzymes, Factors that influence the properties of Enzymes, Molecular mechanism of action of some model enzymes.
- **Module 4: Intermediary Metabolism:** Intermediary Metabolism: Overview of the Classical Pathways and their Regulation, Special features of Metabolism in Photo-autotrophs.

Recommended Reading

1. Haynie D T (2008) Biological Thermodynamics, Cambridge University Press
2. Nelson D L and Cox M (2017) Lehninger Principles of Biochemistry, W H Freeman
3. Atkins P and Paula J (20111) Physical Chemistry for the Life Sciences, W H Freeman

4. Palmer T (1995) Understanding Enzymes, Ellis Horwood Ltd

BMB415: Mathematical biology I (Credits: 2 | Marks: 25)

Course Objectives

1. To provide a foundational mathematical framework tailored for biological systems, translating geometric and logical relationships into precise algebraic expressions.
2. To establish a rigorous understanding of multi-variable calculus, series convergence, and spatial vector systems to analyze complex multi-dimensional properties in structural biology.
3. To develop the theoretical foundation of linear operators and vector calculus.
4. To train students to perform matrix operations, compute eigenvalues/eigenvectors, and handle changes of bases to model coordinate normalization profiles.
5. To equip students with foundational probability theory, conditional probability mechanics, and Bayes' theorem to systematically relate experimental probability data to standard statistical significance thresholds.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Construct geometric and algebraic solutions for linear inequalities containing multiple variable parameters.
- **CO-2:** Evaluate the convergence boundaries of multi-variable Taylor series expansions for macromolecular approximations.
- **CO-3:** Apply the Gram-Schmidt orthogonalization algorithm to derive normalized, independent scalar product bases.
- **CO-4:** Solve matrix operator transformations to deduce spatial rotations, structural scaling volume factors, and coordinate eigenvalues.
- **CO-5:** Apply conditional probability models and Bayes' theorem equations to calculate scientific significance thresholds from raw datasets.

Course Modules

- **Module 1: Linear Inequalities:** Algebraic solutions, graphical representation, inequalities in two variables.
- **Module 2: Calculus:** Functions and graphs; Taylor series, convergence, multivariable series.

- **Module 3: Vector and Metric Spaces:** Vectors and coordinate systems, vector operations. Axioms and examples of vector spaces, linear independence, norms, bases and scalar products, Gram-Schmidt orthogonalization, infinite dimensions, metric spaces; applications.
- **Module 4: Operators and Matrices:** The idea of an operator, definition of an operator, examples of operators; gradient, divergence and curl operators, application in electrostatics and electrodynamics. Matrices as operators, matrix multiplication, inverses, rotations, areas, volumes, determinants, eigenvalues and eigenvectors, change of basis, matrix normalization.
- **Module 5: Probability:** Basic notions from probability theory, how to calculate the probability of independent events, conditional probability, Baye's theorem, Relating probability and statistical significance.

Recommended Reading

- Nearing, J. (2010) Mathematical Tools for Physics, Dover Publications.
- Khanal, Arun Bhadra (2016) Mahajan's Methods in Biostatistics for Medical Students and Research Workers, Jaypee Brothers Medical Publishers (P) Ltd.

BMB416: Computer programming (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives

1. Introduce the fundamental structural architecture of Linux-based operating systems and shell command interpreters to manage large-scale computational biological workflows. Establish an operational framework in Python syntax logic, data types, and looping structures tailored for scientific data handling.
2. Equip students with the practical coding skills required to execute shell pipelines, command redirections, and script configurations for file management. Train students to construct modular subprograms, file handlers, and array manipulations in Python and Octave to parse, filter, and analyze three-dimensional structural coordinate files (PDB) and sequence alignments (FASTA).

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Configure custom Linux shell environments and implement file system pipelines using redirection and command filters.
- **CO-2:** Develop functional Python scripts utilizing conditional selection blocks, logical loops, and structured file I/O operations.
- **CO-3:** Implement modular subprograms and multidimensional arrays to parse and automate the analysis of macromolecular sequence datasets.
- **CO-4:** Execute matrix arithmetic algorithms and numerical biological models within the GNU Octave computing environment.

Course Modules

- **Module 1: Linux Operating System and Shell:** Introduction to the structure of a Linux based OS, shell command interpreters, configuring shell environment, basic shell commands, handling file systems, editing files, file permissions, file redirection and pipes.
- **Module 2: Python for Bioinformatics:** Variables, data types, declarations, expressions, input and output, selection and looping, file operations, arrays, subprograms. Applications in sequence and structure data handling.

BMB417: Biological data analysis (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives

1. To establish a thorough practical grasp of biostatistical modeling, differentiating between discrete and continuous probability layouts (Binomial, Poisson, Gaussian).
2. To Provide an operational understanding of null-hypothesis significance testing, identifying boundaries separating parametric from non-parametric statistical checks.
3. To train students to write custom scripts within the R programming language to read, manipulate, concatenate, and normalize high-dimensional biological data objects.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Determine data dispersion properties and evaluate compliance with standard probability distributions using R graphics packages.
- **CO-2:** Construct complex, multi-scale data objects including data frames, conversion matrices, and conditional logical loops in R.
- **CO-3:** Execute Student's t-tests, Chi-square independence validations, and estimate confidence intervals on biological samples.
- **CO-4:** Formulate linear and multiple regression equations while tracking residual variances and calculating experimental power bounds.

Course Modules

- **Module 1: Foundation of Biostatistics:** Random variables; Uniform distribution, Binomial distribution; Poisson's distribution. Functions of random variables.. Gaussian distribution. Standard Normal distribution. Central limit theorem. t-distribution. Pairwise t-tests. Confidence interval estimation for z-test, t-test. Hypothesis testing. Type I and Type II errors. Chi-square distribution. Contingency chi-square. Tests of independence, tests for homogeneity. Hypothesis testing continued with z-distribution, t-distribution and chi-square distributions.
- **Module 2: R Language Environment:** Introduction to R. Objects and data. Working methodology of R. Use of R as a calculator. Reading data from a file, saving data. Generation of regular and random sequences. Creating and converting objects. Concatenation of vectors. Types

of data. Features of data distribution. Data frames, matrices, functions, operators and loops. Sample spaces, conditional probability and Bayes' theorem. Graphics with R; graphical functions. Low level plotting commands. Packages.

BMB418: Experiments in molecular biology (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives.

1. To connect the theoretical physical principles of macromolecular transactions with real-world laboratory workflows, analyzing how modifications at the DNA level change downstream protein expressions.
2. To establish a definitive understanding of the biophysical rules governing electrophoresis, multi-dimensional separations, and affinity/ion-exchange chromatography.
3. To equip students with the practical skills to isolate plasmid DNA, calculate purity indices spectrophotometrically, and perform site-directed restriction digestions.
4. To train students to engineer recombinant expression vectors via ligation, measure bacterial transformation kinetics, and systematically purify target proteins using affinity columns and Western blot immunodetections.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Isolate plasmid DNA and evaluate structural forms and absolute chemical purity ratios using spectrophotometric coordinates.
- **CO-2:** Formulate and execute a gene cloning layout utilizing restriction digestion, ligation, and competent cell transformations.
- **CO-3:** Express recombinant targets in E. coli and perform downstream processing using one-step affinity chromatography columns.
- **CO-4:** Validate target protein molecular weight and purity boundaries using SDS-PAGE and Western blot immunoassay profiling.

Course Modules

- **Module 1: Plasmid Preparation and Verification:** Agarose gel electrophoresis of DNA and extraction and purification of Nucleic acid: Plasmid DNA preparation and identification of various structural forms of plasmid, Estimation of the purity of the isolated Plasmid DNA spectrophotometrically, Digestion of DNA by restriction enzyme; Purification of DNA from gel.

- **Module 2: Gene Cloning Paradigm:** How to clone a gene (overview of the procedure), cloning by PCR, characterization of plasmid clones (PCR, DNA sequencing).
- **Module 3: Bacterial Transformation:** Preparation of competent cells by $CaCl_2$ method. Ligation, preparation of competent cells and transformation of ligated DNA to *E. coli*, measurement of transformation efficiency.
- **Module 4: Expression and Purification of Proteins:** Expression of a recombinant Protein in *E.coli* and one step purification of the protein by the affinity column method. Estimation of the purity of the isolated protein by SDS-PAGE and Western blot.

Recommended Reading

- Wilson, K. and Walker, J. (2010) *Principles and Techniques of Biochemistry and Molecular Biology*, 7th ed., Cambridge University Press.
- Dale, J. W., Schantz, M. von, and Plant, N. (2011) *From Genes to Genomes: Concepts and Applications of DNA Technology*, 3rd ed., Wiley.

BMB421: Molecular biology II (Credits: 2 | Marks: 25)

Course Objectives

1. To provide a comprehensive understanding of eukaryotic transcriptional regulation, detailing RNA Polymerase assembly, Mediator complex interactions, and ATP-dependent chromatin remodeling mechanisms.
2. To establish a deep molecular framework regarding post-transcriptional processing events, exploring splicing variations, chemical modifications, and small non-coding RNA (siRNA/miRNA) gene silencing tracks.
3. To examine the structural and kinetic controls governing eukaryotic translation cycles, detailing checkpoint machinery, ribosomal stalling, and translational repression networks.
4. To dissect the physical pathways of target protein post-translational modifications and cell degradation coordinates governed by the ubiquitin-proteasome pathway.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Understand the eukaryotic promoter, enhancer, and chromatin remodeling layouts to predict target transcription efficiency.
- **CO-2:** Differentiate between alternative splicing tracks and trace the structural biogenesis paths of microRNA silencing networks.
- **CO-3:** Map molecular checkpoints regulating eukaryotic translation initiation, elongation, and structural termination events.
- **CO-4:** Model post-translational updates and calculate the kinetic degradation routes of proteins inside the ubiquitin-proteasome hub.

Course Modules

- **Module 1: Eukaryotic Transcription:** Transcription in Eukaryotes: RNA Polymerases, Promoters, Enhancers and Silencers, Transcription Factors, Mediator Complex, Activators, Interaction among Activators, Chromatin remodeling, Regulation of Transcription, Epigenetic regulation.

- **Module 2: RNA Processing and Control:** RNA Processing: Splicing, Capping and Polyadenylation, Post-Transcriptional Control of Gene Expression, RNA Editing, mRNA Stability, siRNA, miRNA.
- **Module 3: Eukaryotic Translation and Proteolysis Networks:** Translation in Eukaryotes: Ribosomes, Initiation, elongation and termination, Translational regulation, Translation Repression, Post-translational modifications and mechanisms of protein degradation.

Recommended Reading

- Krebs, J. E., Goldstein, E. S., and Kilpatrick, S. T. (2018) *Lewin's GENES XII*.
- Watson, J. D. et al. (2017) *Molecular Biology of the Gene*, 7th ed., Pearson.
- Weaver, R. (2011) *Molecular Biology*, 5th ed., McGraw-Hill Education.

BMB422: Cell biology II (Credits: 2 | Marks: 25)

Course Objectives

1. To provide a comprehensive understanding of the internal organization and physical connectivity of eukaryotic cells.
2. To explore the mechanical and molecular principles governing intracellular transport, the structural dynamics of the cytoskeleton, and the mechanisms by which cells interact with their environment and one another to form multicellular structures.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Analyze the structural and functional distinctions between the ER, Golgi, endosomes, and lysosomes; Deconstruct the molecular mechanisms of vesicular traffic, including the role of coat proteins and SNARE proteins in maintaining compartmental identity; Differentiate between the pathways of endocytosis and exocytosis, explaining how cells regulate protein secretion and nutrient uptake.
- **CO-2:** Explain the self-assembly and dynamic instability of actin filaments, microtubules, and intermediate filaments; Relate the activity of molecular motors (myosin, kinesin, and dynein) to intracellular transport and cellular motility; Describe the physiological process of muscle contraction through the sliding filament model.
- **CO-3:** Categorize the various types of cell junctions (tight, gap, and anchoring) and their roles in epithelial organization; Examine the composition of the extracellular matrix (ECM) and the role of the basal lamina in tissue support; Interpret the bi-directional signaling of integrins (outside-in and inside-out) and how cadherins facilitate selective cell-cell adhesion.

Course Modules

- **Module 1: Endomembrane Organelles:** Structure and function of Endoplasmic reticulum, Golgi apparatus, Endosomes and Lysosomes.
- **Module 2: Intracellular Vesicular Traffic:** Molecular mechanisms of membrane transport and the maintenance of compartmental diversity. Transport from ER to golgi apparatus, transport from the trans-golgi network to lysosomes, transport into the cell from the plasma membrane (endocytosis), transport from the trans-golgi network to the cell exterior (exocytosis).

- **Module 3: Cytoskeleton Structure and Function:** Self-assembly and dynamic structure of cytoskeletal filaments, regulation of cytoskeletal filaments, molecular motors, cytoskeleton and cell behavior, muscle contraction.
- **Module 4: Cell Junctions and Extracellular Matrix Matrix:** Cell junctions, cell adhesion and the extracellular matrix- Cadherins and cell-cell adhesion; tight junctions and the organization of epithelia; passageways from cell-cell-gap junctions and plasmodesmata; the basal lamina, integrins and cell matrix adhesions (outside-in and inside-out signaling).

Recommended Reading

- Alberts, B. et al. (2014) *Molecular Biology of the Cell*, 6th ed., W. W. Norton and Co.
- Cooper, G. M. and Hausman, R. E. (2015) *The Cell: A Molecular Approach*, 7th ed., Sinauer Associates.
- Lodish, H. et al. (2016) *Molecular Cell Biology*, 8th ed., W. H. Freeman.
- Phillips, R. et al. (2012) *Physical Biology of the Cell*, 2nd ed., Garland Science.

BMB423: Biomolecules II (Credits: 2 | Marks: 25)

Course Objectives

1. To apply the basic laws of polymer physics and statistical mechanics to macromolecular chains, deriving partition functions, persistence lengths, and random coil distributions within various solvent systems.
2. To establish a rigorous physical chemistry framework for evaluating phase transitions, helix-coil dynamics, and the thermodynamics of multi-component binding interactions.
3. To decode high-order structural topographies including protein domains, structural cooperativity models, and allosteric state networks.
4. To analyze the continuum mechanics of nucleic acids, parsing DNA bending dynamics, nucleosome folding constraints, supercoiling topology, and RNA quaternary architectures.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Calculate biopolymer persistence lengths and apply Flory excluded volume principles to characterize random coil dimensions.
- **CO-2:** Model the phase mechanics of helix-coil transitions and evaluate hybridization thermodynamics using DNA curves.
- **CO-3:** Dissect protein tertiary folds and compare statistical models of allosteric cooperativity under ligand binding stress.
- **CO-4:** Evaluate DNA supercoiling constraints, topological linking numbers, and high-order nucleosome chromatin compaction arrays.

Course Modules

- **Module 1: Statistical Mechanics of Biopolymers:** Statistical mechanics of Biopolymers: Polymer chains and configurational partition functions, statistics of random coils, persistence length, Flory theory and theta solvents, probability distributions and physics of random coil polymers.
- **Module 2: Thermodynamics and Kinetics of Macromolecules:** Thermodynamic and kinetics of biomolecules: Thermodynamics of helix-coil transition, thermodynamics and kinetics of DNA - Cot Curve, Thermodynamics of biomolecular interactions and assembly.

- **Module 3: Advanced Structural Aspects of Interaction:** Advanced structural aspects of protein, nucleic acids and their interactions: Protein tertiary structure; domains and folds, protein folding and cooperativity, quaternary structure and allosteric interactions. Protein-protein and protein-nucleic acid interaction. Flexibility and bending of DNA. Nucleosome and chromatin model; supercoiled DNA; RNA tertiary structure; tRNA structure and folding. G-quadruplex.

Recommended Reading

- Tinoco, I. et al. (2014) *Physical Chemistry: Principles and Applications in Biological Sciences*, Pearson.
- Atkins, P. and de Paula, J. (2010) *Physical Chemistry for the Life Sciences*, 2nd ed., Oxford University Press.
- Cantor, C. R. and Schimmel, P. R. (1980) *Biophysical Chemistry*, Part II, 1st ed., W. H. Freeman and Co.
- Jackson, M. B. (2006) *Molecular and Cellular Biophysics*, Cambridge University Press.

BMB424: Physico-chemical techniques (Credits: 4 | Marks: 50)

Course Objectives

1. To learn the physics of how light interacts with biological molecules across different energy scales (electronic, vibrational, and optical rotation).
2. To understand how optical tools like Circular Dichroism (CD) and Infrared/Raman spectroscopy reveal the secondary structures of proteins and the shapes of DNA.
3. To examine how the physical traits of a protein in solution (such as its weight, hydration layer, and shape) dictate how it moves, flows, and separates under physical forces.
4. To master the design, operational rules, and resolution limits of high-powered optical, confocal, and electron microscopes (TEM/SEM).
5. To gain a practical understanding of multi-component instruments used to isolate and study cell samples, including centrifuges, flow cytometers (FACS), and mass spectrometers (MALDI-TOF).

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Calculate the wavelength of maximum light absorption (λmax) for conjugated biological molecules using standard empirical rules.
- **CO-2:** Explain molecular relaxation and calculate structural spacing or environment updates using fluorescence quenching and energy transfer (FRET) equations.
- **CO-3:** Identify protein and nucleic acid structural folds by analyzing peaks and shifts in Circular Dichroism (CD), Infrared, and Raman spectra.
- **CO-4:** Determine the resolution limits of different microscopes using Abbe's law and evaluate the role of deconvolution in sharp confocal imaging.
- **CO-5:** Use Perrin's and Stokes' equations to calculate a protein's size, shape, and frictional properties from experimental solution data.
- **CO-6:** Choose the correct separation or mass-testing strategy for a given experiment, matching the biological sample with the right centrifuge gradient, flow cytometry dye, or mass spectrometry matrix.

Course Modules

- **Module 1: Electronic Spectroscopy:** Molecular spectroscopy – quantum mechanical principles. Electronic spectroscopy: UV-Vis Spectroscopy: Parameters of absorption spectra; molecular basis of light absorption by molecules like DNA, RNA, protein and other biomolecules; calculation of λ_{max} for linear conjugated molecules with examples; calculation of λ_{max} for circular conjugated molecules with examples; working principle of UV-Vis absorption spectrophotometer; application in bio-world.
- **Module 2: Fluorescence Spectroscopy:** Jablonski diagram; Stokes shift; fluorescence emission parameters; biomolecules that have fluorescence; intrinsic protein fluorescence from aromatic amino acids; other natural fluorophores, green fluorescence protein (GFP) and its mutants; extrinsic fluorescence probes; protein fluorescence; instrumentation for fluorescence spectroscopy; fluorescence quenching; polarization and anisotropy, effect of solvent on fluorescence emission, fluorescence resonance energy transfer (FRET).
- **Module 3: Chiral and Vibrational Spectroscopy:** Chiral molecules and optical activity: Physical basis of circular dichroism (CD) different ranges of CD (visible, near, far and vacuum-UV), CD spectra of interacting chromophores; electronic transitions of the peptide group; CD spectral signatures for different conformations of proteins; conformational analysis of DNA via CD spectroscopy; induced circular dichroism with typical applications to studies of biomolecular interactions.

  Vibrational spectroscopy (Infrared and Raman spectroscopy): Molecular vibrations; harmonic and Morse potentials; fundamental and overtone modes; group frequencies; influence of hydrogen bonding and isotopic substitution on vibrational frequencies; physical basis of infrared and Raman spectra; resonance Raman spectroscopy; FT-IR and Raman spectrometers and their working principles; amide vibrational modes and side chain modes of proteins; applications of IR and Raman to structural analyses of biological macromolecules; typical empirical (including biomedical) applications of vibrational spectroscopy.

- **Module 4: Advanced Microscopy and FACS:** Design and fundamental principles of light and fluorescence microscopes; the fundamental principles of transmission and scanning electron microscopy; sample preparation for microscopy. Structure and function of a confocal laser scanning microscope; the principle and use of deconvolution in fluorescence microscopy.
- **Module 5: Hydrodynamics and Analytical Mass Spectrometry:** Describing macromolecules: Size, shape and frictional coefficient of macromolecules, bound water, molecular weight,

Perrin's equation, shape factor, partial specific volume. Transport properties: Stokes' law, diffusion, Viscosity: intrinsic and specific viscosity. Sedimentation and ultracentrifugation: flow equation, sucrose, CsCl, alkaline sucrose gradients and applications. Principle of MALDI-TOF and its applications.

Recommended Reading

- Lakowicz, J. R. (2006) *Principles of Fluorescence Spectroscopy*, 3rd ed., Springer.
- Cantor, C. R. and Schimmel, P. R. (1980) *Biophysical Chemistry*, Part II, 1st ed., W. H. Freeman and Co.
- Banwell, C. N. and McCash, E. M. (1994) *Fundamentals of Molecular Spectroscopy*, 4th ed., McGraw-Hill.
- Hollas, J. M. (2004) *Modern Spectroscopy*, 4th ed., Wiley.
- Campbell, I. D. and Dwek, R. A. (1984) *Biological Spectroscopy*, Addison-Wesley.
- Tinoco, I. et al. (2014) *Physical Chemistry: Principles and Applications in Biological Sciences*, Pearson Education.

BMB425: Mathematical biology II (Credits: 2 | Marks: 25)

Course Objectives

1. To establish a mathematical toolkit for signal processing using Fourier series and transform.
2. To provide a basic introduction to ordinary and partial differential equations (ODEs/PDEs) to model biophysical systems.
3. To train students to formulate and solve linear programming problems using graphical and matrix optimization methods.
4. To introduce the mathematical constraints of Pareto efficiency and Pareto Front geometry to analyze biological fitness landscapes and multi-task evolutionary compromises.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Apply Fourier Transform algorithms and the Convolution Theorem to decode time-series datasets and structural signals.
- **CO-2:** Formulate linear programming matrices to calculate optimal solution coordinates under strict boundary constraints.
- **CO-3:** Solve first-order and simultaneous differential equations to model spatial-temporal biological dynamics.
- **CO-4:** Map Pareto Front geometries to predict target fitness compromises across competing evolutionary tasks.

Course Modules

- **Module 1: Linear Programming and Optimization:** Introduction, graphical methods for solving linear programming problems (constraints and optimal solutions).
- **Module 2: Pareto Optimization Theories:** Basic concept of Pareto optimization, Fitness landscape for single task, multiple tasks and trade-offs, geometry of Pareto front.
- **Module 3: Fourier Analysis:** Fourier analysis: Fourier series, choice of basis, Fourier transform
- **Module 4: Differential Equations and Dynamical Systems:** Differential equations: First Order differential equations, Systems of differential equations, introduction to partial differential equations. Introduction to dynamical systems theory. Applications in biological systems.

Recommended Reading

- Nearing, J. (2010) Mathematical Tools for Physics, Dover Publications.
- Deb, K. (2001) Multi-objective optimization using evolutionary algorithms, Wiley
- Pipes, L. A. (1946) Applied mathematics for engineers and physicists. Digital library of India.
- Jones, D. S. et al. (2009) Differential equations and mathematical biology, CRC press

BMB426: Experiments in cell biology (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives

1. To provide the foundational laboratory skills required to maintain, manipulate, and analyze mammalian cells and tissues.
2. To gain proficiency in aseptic cell culture techniques, transfection methods for protein expression, and histological staining protocols (HandE and IHC) used to visualize cellular architecture and protein localization.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Distinguish between primary, finite, and immortalized cell lines, selecting the appropriate model for specific research goals; Demonstrate mastery of aseptic techniques, including subculturing (trypsinization), cryopreservation, and thawing procedures; Quantify cell populations accurately using a hemocytometer and evaluate health through viability assays like Trypan Blue and MTT.
- **CO-2:** Compare and contrast transient and stable transfection methods for introducing foreign DNA into mammalian cells; Apply molecular tagging techniques (e.g., GFP tagging) to monitor protein dynamics in real-time; Design immunofluorescence experiments using direct or indirect labeling to localize proteins within specific subcellular compartments.
- **CO-3:** Learn the full sequence of tissue processing, from formalin fixation and paraffin embedding to microtomy (sectioning); Understand the HandE staining protocol, the chemical basis of Basophilia (Hematoxylin binding to DNA) and Acidophilia (Eosin binding to proteins); Learn Immunohistochemistry (IHC) protocols, including critical steps like Heat-Induced Epitope Retrieval (HIER) and DAB chromogen detection to identify specific antigens in tissue sections.

Course Modules

- **Module 1: Mammalian Cell Culture and Visualization:**
  -Types of Cell Culture: Primary Culture, Secondary (Passaged) Culture, Finite Cell Lines, Continuous (Immortalized) Cell Lines. Visualization of cells under microscope.

-Growing adherent cells: Culture conditions, trypsinizing and subculturing cells from a monolayer. Freezing cells grown from monolayer and suspension cultures and thawing and recovering frozen cells.

-Cell counting using a hemocytometer.

-Assessing cell viability using Trypan blue staining and learning other cytotoxicity assays such as MTT assay, Alamar blue assay, LDH assay.

-Mammalian cloning vectors and GFP tagging proteins for direct visualization. Methods used to transfect mammalian cells for protein expression transiently and stably.

-Immunofluorescence labelling of protein targets within cells: Direct and indirect.

-Labeling protocol: Cell fixation, permeabilization, blocking, staining with primary and secondary antibodies, nuclear counter staining or specific organelle counter staining for protein localization in specific organelles.

- **Module 2: Tissue Processing and HandE / IHC Staining:** Hematoxylin and Eosin (HandE) and Immunohistochemistry (IHC). Principles of Routine Staining of tissue sections: Basophilia vs. Acidophilia, understanding why nucleic acids (DNA/RNA) bind to Hematoxylin and why proteins bind to Eosin.

  Fundamentals of Tissue Processing: Fixation: 10% Neutral Buffered Formalin. Processing: Dehydration (Alcohols), Clearing (Xylene), and Infiltration (Paraffin). Microtomy: Sectioning at 4–5 microns. Deparaffinization: removal of paraffin using Xylene. Hydration: alcohol series down to water. Nuclear Staining with Hematoxylin and Counterstaining with Eosin Y.

  For IHC: Antigen Retrieval and Blocking: HIER (Heat-Induced Epitope Retrieval). Endogenous Peroxidase Blocking using H2O2. Primary Antibody incubation. Secondary Antibody conjugated with HRP. Detection System: DAB chromogen producing a brown precipitate. Dehydration, clearing, and coverslip mounting.

Recommended Reading

- Celis, J. E. (1997) *Cell Biology: A Laboratory Handbook*, 2nd ed., Academic Press.

BMB427: Physico-chemical techniques (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives

1. To connect basic laws of photophysics, quantum optics, and physical chemistry with practical laboratory measurements of biomolecular matrices.
2. To establish a rigorous operational understanding of steady-state spectroscopy, tracking how micro-environmental parameters update macromolecular configurations.
3. Equip students with the quantitative skills to record absorption profiles, monitor fluorescence intensity shifts, and analyze resonance changes.
4. To train students to mathematically derive binding parameters, dissociation constants, and stoichiometry factors from raw data using Scatchard models and FRET ruler mechanics.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Evaluate hyperchromicity shifts to calculate melting temperatures for duplex DNA and non-canonical G-quadruplexes.
- **CO-2:** Quantify fluorescence quenching parameters using Stern-Volmer derivations to chart protein structural alterations.
- **CO-3:** Construct Scatchard plots from protein-ligand steady-state fluorescence datasets to deduce absolute binding limits.
- **CO-4:** Compute energy transfer efficiencies using singlet-singlet FRET equations to map intramolecular donor-acceptor spacing.

Course Modules

- **Module 1:** Determination of DNA (B DNA/ G-quadruplex) melting curve by spectrophotometry.
- **Module 2:** Enhancement of fluorescence activity of Ethidium Bromide upon interaction with double stranded DNA.
- **Module 3:** Fluorescence quenching of protein (BSA) by Acrylamide, and study of the effect of microenvironment on intrinsic fluorescence.
- **Module 4:** Fluorescence studies of protein-ligand binding: Binding of ANS a fluorescence probe with BSA. Estimation of binding parameters *via* Scatchard plot analysis. FRET studies (Trp to ANS FRET).

- **Module 5:** Studying the effect of solvent polarity on ANS fluorescence by examining emission spectra of ANS in varying concentrations of ethanol-water mixtures.

Recommended Reading

- Holtzhauer, M. (2006) *Basic Methods for the Biochemical Lab*, Springer.
- Nadeau, J. L. (2015) *Introduction to Experimental Biophysics*, CRC Press.

BMB428: Bioinformatic tools and techniques (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives

1. To provide an active conceptual framework in data mining and algorithmic analysis, enabling students to evaluate the biological annotation quality and structural validation criteria of public repositories.
2. To establish a definitive computational understanding of the scoring logic, gap penalties, and evolutionary substitution models embedded in sequence search engines.
3. To equip students with the computational skills to retrieve genomic, transcriptomic, and 3D coordinate packages from international databases.
4. To train students to execute global/local pairwise alignments, build multiple sequence alignments (MSA) to identify highly conserved functional motifs, and reconstruct valid molecular phylogenetic trees using character- and distance-based workflows.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Query and extract integrated sequence, structure, and functional annotations from NCBI, UniProt, Ensembl, and the PDB.
- **CO-2:** Implement global Needleman-Wunsch and local Smith-Waterman matrix algorithms to evaluate pairwise sequence alignments.
- **CO-3:** Optimize database BLAST heuristic parameters, filtering matches according to mathematical Expectation values.
- **CO-4:** Reconstruct molecular phylogenetic trees from multiple sequence alignments using distance and character criteria.

Course Modules

- **Module 1: Database Extraction :** Retrieval of biological information from widely used resources (e.g. NCBI, Uniprot, Ensembl); resources of sequence, structure, interaction and function of biomolecules.
- **Module 2: Alignment Informatics and Tree Reconstruction:** Pair-wise and multiple sequence alignments; searching sequence databases; construction of phylogenetic trees.

- **Module 3: Structure prediction of biomolecules:** Prediction of secondary and tertiary structures of proteins using comparative modelling tools. Nucleic acid secondary structure prediction.
- **Module 4: Multivariate Statistics and Dimension Reduction:** Correlation coefficients. Principal Component Analysis (PCA) theory. Eigenvalues and eigenvectors in biological data. High-dimensional data visualization. Clustering techniques for omics profiles.

BMB511: Cell biology III (Credits: 2 | Marks: 25)

Course Objectives:

1. To provide students with a deep, molecular-level understanding of how cells reproduce, communicate, and integrate external signals to dictate fate, metabolism, and survival.
2. To explore the mechanics and regulation of the cell cycle, mitosis, and meiosis, alongside the intricate biochemistry of cell signaling pathways — ranging from ligand-receptor interactions to intracellular cascades and gene expression.
3. To connect physiological signaling networks (insulin, inflammation cascades) to pathological states like oncogenesis.

Course Outcomes (COs):

By the end of this course, students will be able to:

- **CO-1:** Map the sequential stages of the cell cycle, mitosis, meiosis, and cytokinesis, and evaluate the molecular checkpoint mechanisms and regulatory proteins (such as Cyclins and CDKs) that ensure genomic integrity.
- **CO-2:** Differentiate between the four primary forms of signaling (juxtacrine, endocrine, paracrine, and autocrine) and predict how the chemical nature of a ligand (hydrophilic *vs.* hydrophobic) determines its specific receptor binding and life cycle.
- **CO-3:** Compare and contrast the structure, activation, and downstream signaling of major receptor classes, including G Protein-Coupled Receptors (GPCRs), Receptor Tyrosine Kinases (RTKs), non-protein tyrosine kinase receptors, and intracellular nuclear receptors.
- **CO-4:** Trace the biochemical pathways of key second messengers and downstream kinase cascades highlighting the balance between phosphorylation and dephosphorylation.
- **CO-5:** Explain how complex physiological processes — such as insulin-mediated glucose regulation and TNF-α-mediated inflammation — are controlled via pathway cross-talk, feedback loops, and receptor desensitization/endocytosis mechanisms.
- **CO-6:** Apply knowledge of normal cellular communication to analyze how "molecular mutiny" (*e.g.*, constitutive kinase activation, evasion of apoptosis, or checkpoint failure) drives uncontrolled cell proliferation and cancer development.

Course Modules

- **Module 1: Cell Division and Cell Cycle:** General strategies and stages of the cell cycle, mitosis and meiosis, cytokinesis, control and regulation of the cell cycle.
- **Module 2: Cellular Communication and Receptor Dynamics:** The modes of cell signaling: Juxtacrine, Endocrine, Paracrine, Autocrine. Signal Life Cycle: Reception, transduction, response and termination. Signaling ligands: Hydrophilic vs. Hydrophobic. Hormones and their receptors; GPCRs, RTKs, non-protein tyrosine kinase receptors.
- **Module 3: Internal Cascades and Transductions:** Cyclic AMP (cAMP): PKA. Inositol Phospholipid Pathway: IP3 and DAG releasing Ca^{2+}. Calcium as a Universal Signal: Calmodulin. Phosphorylation Cascades: "Kinase vs. Phosphatase". Signaling pathways: MAPK/ERK Pathway, PI3K/Akt pathway and mTOR, JAK-STAT pathway, signaling via TNF-α, Insulin signaling pathway and glucose regulation.
- **Module 4: Termination and Oncogenic Mutations:** Feedback Loops, Receptor Desensitization, Cross-talk. Molecular Mutiny: The Breakdown of Cellular Communication in Cancer and Cell death.

Recommended Reading

- Alberts, B. et al. (2014) *Molecular Biology of the Cell*, 6th ed., W. W. Norton and Co.
- Cooper, G. M. and Hausman, R. E. (2015) *The Cell: A Molecular Approach*, 7th ed., Sinauer Associates.
- Lodish, H. et al. (2016) *Molecular Cell Biology*, 8th ed., W. H. Freeman.
- Berridge, M. J. (2014) *Cell Signalling Biology*, Portland Press.
- Bradshaw, R. A. and Dennis, E. A. (2003) *Handbook of Cell Signaling*, Academic Press.

BMB512: Developmental biology (Credits: 2 | Marks: 25)

Course Objectives

1. To trace historical foundations, transitioning from classical embryology to modern molecular genetics.
2. To analyze how differential gene expression allows a single genome to generate specialized cell fates.
3. To deconstruct cellular events of fertilization, acrosome pathways, and polyspermy blocks.
4. To compare early cleavage setups across taxa based on yolk distributions.
5. To examine genetic segments, mammalian Hox complexes, morphogen induction fields, and vertebrate organ regionalization profiles.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO 1:** Select and justify the appropriate model organism and molecular technique (Fate mapping, In Situ Hybridization, CRISPR/Cas9) to investigate specific developmental questions.
- **CO 2:** Explain how cells with identical DNA differentiate into specialized tissues via transcriptional, post-transcriptional, translational, and epigenetic regulatory mechanisms.
- **CO 3:** Detail the step-by-step signal transduction pathways involved in the acrosome reaction, egg activation, and the fast/slow blocks to polyspermy.
- **CO 4:** Classify embryonic cleavage types based on yolk distribution and predict the structural outcomes of blastulation and the Mid-Blastula Transition across different taxa.
- **CO 5:** Illustrate the cellular movements during gastrulation and explain the molecular function of the Spemann-Mangold Organizer and Hensen's Node in establishing body axes.
- **CO 6:** Analyze the maternal and zygotic genetic cascades (Drosophila gap, pair-rule, and segment polarity genes) and evaluate how the mammalian Hox complex provides positional identity to body segments.
- **CO 7:** Differentiate between induction and competence, and diagram how opposing morphogen gradients establish spatial, temporal, and positional boundaries in the developing vertebrate neural tube.

Course Modules

- **Module 1: Foundations and Gene Expression Patterns:** History of developmental biology. Techniques in developmental biology and model organisms. The pattern of Differential gene expression during development.
- **Module 2: Fertilization Kinetics and Early Cleavage:** Early Embryonic Development: Structure and function of Gametes. Egg activation. Acrosome reaction and signal transduction. Cellular and Biochemical mechanisms during fertilization and strategies for monospermy and conservation of species specificity. Cleavage and Types of cleavage and blastulation in sea urchin, frog, bird and mammals. Mid-blastula transition.
- **Module 3: Gastrulation and Axis Topologies:** Gastrulation: Gastrulation in frog and chick. Specifying body axes in amphibian and bird, primary organizer and Cellular movements. Early development and axis specification of Drosophila, Hox complex in mammals.
- **Module 4: Signal Inductions and Later Organogenesis:** Induction and competence: Cell-cell communication. Cell surface receptor and signal transduction pathways. Temporal and positional specificity in neural induction and neural competence in vertebrates. Molecular signaling by inducers and hierarchy in anterior-posterior, dorsal-ventral polarity of neural tube. Later Embryonic Development: Limb and Eye development, Organogenesis, Specification of Neural Crest, Post embryonic development- Regeneration. Implications of Developmental Biology in Modern Medicine.
- **Module 5: Plant Growth Systems and Meristems:** Growth and Development: Overview; embryogenesis; the origin of polarity; cell fate acquisition and lineage specification. Cellular plasticity (totipotency, pluripotency, dedifferentiation, redifferentiation, transdifferentiation). Meristematic tissues: Organization of root, shoot and floral meristem. De Novo organogenesis: lateral root and nodule development. Phyllotaxis; Floral transition.

Recommended Reading

- Wolpert, L., Tickle, C. and Arias, A. M. (2015) *Principles of Development*, 5th ed., Oxford University Press.
- Gilbert, S. F. and Barresi, M. J. F. (2023) *Developmental Biology*, 13th ed., Oxford University Press.
- Taiz, L., Zeiger, E., Møller, I. M., and Murphy, A. *Plant Physiology and Development*, Sinauer Associates.

BMB513: Evolution and ecology (Credits: 2 | Marks: 25)

Course Objectives:

1. To provide a clear evolutionary context spanning astronomical origins, reducing-to-oxidizing atmospheric updates, prebiotic assemblies, and the Neo-Darwinian synthesis.
2. To analyze variation parameters, allele profiles, and mathematical HWE validations inside microevolution.
3. To track hominid evolutionary chains, cultural adaptations, and modern Anthropocene selection footprints.
4. To evaluate biotic and abiotic interactions, niche dynamics, and elementary ecological modeling.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Explain the geological history of Earth and plate tectonics.
- **CO-2:** Describe the chemical origin of life and cellular evolution.
- **CO-3:** Contrast historical and modern theories of evolution.
- **CO-4:** Identify the sources of genetic variation in populations.
- **CO-5:** Trace human evolutionary history and anthropological impacts.
- **CO-6:** Distinguish between fundamental and realized ecological niches, and evaluate how factors like resource partitioning reduce competition.

Course Modules

- **Module 1: Lithosphere and Atmosphere Evolution:** Cosmic Dawn: first ten billion years and the origin of Earth. Atmospheric Shifts: reducing to the modern oxidizing atmosphere. Lithosphere Dynamics: rock cycles. Continental Drift: mechanisms of plate tectonics, supercontinents.
- **Module 2: Protocell Formations and Endosymbiosis:** Chemical Evolution: Prebiotic synthesis, RNA world hypothesis, molecular self-assembly. Membrane Bound Systems: protocells and lipid bilayers. Cellular Leap: prokaryotic emergence. Endosymbiotic Theory: mitochondria and chloroplasts. Multicellularity tracks.

- **Module 3: Synthesis of Evolutionary Models:** Early Theories: Lamarckism. Darwinian Revolution: variation, adaptation, natural selection. Genetic Basis: Mendelian inheritance role. Mutational Theory: fluctuation test. Modern Synthesis: integration with genetics.
- **Module 4: Variation Sources and Speciation Mechanics:** Individual Variation: crossover, independent assortment. Population Dynamics: gene pools, allele frequencies, Hardy-Weinberg Principle. Drivers of Microevolution: gene flow, genetic drift, mutation pressure. Speciation: reproductive isolation networks leading to allopatric and sympatric speciation.
- **Module 5: Anthropological Lineages and Ecological Modeling:** Primate Lineage: Hominid evolution fossil records. Modern Human: Homo sapiens emergence, migration models. Cultural Evolution: language, agriculture. Anthropogenic Selection: human influences on modern evolution, artificial selection. Foundations of elementary ecological modeling and population equations.
- **Module 6: Environment:** Physical and biotic environment, Biotic and abiotic interactions, the laws of limiting factors
- **Module 7: Habitat and Niche:** Concept of habitat and niche, niche width and overlap, fundamental vs realized niche, resource partitioning and character displacement
- **Module 8: Population and Community Ecology**: Characteristics of a population, population growth curves, population regulation, life history strategies (r and K selection), species interactions, competition. Introduction to community ecology.

Recommended Reading

- Hall, B. K. and Hallgrimsson, B. (2013) *Strickberger's Evolution*, 5th ed., Jones and Bartlett Learning.
- Shanker Kartik (2024) Ecology, evolution and everything, IISc Press.

BMB514: Cellular basis of immunity and host pathogen interaction (Credits: 2 | **Marks:** 25)

Course Objectives

1. To study the mechanisms of the human immune response, balancing early innate defenses like phagocytes and signaling paths with targeted acquired systems like antibodies.

2. To analyze the lifecycle of a pathogen inside a host, exploring entry points, evasion of host systems, and the function of virulence factors and toxins.

3. To study specific, real-world infectious profiles by tracking the different mechanisms used by bacterial, viral, and parasitic agents.

4. To explore how pathogens regulate their disease-causing genes and learn the molecular tools used to identify these targets in a laboratory.

5. To understand modern healthcare strategies against infectious diseases, examining how vaccines function, how antimicrobials destroy pathogens, and the mechanisms behind antimicrobial resistance (AMR).

Course Outcomes (COs)

By the end of this course, students will be able to:

CO-1: Explain the signaling pathways of both the innate and acquired immune systems, tracking how the body recognizes antigens and activates cell-mediated defenses.

CO-2: Map how pathogens enter host cells, bypass cellular defenses, and release toxins using specialized delivery systems.

CO-3: Apply modified Koch's principles to verify the relationship between a specific microorganism and a disease state.

CO-4: Analyze and compare the distinct pathogenic lifestyles and infectious strategies of key model organisms, including intracellular bacteria (Mycobacterium tuberculosis), opportunistic pathogens (Staphylococcus aureus), viral agents (Influenza virus), and parasites (Entamoeba histolytica).

CO-5: Use molecular screening methods to identify unknown bacterial virulence genes and evaluate their regulatory mechanisms.

CO-6: Critically evaluate the mechanisms of vaccinations and antimicrobials, and formulate an understanding of the genetic basis and challenges surrounding Antimicrobial Resistance (AMR).

Course Modules

Module 1: Cellular Basis of Immunity: The first line of defence (Innate immunity) – Phagocytes, complement cascades, cytokines, TLRs and their signalling pathways. The second line of defence (Acquired immunity) – Antibodies, Cytotoxic T lymphocytes, Antigen processing and presentation.

Module 2: Host-pathogen interaction: Linking a microbe to a disease – the Koch's principle and its modifications. Entry of pathogens into host cells and mechanisms of evasion of host cell defences. Toxins and virulence factors – their mode of action and delivery using secretion systems. Regulation of virulence gene expression. Molecular methods to identify virulence genes.

Module 3: Cases studies: Mycobacterium tuberculosis –intracellular pathogen, Staphylococcus aureus – an opportunistic pathogen, Influenza virus – a viral pathogen and Entamoeba histolytica - a parasite.

Module 4: Prevention and therapy: Vaccinations, antimicrobials, antimicrobial resistance (AMR)

Recommended Reading:

- Kenneth Murphy and Casey Weaver (2016) Janeway's Immunobiology, 9th Edition. Garland Science.
- Jenni Punt, Sharon Stranford, Patricia Jones, and Judith A. Owen (2018) Kuby Immunology. 8th Edition. W. H. Freeman.
- Brenda A. Wilson, Malcolm F. Winkler, and Brian T. Ho (2019) Bacterial Pathogenesis: A Molecular Approach. Washington, 4th Edition. ASM Press.
- Jane Flint, Vincent R. Racaniello, Glenn F. Rall, and Anna Marie Skalka (2015) Principles of Virology, 4th Edition. ASM Press.
- Michael T. Madigan, Kelly S. Bender, et al. (2018) Brock Biology of Microorganisms, 15th Edition. Pearson.
- Kathleen Park Talaro and Barry Chess (2018) Foundations in Microbiology, 10th Edition. McGraw-Hill Education.

- Kateryna Kon and Mahendra Rai (2016) Antibiotic Resistance: Mechanisms and New Antimicrobial Approaches, 1st Edition . Academic Press.

BMB515: Biomolecules III (Credits: 2 | Marks: 25)

Course Objectives

1. To enable students to critically evaluate how uniform magnetic fields, paired with specialized radiofrequency pulses and spatial linear gradients, differentiate structural chemistry (MRS) from spatial anatomy (MRI).
2. To establish a thorough mathematical understanding of Fourier operations across multiple modalities: time-to-frequency transformations in FT-NMR, k-space-to-real-space translation in MRI, and reciprocal-space structure factors in X-ray diffraction.
3. To train students to interpret validation boundaries across structural disciplines, including Rfree parameters in crystallography, NOE restraints in MRS, and FSC curves in single-particle Cryo-EM.
4. To train students to compute the necessary magnetic field gradient strengths and RF bandwidths required to isolate a specific slice or volume during spatial encoding in MRI.
5. To equip students with the skills to read 2D NMR spectral topologies (COSY/TOCSY) for assigning polypeptide backbones and establishing high-resolution proximity constraints.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Deconstruct 2D COSY and TOCSY spectral cross-peaks to map scalar coupling networks and establish sequential amino acid resonance assignments in polypeptide backbones.
- **CO-2:** Formulate the exact sequence of slice-selection, phase-encoding, and frequency-encoding gradients needed to target a specific spatial plane, and calculate the resulting coordinate parameters within k-space.
- **CO-3:** Differentiate between T1, T2, and Proton Density pulse parameters (TR and TE) to predict or optimize image contrast profiles between different biophysical tissues.
- **CO-4:** Apply Bragg's Law and structure factor calculations to predict diffraction spot intensities, and evaluate the reciprocal lattice space to identify systematic absences caused by screw axes or glide planes.
- **CO-5:** Select and justify the optimal structural biology method (MAD, SAD, or Molecular Replacement) required to recover lost phase information from an unknown protein crystal data set.

- **CO-6:** Integrate 2D alignment coordinates, sorting metrics, and Fourier Shell Correlation criteria to construct, refine, and validate a 3D structural model from raw Cryo-EM particle datasets.

Course Modules

- **Module 1: Macromolecular Magnetic resonance spectroscopy**: Quantum model for spin 1/2 nuclei; Classical Model; FT-NMR, NMR spectrometer and pulse sequence, Chemical shift; J-coupling; Relaxation; Rates and mechanisms, Correlation time, Spin decoupling; NOE, Spin echo, Applications of NMR in macromolecules, Multi-dimensional NMR; COSY; TOCSY, NOESY; Protein NMR; General Principles; Resonance Assignment.
- **Module 2: Elementary MRI Principles:** Spatial encoding gradients, magnetic field gradients, slice selection, frequency and phase encoding. k-space trajectories and frequency domains. 2D Inverse Fourier Transformation. Image contrast mechanics: T1, T2, and Proton Density weighting profiles.
- **Module 3: X-Ray Crystallography Diffraction:** Crystals; Types of lattices and symmetry, Scattering by atoms and molecules; Scattering in terms of Fourier transforms, Interference from sets of atoms and Bragg's Law, Reciprocal lattice and systematic absences, Electron density calculations and phase problem; Solutions to phase problem, Patterson function, Model building and Refinement.
- **Module 4: Elementary Cryo-Electron Microscopy:** Vitrification mechanics: liquid ethane plunge freezing, amorphous vitreous ice controls. Contrast Transfer Function (CTF), Motion Correction**,** defocus operations, phase flipping corrections. Single Particle Analysis (SPA) workflow: alignment, classification, 3D back-projection, Fourier Shell Correlation (FSC) criteria, Local vs global resolution; Map sharpening; Model fitting; Validation concepts.

Recommended Reading

- Michael Lipton (2010) Totally Accessible MRI, Springer.
- Thomas Engel et al. (2019) Quantum Chemistry and Spectroscopy 4th Edition, Pearson.
- Jan Drenth (2007) Principles of Protein X-Ray Crystallography 3rd Edition, Springer.
- Ignacio Tinoco, Jr. et al. (2014) Physical Chemistry: Principles and Applications in Biological Sciences, 5th Edition, Pearson.
- James Keeler (2002) Understanding NMR Spectroscopy, Free Web Edition.

- Sherwood, D. and Cooper, J. (2010). Crystals, x-rays and proteins: comprehensive protein crystallography. Oxford university press.
- Ipsita Banerjee (2025) Notebook on Structural Biology Techniques: Study Guide for Practitioners, World Scientific.
- Subrata Pal (2023) Mathematical Approaches to Molecular Structural Biology. Academic Press
- Subrata Pal (2026) Fundamentals of Molecular Structural Biology 2nd Edition, Academic Press
- Joachim Frank (2006) Three-Dimensional Electron Microscopy of Macromolecular Assemblies, 2nd Edition, OUP
- Joachim Frank (2006) Electron Tomography, 2nd Edition, Springer.

BMB 516: Genetics and genomics (Credits: 4 | Marks: 50)

Course Objectives

1. To enable students to critically distinguish between monogenic, complex non-Mendelian, and multifactorial patterns of disease transmission using precise clinical pedigree metrics.
2. To establish a molecular and geometric understanding of how phenomena like random X-inactivation, dynamic repeat mutations, imprinting boundaries, and tissue mosaicism alter classical genomic inheritance ratios.
3. To provide a comprehensive mathematical foundation in population dynamics, allowing students to map how selection, drift, migration, and mutation dynamically shift allele frequencies across evolutionary time.
4. To train students to mathematically construct polygenic threshold models, calculate familial recurrence risks, and map continuous genomic liabilities to clinical disease states.
5. To equip students with the statistical skills required to calculate allele frequencies from raw population data and evaluate deviations from Hardy-Weinberg Equilibrium.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Analyze multi-generational pedigrees to identify and differentiate non-canonical modes of transmission, accounting explicitly for maternal inheritance, skewed lyonization, pseudoautosomal crossover, and dynamic triplet expansions.
- **CO-2:** Differentiate between allelic, locus, and clinical heterogeneity when analyzing clinical profiles, and apply mathematical corrections to eliminate ascertainment biases during familial link analysis.
- **CO-3:** Predict the phenotypic outcomes of localized chromosomal mutations or deletions by constructing biochemical models of parent-of-origin genomic imprinting and somatic mosaicism.
- **CO-4:** Calculate familial disease liability scores and predict clinical recurrence risks for multifactorial traits by fitting patient pedigree data to normal liability distributions.
- **CO-5:** Compute expected genotype distributions from multi-allelic population datasets, execute Chi-Square goodness-of-fit equations, and interpret whether a population is deviating from statistical equilibrium.

- **CO-6:** Formulate differential equations to calculate how specific selection coefficients, genetic drift variables, or migration rates alter the long-term equilibrium states of deleterious alleles within a breeding population.

Course Modules

- **Module 1: Classical Genetics and Pedigree Heterogeneity:** Introduction to genetics; monogenic versus multifactorial inheritance. Gene, locus, allele, allele frequency; Mendelian pedigree patterns. Complications to Mendelian patterns - Co-dominance; mitochondrial inheritance; ascertainment bias; heterogeneity (allelic, locus, clinical heterogeneity). Lyonization, pseudoautosomal segregation; anticipation; imprinting; mosaics and chimeras.

- **Module 2: Elements of Population Genetics**

  Definitions of genotype (P, Q, R) and allele (p, q) frequencies; the directional constraint of gene pool tracking; The Hardy-Weinberg Principle; Historical significance in preserving variation against blending inheritance models.

  Parameterizing selection: Relative fitness and selection coefficients; Normalization via Mean Fitness; Selection against recessive homozygotes; Case studies.

  Mutation-Selection Balance; Equilibrium dynamics; Heterozygote Advantage (Overdominance): Asymmetric and symmetric selection coefficients and stable balancing equilibria; classic biophysical paradigm of Sickle-Cell Anemia (AS) and malaria resistance; Frequency-Dependent Selection: Dynamics of rare-allele advantages.

  The Wahlund Effect; Migration Dynamics: Gene flow as an evolutionary homogenizer; Migration-Selection Balance.

- **Module 3: Genome Architecture and Structural Genomics**

  High-Resolution Chromatin Topography: Three-dimensional organization of the genome; Hierarchical folding, Topologically Associating Domains (TADs), and Lamina-Associated Domains (LADs). Principles of Chromosome Conformation Capture techniques.

Advanced Sequencing Paradigms: Comparative evaluation of Next-Generation Sequencing (NGS) cyclic reversible termination chemistry versus Third-Generation single-molecule real-time (SMRT) and synthetic/protein nanopore sequencing.

- **Module 4: Functional Genomics and Epigenomic Landscapes**

  The Transcriptional Continuum: High-throughput transcriptomics via RNA-Seq; library preparation variations (total RNA vs. mRNA-Seq vs. nascent RNA sequencing). Statistical frameworks for differential gene expression analysis. Single-cell RNA sequencing (scRNA-Seq) principles and dimensionality reduction pipelines.

  Epigenetic Modification Mapping: Molecular mechanisms and genome-wide profiling of DNA methylation (Bisulfite sequencing/WGBS) and histone modifications. Chromatin accessibility profiling using ChIP-Seq and ATAC-Seq.

  Non-Coding Regulatory Elements: Functional classification of the non-coding genome; long non-coding RNAs (lncRNAs), microRNAs (miRNAs), and enhancers.

- **Module 5: Comparative Genomics and Systems Interactivity**

  Evolutionary and Comparative Sequence Analysis: Algorithms for whole-genome alignments. Detection of orthologs, paralogs, and xenologs. Identification of evolutionary constraints, highly conserved elements, and genomic islands.

  Metagenomics and Environmental Sequencing: Culture-independent genomic analysis; 16S/18S rRNA amplicon sequencing vs. shotgun metagenomics. Computational binning, taxonomic assignment, and functional metabolic profiling of complex microbiomes.

Recommended Reading:

- Meneely, P. (2014) Genetic Analysis: Genes, Genomes and Networks in Eukaryotes. 2nd edition. Oxford University Press.
- Hawley, R. S. and Walker, M. (2003) Advanced Genetic Analysis: Finding Meaning in a Genome. 1st edition. Wiley-Blackwell.

- Korf, B. R. and Irons, M. B. (2013) Human Genetics and Genomics. 4th edition. Wiley-Blackwell.
- Mark Ridley (2004) Evolution, 3rd edition Blackwell Publishing.
- Helmut Schiessel (2013) Biophysics for Beginners: A Journey through the Cell Nucleus, Routledge.

BMB517: Systems and integrated biology (Credits: 4 | Marks: 50)

Course Objectives

1. To introduce foundational concepts of systems biology and integrated multi-scale biological hierarchies.
2. To familiarize students with advanced experimental and data-generation techniques for biomolecular analysis.
3. To develop mathematical and computational skills for modeling biological networks and metabolic pathways.
4. To impart knowledge on dynamic systems, stability, and stochastic behaviors in cellular physiology.
5. To foster critical thinking through research literature analysis of genotype-to-phenotype relationships.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Explain biological systems from atoms to ecosystems using an integrated, multi-disciplinary approach.
- **CO-2:** Select appropriate experimental tools to analyze biomolecules and handle large-scale systems biology data.
- **CO-3:** Apply mathematical tools and structural modeling to analyze biological network kinetics and biochemistry.
- **CO-4:** Analyze cellular dynamics using phase planes, stability analysis, and bifurcation theories.
- **CO-5:** Evaluate ecological models, gene regulatory networks, and the limitations of whole-cell physiology modeling.
- **CO-6:** Critique contemporary research papers to synthesize solutions for complex cell-biological problems.

Course Modules

- **Module 1: Systems Theory Foundations:** An integrated view of biology – from atoms to ecosystems (what is systems, need of systems and integrated approach).

- **Module 2: Experimental Multi-Scale Data Generation:** A summary on experimental techniques to study biomolecules and biomolecular interactions. Experimental techniques used in small and large scale data generation for systems biology study.
- **Module 3: Large-Scale Omics and Systems Integration:** Omics data pipelines. Multi-omics data normalization techniques. Network-based data integration strategies. Embedding data into structural systems models.
- **Module 4: Network Informatics and Systems Biochemistry:** Mathematical tools to study the theory of networks and its application to understand different levels of biological systems; systems biochemistry - alternate approaches; structural and kinetic modeling; basics of kinetic modeling - its advantages and disadvantages in studying biological systems; structural modeling in metabolism.
- **Module 5: Dynamical systems**: Definition and examples; phase plane analysis; nullclines; stability analysis; bifurcation analysis; signal transduction; ultrasensitivity; gene regulatory networks; stochastic modelling.
- **Module 6: Practical Seminar Presentation Component:** Apart from the coursework, students will be assigned recent papers on systems biology for seminar presentations.

Recommended Reading:

- Alon U (2020) An introduction to systems biology: Design principles of Biological circuit., Chapman and Hall
- Klipp E. et al. (2016) Systems Biology: A Textbook, Wiley-VCH

BMB518: Molecular and cell biology techniques (Practical) (Credits: 2 | Marks: 25)

- *Assessment Strategy:* Continuous Laboratory Assessment Model followed by *viva voce.*

Course Objectives

1. Advanced Molecular Biology Technique syllabus bridges foundational theory and cutting-edge laboratory applications. It typically trains students on gene manipulation, "omics" analysis, and genome editing.

   Advanced Molecular Biology Techniques connect the cellular basis of immunity and cell line manipulations with advanced automated diagnostic validation pipelines. Train students to gate flow cytometric data, isolate and identify apoptotic phases, change in mitochondrial membrane potentials, and analyze organelle co-localizations under high-resolution fluorescence microscopes.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Analyze flow cytometric data sets using precise multi-parameter gating loops.
- **CO-2:** Distinguish apoptotic phases (Viable vs. Early vs. Late) using Annexin V / PI quadrant statistics.
- **CO-3:** Compute mitochondrial membrane polarization changes via JC-1 aggregate/monomer ratios.
- **CO-4:** Map protein co-localization boundaries using vital dye organelle trackers and immunofluorescence.

Course Modules

Module 1: Flow Cytometric Gating and Cell Cycle Analysis: Analysing flow cytometric data: Cell Surface Phenotyping: Gating hierarchy. Expression data comparisons (Percentage (%) vs. MFI). Cell Cycle Analysis: phase quantification identifying G0/G1 (2n), S, and G2/M (4n) populations; Sub G1 Peak identifying fragmented apoptotic DNA.

Module 2: Apoptosis and MMP Analysis: Analysing apoptosis and cell death: Annexin V / PI (or 7-AAD) Assay quadrant analysis distinguishing viable (A^-/PI^-), Early Apoptotic (A^+/PI^-), and Late Apoptotic/Necrotic (A^+/PI^+) cells. Analysing Mitochondrial Membrane Potential: JC-1 dye checking J-Aggregates (Red): High potential vs. Monomers (Green): Depolarized.

Module 3: Multiplex Fluorescence Microscopy: Visualizing cell structure and protein localization using fluorescence microscopy: Immunofluorescence (IF): Direct vs. indirect. Organelle Tracking using organelle specific vital dyes and protein co-localization.

Module 4: Immunohistochemistry Expression Profiles: Analysing immunohistochemistry (IHC) data: protein expression and activation in tissue samples; assessing tissue inflammation by identifying inflammatory cells and tracking mucosal thickness parameters.

Module 5: Advanced Nucleic Acid Manipulation and Amplification

High-Throughput PCR Methods: Multiplex PCR, nested PCR, real-time quantitative PCR (RT-qPCR) for gene expression. Cloning and Mutagenesis: Site-directed mutagenesis and cloning techniques.

Sequencing Technologies: Next-Generation Sequencing (NGS) platforms, RNA-seq and Single-Cell RNA sequencing (scRNA-seq).

Module 6: Genome Editing and Synthetic Biology

CRISPR-Cas Systems: Mechanism, guide RNA (gRNA) design, off-target analysis, and genome engineering (knock-outs/knock-ins).

Module 7: Protein Analysis and Interactions

Protein Expression and Purification: Recombinant protein expression in bacterial/eukaryotic systems and affinity chromatography (His-tag, GST-tag).

Macromolecular Interactions: Yeast two-hybrid screening, ChIP-seq, EMSA.

Structural Techniques: Mass spectrometry for proteomics and Cryo-Electron Microscopy (Cryo-EM) principles.

Module 8: Functional Genomics and Epigenetics

Gene Silencing: RNA Interference (RNAi), siRNA, and miRNA applications.

Epigenetic Profiling: Sequencing for DNA methylation and ATAC-seq for chromatin accessibility.

Gene Delivery: Viral vectors (Lentivirus, Adenovirus), electroporation, and microinjection.

Recommended reading:

1. Flow cytometry protocols (Methods in Molecular Biology series) by Teresa S. Hawley and Robert G. Hawley.
2. Fluorescence Microscopy: Cellular and Molecular Imaging by F.S. Ligler and C.R. Taitt
3. Bancroft's Theory and Practice of Histological Techniques by S. Kim Suvarna, Christopher Layton, and John D. Bancroft.
4. Advanced Methods in Molecular Biology and Biotechnology: A Practical Lab Manual by Khalid Z. Masoodi

BMB521: M.Sc. Thesis (Research) (Credits: 12 | Marks: 150)

Course Objectives

1. To execute an original, independent laboratory or theoretical research project under the mentoring of a designated departmental faculty member.
2. To train students to manage bench timelines, document daily experimental logs, present data summaries in review forums, and assemble a formal scientific thesis report defensible before a panel of external field experts.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Design and execute a research plan to address an open biological problem.
- **CO-2:** Maintain systematic scientific records and data sheets.
- **CO-3:** Formulate and structure a comprehensive research thesis following standard scientific publishing criteria.
- **CO-4:** Defend research data and theoretical models before a formal panel of internal and external academic examiners.

Evaluation Framework

- Project assignment is finalized by the Departmental Committee based on student preferences and previous performances.
- The final thesis is evaluated by an external expert followed by a seminar and viva-voce examination.
- **Allotment of Marks:** Internal assessment by the supervisor: 40% | Seminar + Report + Viva-voce: 60%.

BMB522: Research methodology and project writing (Practical) (**Credits:** 4 **Total Marks:** 50)

Course Objectives

1. To provide an advanced theoretical and operational understanding of the scientific method, experimental design, and the statistical or structural validation of biological data.
2. To establish a clear structural framework regarding the global intellectual property regime, patentability criteria, and the legal protocols of patent drafting and clinical translation.
3. To train students to identify, prevent, and mitigate scientific misconduct (plagiarism, data falsification, and fabrication) according to international publishing standards.
4. To equip students with the ethical reasoning and regulatory knowledge required to safely navigate animal welfare codes, human clinical trial protocols, and genetically modified organism (GMO) biosafety constraints.

Course Outcomes (COs)

By the end of this course, students will be able to:

- **CO-1:** Formulate testable, data-driven biophysical hypotheses and construct rigorous, statistically controlled experimental designs.
- **CO-2:** Detect and eliminate instances of academic plagiarism, falsification, and questionable research practices using standard screening software and the COPE guidelines.
- **CO-3:** Design and evaluate institutional bioethics protocols for projects involving animal models, human tissue samples, or recombinant DNA vectors.
- **CO-4:** Map the landscape of a specific technology area using international patent databases to assess the criteria of novelty, inventive step, and industrial applicability.
- **CO-5:** Structure a formal, multi-tiered research grant proposal or patent specification file adhering to standard statutory frameworks.

Course Modules

Module 1: Philosophy of Science and Experimental Design

- **The Scientific Method:** Formulation of research hypotheses; deductive vs. inductive reasoning layouts; identifying knowledge gaps in structural biology and multi-omics.
- **Experimental Controls and Optimization:** Selecting negative, positive, and vehicle controls; blind and double-blind experimental setups; reducing selection and measurement biases.

- **Data Reproducibility and Sampling:** Defining sample sizes, power analysis, and technical vs. biological replicates; handling outliers and managing raw data sheets in computational laboratories; open-access data sharing and version control frameworks (e.g., GitHub, Zenodo).

Module 2: Scientific Integrity, Misconduct and Publishing Ethics

- **The Ethics Matrix:** Fundamental principles of research integrity; values of objectivity, honesty, and accountability in the laboratory.
- **Scientific Misconduct (The Triad of FFP):** Explicit boundary definitions for Fabrication, Falsification, and Plagiarism. Questionable Research Practices (QRPs): image manipulation, selective data reporting, p-hacking, and duplicate submissions.
- **Global Publishing Protocols:** Core guidelines established by the Committee on Publication Ethics (COPE); criteria for authorship assignment (first vs. corresponding author contributions, honorary and ghost authorships); managing conflicts of interest and disclosure policies.
- **Navigating the Academic Landscape:** Journal metrics (Impact Factors, CiteScore, h-index, i10-index); identifying and avoiding predatory journals; publishing models: traditional subscription, hybrid, and Open Access options (Creative Commons licensing); leveraging preprint registries (bioRxiv, arXiv) for early dissemination.

Module 3: Bioethics, Biosafety and Environmental Biosecurity

- **Animal and Human Research Ethics:** Regulatory frameworks governing animal experiments; the 3Rs principle (Replacement, Reduction, Refinement); roles of the Institutional Animal Ethics Committee (IAEC). Ethical guidelines for human biomedical research (Declaration of Helsinki); informed consent workflows and privacy protections; functions of the Institutional Ethics Committee (IEC).
- **Recombinant DNA Safety and GMOs:** Biosafety guidelines for handling genetically modified organisms (GMOs) and living modified organisms (LMOs); containment levels (BSL-1 to BSL-4 parameters); roles of the Institutional Biosafety Committee (IBSC) and federal regulatory nodes (e.g., RCGM, GEAC in India).
- **Biosecurity Concerns:** Dual-use research of concern (DURC); biological weapons conventions; environmental safety of synthetic biology and gene-drive interventions.

Module 4: Intellectual Property Rights (IPR) and Patient Dynamics

- **Foundations of IPR:** Conceptual definition of intellectual property; international treaties and conventions (TRIPS Agreement, Paris Convention, Patent Cooperation Treaty (PCT), Madrid Protocol).

- **Forms of IP Protection:** Core operational differences between Patents, Copyrights, Trademarks, Trade Secrets, and Geographical Indications (GIs); Protection of Plant Varieties and Farmers' Rights (PPVandFR).
- **The Mechanics of Patentability:** The three strict criteria for patent grants: Novelty, Inventive Step (Non-obviousness), and Industrial Applicability. Exploring non-patentable subject matter under regional statutory acts (e.g., Section 3 of the Indian Patent Act, highlighting exceptions for naturally occurring biomolecules, micro-organisms, and software codes).
- **Patent Searching and Specification Layouts:** Executing structural prior-art searches across global databases (Google Patents, Espacenet, USPTO, InPASS). Anatomy of a patent application: Provisional vs. Complete Specifications; drafting abstract, description, background, and the legal enforcement boundaries of Patent Claims.

Module 5: Grant Proposal and Project Writing Mechanics

- **The Project Architecture:** Anatomy of a competitive, multi-tiered research grant proposal (modeled after frameworks like ANRF, DBT, SERB, or ICMR).
- **Drafting the Components:** Writing a compelling executive summary; outlining specific, sequential research aims; preparing comprehensive preliminary data sheets; structuring project timelines using Gantt charts.
- **Resource Optimization:** Designing project budgets; justifying capital equipment purchases, consumable expenditures, contingency funds, and manpower requirements; establishing measurable milestones and risk mitigation strategies

Evaluation Framework

- **Case Studies in Misconduct:** Critically analyzing redacted, real-world retractions and image manipulation anomalies sourced from Retraction Watch.
- **Plagiarism Verification:** Hands-on training using professional anti-plagiarism screening tools to interpret similarity reports.
- **Prior-Art Patent Mining:** Assigning students a specific biophysical setup, biochemical modification, or drug molecule to run an exhaustive prior-art landscape report across patent databases.
- **Mock Grant Defense:** Formulating and presenting an original, independent mock research grant proposal before a departmental peer-review panel.

Recommended Reading

- Percie du Sert N et al. The ARRIVE guidelines 2.0: Updated guidelines for reporting animal research. PLoS Biol. (2020) Jul 14;18(7):e3000410. doi: 10.1371/journal.pbio.3000410.
- *On Being a Scientist: A Guide to Responsible Conduct in Research*. (2009) 3rd Edition, National Academies Press.
- Resnik, D. B. (2018) *The Ethics of Science: An Introduction*. Routledge.
- Ganguli, P. (2001) *Intellectual Property Rights: Unleashing the Knowledge Economy*. Tata McGraw-Hill.
- ICMR (2017) NATIONAL ETHICAL GUIDELINES FOR BIOMEDICAL AND HEALTH RESEARCH INVOLVING HUMAN PARTICIPANTS

BMB523: Grand viva (Credits: 4 | Marks: 50)

Course Objectives

1. To evaluate the student's global understanding, integration, and communication of the core principles of biophysics and molecular biology amassed over the course of the degree.
2. To assess the student's capacity to synthesize connections across distinct domains.
3. To test the student's spontaneous problem-solving capacities and readiness to defend structural workflows.
4. To prepare the students to succeed before diverse interview boards in both academic research and industry environments.

Evaluation Framework

Comprehensive oral assessment before a panel of internal and external expert examiners checking cross-disciplinary integration capabilities, spontaneous problem-solving ability, and complete conceptual alignment with the four-semester training.