UNIVERSITY OF DELHI

MASTER OF SCIENCE (BIOPHYSICS AND BIOINFORMATICS)

based on

NEP-PGCF-2024

As approved in the meeting of 'Committee of Courses' held on 06-Feb-2026 and in the meeting of 'Faculty of Interdisciplinary and Applied Sciences' held on 23-Feb-2026, and in the meeting of 'Standing Committee' held on 13-Mar-2026

PROGRAMME BROCHURE

XXXXX Revised Syllabus as approved by Academic Council on XXXX, 2025 and Executive Council on YYYY, 2025

I. About the Department

Department Highlights

The Department of Biophysics was established in 1984 and is part of the FIAS (Faculty of Interdisciplinary and Applied Sciences) at the University of Delhi South Campus. The department currently has five faculty members engaged in various research areas in Biophysics and Bioinformatics.

About the Program

The M.Sc. Biophysics and Bioinformatics program offered by Delhi University is of two years' duration and is divided into four semesters. The various courses of the program are designed to include classroom teaching and lectures, hands-on practical and tutorials, dry and wet laboratory work, and dissertations.

Six categories of courses are being offered in this program: Discipline Specific Core Courses (DSC), Discipline Specific Elective Courses (DSE), Generic Elective Courses (GE), Skill Based courses (SB), Research methods/ tools/ writing courses under Research Track (RT), and Dissertation Research work. Students may opt for any Generic Elective courses offered by any other Department of the Faculty of Interdisciplinary and Applied Sciences. The Core Courses, the Elective Courses and Generic Electives are four credit courses each. As per the University guidelines, the student is required to accumulate twenty-two credits each semester, a total of eighty-eight credits, to fulfill the requirements for a Master of Science (PG) degree in Biophysics and Bioinformatics.

The M.Sc. in Biophysics and Bioinformatics is an interdisciplinary program designed to bridge the gap between biology, physics, and computational sciences. The course integrates biophysical principles, molecular biology, computational biology, and bioinformatics to generate, interpret, and analyze large-scale biological datasets. The curriculum integrates theoretical knowledge with practical skills to train students in modern biophysics and bioinformatics, making them competent for careers in academia, healthcare, pharmaceuticals, and biotechnology industries.

Program Objectives (POs):

The program aims at equipping the students with advanced knowledge and skills in the area of biophysics and bioinformatics, such as to enable them to address present lacunae in biological systems understanding, with the following detailed objectives:

1. Foundational Knowledge in Biophysics & Bioinformatics

- Introduce students to fundamental principles of biophysics, molecular biology, bioinformatics, and computational biology.
- Provide a strong foundation in chemical, physical, and mathematical principles underlying biological processes.
- Equip students with knowledge of macromolecular interactions, protein structure, and cellular mechanisms.

2. Skill Development in Experimental and Computational Techniques

- Train students in molecular biology, genetic engineering, proteomics, and bioinformatics methodologies.
- Develop proficiency in computational biology tools, bioinformatics databases, and molecular modeling.
- Provide hands-on experience in biophysical techniques like spectroscopy, chromatography, and electrophoresis.
- Familiarize students with cell culture techniques and proteomics-based analytical methods.
- Equip students with knowledge of gene regulation, genetic engineering, and genome editing technologies (e.g., CRISPR, TALENs).
- Develop skills in protein-protein interactions, and vaccine development.

3. Application of Biophysics and Bioinformatics in Research and Industry

- Enhance understanding of drug discovery, protein engineering, and genetic manipulation.
- Introduce applications of biophysics in disease modeling, structural biology, and vaccine development.
- Enable students to apply bioinformatics in genome sequencing, phylogenetic analysis, and personalized medicine.

4. Critical Thinking and Problem-Solving

- Encourage students to analyze and interpret biological data using statistical and computational approaches.
- Train students to design experiments for biomolecular research, drug development, and biomedical engineering.
- Develop skills in scientific communication, literature review, and data presentation.

5. Preparing for Advanced Research and Careers in Biotechnology & Healthcare

- Prepare students for careers in biotechnology, pharmaceuticals, computational biology, and academic research.
- Equip students with knowledge of current trends in biotherapeutics, vaccines, and bioenergetics.
- Provide exposure to ethical considerations, regulatory guidelines, and real-world applications in biosciences.

6. Genetic and Structural Insights into Biological Systems:

- Equip students with knowledge of gene regulation, genetic engineering, and genome editing technologies (e.g., CRISPR, TALENs).
- Develop skills in protein-protein interactions, drug discovery, and vaccine development.

7. Application of Biophysical and Bioinformatics Approaches:
    - Bridge the gap between wet-lab experiments and computational biology.
    - Enable the integration of machine learning and AI-driven approaches for analyzing biological datasets.

Program Specific Outcomes (PSOs):

Upon successful completion of the M.Sc. in Biophysics and Bioinformatics, graduates will be well-equipped to contribute to the biotechnology and biological data analysis industries in the following areas:

1. Biotechnology Industry Contributions
- Drug Discovery & Development:
    - Apply computational modeling for drug design and screening.
    - Analyze protein-ligand interactions for pharmaceutical applications.
- Genetic Engineering & Synthetic Biology:
    - Utilize CRISPR, gene editing, and molecular cloning for therapeutic and agricultural advancements.
    - Engineer microbial and plant-based biofactories for biopharmaceuticals and industrial enzymes.
- Bioprocessing & Biomanufacturing:
    - Apply protein purification, expression optimization, and bioanalytical techniques in biopharmaceutical production.
    - Optimize fermentation and metabolic pathways using computational tools.
- Vaccine & Biotherapeutic Development:
    - Design rational vaccines and immunotherapies.
    - Conduct immune response modeling for personalized medicine.

2. Biological Data Science and Analysis
- Big Data Analytics in Life Sciences:
    - Analyze high-throughput genomic, transcriptomic, and proteomic datasets.
    - Use machine learning and AI for predictive modeling in personalized medicine.
- Computational Biology & Bioinformatics Tools:
    - Perform sequence alignment, phylogenetics, and structural modeling.
    - Develop and use databases for genomic and proteomic research.
- Systems Biology & Omics Data Integration:
    - Model biological networks for understanding disease mechanisms.
    - Integrate multi-omics data (genomics, transcriptomics, proteomics) for biomarker discovery.
- Statistical & Programming Skills for Biological Data Analysis:
    - Use R, Python, and bioinformatics pipelines for statistical inference.
    - Apply machine learning algorithms to classify biological patterns and anomalies.

About Program Structure

The M.Sc. Biophysics and Bioinformatics program is a two year program that is divided into four semesters. The program structure is based on the Post Graduate Curricular Framework (PGCF) under (New Education Policy) NEP-2020. The student is required to complete eighty-eight credits for the completion of the course and the award of a degree. The student has to accumulate twenty-two credits in each of the four semesters.

Under PGCF, during the first year of the program, the student is required to study mandatory six Discipline Specific Core courses (three DSC in each semester), and a total of four Discipline Specific Elective courses (two DSE in each semester). The student can also opt for 1GE from another sister department from FIAS instead, thus making this combination as 1DSE+1GE. In addition, the student will also be required to study 1 mandatory Skill based course (SBC) of 2 credits in each semester of the first year.

In the second year of the program, the student will choose any one of the two structures: Program Structure 1 (PG with only coursework), or Program Structure 2 (PG with coursework and research). Program structure 2 has a dissertation option that is continuous in both semesters. The Program Structure 3 (PG with research) is not being offered currently (as per the university guidelines). Both Structures- 1 and 2, require the student to complete two DSC in each semester. A student is expected to complete 3 DSE or 2DSE+GE combination in both semesters under structure-1. In Structure-2, a student has to opt for 2DSE or 1DSE+GE combination in both semesters along with a dissertation. Structure-1 also includes a 2 credit Skill based course in each semester. The details of the course credits and the courses available under each category of courses (DSC, DSE, GE, SB, RT) are elaborated in the tables ahead.

A minimum of 75% attendance in the practical and theory classes would be mandatory requirement for appearing in exams and obtaining the degree.

Course Credit Scheme

Program Structure-1: (PG with only coursework)

Sem	*Core courses (DSC)*		*Elective courses (DSE/GE)*		*Skill based courses (SB)*		*Res Track courses (RT)*		*Dissertation/ Project*		*Total Credits*
	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	
I	3	12	2	8	1	2	-	-	-	-	22
II	3	12	2	8	1	2	-	-	-	-	22
III	2	8	3	12	1	2	-	-	-	-	22
IV	2	8	3	12	1	2	-	-	-	-	22
Total Credits	**40**		**40**		**8**		**-**		**-**		**88**

Program Structure-2: (PG with coursework + research)

Sem	*Core courses (DSC)*		*Elective courses (DSE/GE)*		*Skill based courses (SB)*		*Res Track courses (RT)*		*Dissertation/ Project*		*Total Credits*
	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	
I	3	12	2	8	1	2	-	-	-	-	22
II	3	12	2	8	1	2	-	-	-	-	22
III	2	8	2	8	-	-	-	-	1	6	22
IV	2	8	2	8	-	-	-	-	1	6	22
Total Credits	**40**		**32**		**4**		**-**		**12**		**88**

Program Structure-3: (PG with research) (not being offered currently *)

Sem	*Core courses (DSC)*		*Elective courses (DSE/GE)*		*Skill based courses (SB)*		*Res Track courses (RT)*		*Dissertation/ Project*		*Total Credits*
	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	No. of Courses	Total Credit	
I	3	12	2	8	1	2	-	-	-	-	22
II	3	12	2	8	1	2	-	-	-	-	22
III	1	4	1	4	-	-	2	4	1	10	22
IV	-	-	1	4	-	-	1	2	1	16	22
Total Credits	**28**		**24**		**4**		**6**		**26**		**88**

SEMESTER-WISE PROGRAM STRUCTURE of M.Sc. BIOPHYSICS AND BIOINFORMATICS COURSE (NEP-PGCF)

First year (Common in Program Structure 1, 2 and 3)

Semester-1 ***** *(a student can opt for either two DSE course, or one DSE with one GE)*

	Credits in each course			
	Theory	Tutorial	Practical	Credits
Discipline Specific Core (DSC) courses				
BP-DSC01: Biophysical Chemistry	3	0	1	4
BP-DSC02: Molecular Biology	3	0	1	4
BP-DSC03: Protein Sciences: Emerging Frontiers	3	0	1	4
Discipline Specific Elective (DSE) courses*				
#BP-DSE01: Cellular Proteomics	3	1	0	4
BP-DSE02: Statistics and Programming for Life Sciences	3	0	1	4
BP-DSE03: Vaccines and Biotherapeutics	3	0	1	4
Generic Elective courses*				
#BP-DSE01: Cellular Proteomics	3	1	0	4
Skill-based course/ workshop/ Specialized laboratory/ Hands on Learning				
BP-SBC01: Specialised Laboratory – I: Molecular Biology	0	0	2	2
Research Methods/ Tools/ Writing				
-	-	-	-	-
Dissertation/ Academic Project/ Entrepreneurship/ Intensive problem-based research				
-	-	-	-	-
Total credits				22

#BP-DSE01 is designed to be of Interdisciplinary nature and is open to students from other departments as well.

SEMESTER-WISE PROGRAM STRUCTURE of M.Sc. BIOPHYSICS AND BIOINFORMATICS COURSE (NEP-PGCF)

First year (Common in Program Structure 1, 2 and 3)

Semester-2 * *(a student can opt for either two DSE course, or one DSE with one GE)*

	Credits in each course			
Course	Theory	Tutorial	Practical	Credits
Discipline Specific Core (DSC) courses				
BP-DSC04: Computational Biology and Bioinformatics	3	0	1	4
BP-DSC05: Cellular Biophysics and Bioenergetics	3	0	1	4
BP-DSC06: Genetic Engineering	3	0	1	4
Discipline Specific Elective (DSE) courses*				
#BP-DSE04: Environmental Biophysics	3	1	0	4
BP-DSE05: Biophysical methods: Fundamental Techniques	3	0	1	4
BP-DSE06: Text Mining Methods in Biology	3	0	1	4
Generic Elective courses*				
#BP-DSE04: Environmental Biophysics	3	1	0	4
Skill-based course/ workshop/ Specialized laboratory/ Hands on Learning				
BP-SBC02: Specialised Laboratory – II: Cell Biology and Bioinformatics	0	0	2	2
Research Methods/ Tools/ Writing				
-	-	-	-	-
Dissertation/ Academic Project/ Entrepreneurship/ Intensive problem-based research				
-	-	-	-	-
Total credits				22

#BP-DSE04 is designed to be of Interdisciplinary nature and is open to students from other departments as well.

Second Year: Program Structure -1 (PG with only coursework)

Semester-3 * *student can opt for either three DSE OR two DSE with one GE*

	Credits in each course			
Course	Theory	Tutorial	Practical	Credits
Discipline Specific Core (DSC) courses				
BP-DSC07: AI (Artificial Intelligence) in Drug Design	3	0	1	4
BP-DSC08: Physiological Biophysics	3	0	1	4
Discipline Specific Elective (DSE) courses*				
#BP-DSE07: Biophysical Methods: Frontiers	3	1	0	4
BP-DSE08: Biomolecular Interactions	3	0	1	4
BP-DSE09: Infection and Immunity	3	0	1	4
BP-DSE10: Protein Aggregation, misfolding and disorders	3	0	1	4
Generic Elective courses*				
#BP-DSE07 Biophysical Methods: Frontiers	3	1	0	4
Skill-based course/ workshop/ Specialized laboratory/ Hands on Learning				
BP-SBC03: Specialised Laboratory – III: Protein Chemistry	0	0	2	2
Research Methods/ Tools/ Writing				
-	-	-	-	-
Dissertation/ Academic Project/ Entrepreneurship/ Intensive problem-based Research				
-	-	-	-	-
Total credits				22

#BP-DSE07 is designed to be of Interdisciplinary nature and is open to students from other departments as well.

Semester-4 **student can opt for either three DSE OR two DSE with one GE*

Course	Theory	Tutorial	Practical	Credits
Discipline Specific Core (DSC) courses				
BP-DSC09: High-Throughput Biology	3	0	1	4
BP-DSC10: Molecular Biophysics	3	0	1	4
Discipline Specific Elective (DSE) courses*				
#BP-DSE11: Algorithms in Computational Biology	3	1	0	4
BP-DSE12: Combating diseases: leveraging in-silico approaches	3	0	1	4
BP-DSE13: Protein Engineering and applications	3	0	1	4
BP-DSE14: Cellular and molecular neurophysiology	3	0	1	4
Generic Elective courses*				
#BP-DSE11: Algorithms in Computational Biology	3	1	0	4
Skill-based course/ workshop/ Specialized laboratory/ Hands on Learning				
BP-SBC-04: Specialised Laboratory – IV: Advanced Analytical Methods	0	0	2	2
Research Methods/ Tools/ Writing				
-	-	-	-	-
Dissertation/ Academic Project/ Entrepreneurship/ Intensive problem-based Research				
-	-	-	-	-
Total credits				22

#BP-DSE11 is designed to be of Interdisciplinary nature and is open to students from other departments as well.

Second Year: Program Structure -2 (PG with Coursework and Research)

Semester-3 * *student can opt for either two DSE OR one DSE and one GE*

	Credits in each course			
Course	Theory	Tutorial	Practical	Credits
Discipline Specific Core (DSC) courses				
BP-DSC07: AI in Drug Design	3	0	1	4
BP-DSC08: Physiological Biophysics	3	0	1	4
Discipline Specific Elective (DSE) courses*				
#BP-DSE07: Biophysical Methods: Frontiers	3	1	0	4
BP-DSE08: Biomolecular Interactions	3	0	1	4
BP-DSE09: Infection and Immunity	3	0	1	4
BP-DSE10: Protein Aggregation, misfolding and disorders	3	0	1	4
Generic Elective courses*				
#BP-DSE07 Biophysical Methods: Frontiers	3	1	0	4
Skill-based course/ workshop/ Specialized laboratory/ Hands on Learning				
-	-	-	-	-
Research Methods/ Tools/ Writing				
-	-	-	-	-
Dissertation/ Academic Project/ Entrepreneurship/ Intensive problem-based Research				
Dissertation: Design Research Proposal	0	0	6	6
Total credits				22

#BP-DSE07 is designed to be of Interdisciplinary nature and is open to students from other departments as well.

Semester-4 * *student can opt for either two DSE OR one DSE and one GE*

Course	Theory	Tutorial	Practical	Credits
Discipline Specific Core (DSC) courses				
BP-DSC09: High Throughput Biology	3	0	1	4
BP-DSC10: Molecular Biophysics	3	0	1	4
Discipline Specific Elective (DSE) courses*				
#BP-DSE11: Algorithms in Computational Biology	3	1	0	4
BP-DSE12: Combating diseases: leveraging in-silico approaches	3	0	1	4
BP-DSE13: Protein Engineering and applications	3	0	1	4
BP-DSE14: Cellular and molecular neurophysiology	3	0	1	4
Generic Elective courses*				
#BP-DSE11: Algorithms in Computational Biology	3	1	0	4
Skill-based course/ workshop/ Specialized laboratory/ Hands on Learning				
-	-	-	-	-
Research Methods/ Tools/ Writing				
-	-	-	-	-
Dissertation/ Academic Project/ Entrepreneurship/ Intensive problem-based Research				
Dissertation: Analysis, Interpretation and Presentation	0	0	6	6
Total credits				22

#BP-DSE11 is designed to be of Interdisciplinary nature and is open to students from other departments as well.

SEMESTER 3

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC CORE COURSE – BP-DSC07: AI (ARTIFICIAL INTELLIGENCE) IN DRUG DESIGN

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSC07: AI (ARTIFICIAL INTELLIGENCE) IN DRUG DESIGN	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- Introduce the drug discovery pipeline and the role of AI, including data types and data-quality challenges.
- Explain machine learning and deep learning methods for target identification, molecular representation, protein structure analysis, and virtual screening.
- Explore generative AI and advanced AI approaches for de novo drug design, lead optimization, and critical evaluation of real-world applications.

Learning Outcomes

The Learning Outcomes of this course are as follows.

- Understand and analyze the AI-enabled drug discovery pipeline, including chemical and biological data types, data-quality challenges, and AI-based target identification approaches.
- Apply and compare machine learning, deep learning, and graph-based models for protein structure analysis, drug–target interaction modeling, virtual screening, and molecular property prediction.
- Evaluate advanced AI methods such as generative AI and multi-objective optimization for de novo drug design, lead optimization, ADMET prediction, and emerging real-world applications in drug discovery.

SYLLABUS OF BP-DSC-07

Theory component (45 hours)

Unit I: Drug Discovery Pipeline and the AI Revolution (6 hours)

Overview of the traditional drug discovery pipeline: target identification, lead discovery, lead optimization, preclinical and clinical stages; limitations of conventional experimental and computational approaches; emergence of AI in drug discovery post-2010 due to data explosion, high-dimensional chemical and biological spaces, and advances in computing power; overview of AI paradigms (machine learning, deep learning, generative AI) and their roles across different stages of the drug discovery process.

Essential Reading:

a) Paul, S. M. et al. How to improve R&D productivity: the pharmaceutical industry's grand challenge. Nature Reviews Drug Discovery (2010). 9(3):203-14. doi: 10.1038/nrd3078.
b) Schneider, G. Automating drug discovery. Nature Reviews Drug Discovery (2018).
c) Zhavoronkov, A. et al. Artificial intelligence for drug discovery, biomarker development, and generation of novel chemistry. Molecular Pharmaceutics (2019).
d) Vamathevan, J. et al. Applications of machine learning in drug discovery and development. Nature Reviews Drug Discovery (2019).

Unit II: Chemical and Biological Data Foundations for AI-assisted Drug Discovery (6 hours)

Types of data used in AI models: chemical representations (SMILES, molecular fingerprints, descriptors), protein sequences and structures, bioactivity and assay data, omics datasets, and phenotypic screening data; data curation, preprocessing, quality control, bias, and imbalance; challenges of sparse, noisy, and heterogeneous biological data; public databases, data integration, and data-sharing challenges; limitations of traditional molecular descriptors and motivation for learned representations.

Essential Readings:

a) Bajorath, J. Chemoinformatics and computational chemical biology. Journal of Chemical Information and Modeling (2014).
b) Wu, Z. et al. MoleculeNet: a benchmark for molecular machine learning. Chemical Science (2018).
c) Rifaioglu, A. S. et al. Recent applications of deep learning and machine intelligence on in silico drug discovery. Briefings in Bioinformatics (2019).
d) Kearnes, S. et al. Molecular graph convolutions: moving beyond fingerprints. Journal of Computer-Aided Molecular Design (2016).

Unit III: AI for Target Identification, Protein Structure, and Virtual Screening (20 hours)

AI-based target identification and validation: systems biology approaches, network and pathway analysis, disease gene prioritization, and integration of multi-omics data; case studies of AI-assisted target discovery.

AI for protein structure and drug–target interactions: conceptual overview of protein structure prediction, AI-assisted binding affinity prediction, structure-aware drug design, and protein–ligand interaction modeling.

Machine learning and deep learning for virtual screening: ligand-based and structure-based virtual screening, deep learning models for activity prediction, CNNs and graph-based molecular representations, advantages of AI over classical docking, and selected case studies.

Essential Readings:

a) Barabási, A.-L., Gulbahce, N., & Loscalzo, J. Network medicine: a network-based approach to human disease. Nature Reviews Genetics (2011).
b) Jumper, J. et al. Highly accurate protein structure prediction with AlphaFold. Nature (2021).
c) Yang, X. et al. Concepts of artificial intelligence for computer-assisted drug discovery. Chemical Reviews (2019).
d) Chen, H. et al. The rise of deep learning in drug discovery. Drug Discovery Today (2018).

Unit IV: Graph Neural Networks, Generative AI, and Lead Optimization (13 hours)

Molecules as graphs and molecular representation learning; graph-based representations and Graph Neural Networks (GNNs) for property prediction, toxicity assessment, and drug–target interaction prediction; applications in lead identification.

Generative AI for de novo drug design: chemical space exploration; generative models including VAEs, GANs, transformer-based architectures, and reinforcement learning for molecular optimization.

AI in lead optimization and ADMET prediction: optimization of potency, selectivity, and stability; AI models for ADMET, toxicity, pharmacokinetics, and bioavailability; multi-objective optimization and reducing late-stage drug attrition; illustrative case studies of AI-designed molecules.

Essential Readings:

a) Gilmer, J. et al. Neural message passing for quantum chemistry. International Conference on Machine Learning (ICML) (2017).
b) Duvenaud, D. et al. Convolutional networks on graphs for learning molecular fingerprints. NeurIPS (2015).
c) Gómez-Bombarelli, R. et al. Automatic chemical design using a data-driven continuous representation of molecules. ACS Central Science (2018).
d) Polykovskiy, D. et al. Molecular sets (MOSES): A benchmarking platform for molecular generation models. Frontiers in Pharmacology (2020).
e) Chen, R. et al. Artificial intelligence in ADMET prediction: current status and future perspectives. Drug Discovery Today (2020).

Practical component (30 hours)

1. Generation of molecular descriptors and fingerprints of a potential drug molecule.
2. To curate and clean bioactivity datasets and to build classical ML models for QSAR.
3. To identify potential disease targets using network analysis.
4. Comparison of docking vs ML-based predictions.
5. To implement a neural network for activity classification and property prediction.
6. To generate novel molecules using generative models.
7. To optimize compounds for activity and ADMET simultaneously.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC CORE COURSE – BP-DSC08: PHYSIOLOGICAL BIOPHYSICS

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSC08: PHYSIOLOGICAL BIOPHYSICS	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- Students will be able to enumerate the various processes & mechanisms controlling the physiological viability and function
- Students will understand the physical principles involved in physiological function of various organs and their sustenance.
- Students will understand the integration of principles of physiological functioning & sustenance at the whole body level.

Learning Outcomes

The Learning Outcomes of this course are as follows.

- Should be able to design nutrition.
- Should be able to understand blood related disorders and recommend precautions.
- Should understand functioning of healthy muscles and diagnose muscle disorders.
- Should understand the functioning of the heart and recommend its healthy maintenance.
- Should be able to give recommendations for respiratory problems.
- Should understand the biophysical principles of the functioning of the kidney and its maintenance.
- Should understand the role of various hormones in animal & human bodies.

SYLLABUS OF BP-DSC-07

Theory component (45 hours)

UNIT I **(10 hours)**

Levels of structural organization and body systems, Homeostasis, Chemical level of organization, Cellular level of organization
Biophysics of Digestion: Overview of the Digestive System, Phases of Digestion, and Nutrition
Composition, function, and regulation of salivary, gastric, pancreatic, bile, and intestinal juices; Metabolism of Carbohydrates, Protein, Lipids
Biophysics of Respiration: Mechanisms and control of breathing; Transport of oxygen and carbon dioxide; Oxygen dissociation curves of haemoglobin and myoglobin, Bohr effect; Chloride shift; Human respiratory disorders

Essential readings:

a) Principles of Anatomy and Physiology with Study Guide by Gerard J. Tortora
b) Biophysics: A Physiological Approach by Professor Patrick F. Dillon (Author)

UNIT II **(20 hours)**

Biophysics of the circulatory system: Composition and function of blood and lymph, Blood pressure, capillary pressure, Regulation of blood pressure, Role of ionic balance. Blood groups and Rh factors, Blood coagulation, structure and function of haemoglobin, Sickle-cell anemia, thalassemia, and other disorders
Biophysics of Heart: Structure, origin, conduction, and regulation of heartbeat; Cardiac cycle; Electrocardiogram; Disorders of the heart; Atherosclerosis, arrhythmias.
Biophysics of Muscle Function: Ultra-structural, chemical, and physiological basis of skeletal muscle contraction: Molecular mechanisms in muscle contraction.

Essential readings:

a) Principles of Anatomy and Physiology with Study Guide by Gerard J. Tortora
b) Biophysics: A Physiological Approach by Professor Patrick F. Dillon (Author)

UNIT III **(10 hours)**

Structure and Function of the kidney: Physiology of urine formation; Role of the kidney in the regulation of water, salt, and acid-base balance, renal disorders, remedies; Biophysical perspective of the above.
Integration and Control: The endocrine system, hormones and other signalling molecules, hypothalamus, pituitary, parathyroid, adrenal, pancreas, and gonads; Other endocrine elements (pancreatic islets, etc.); Local chemical mediators, prostaglandins; Consequences of endocrine malfunction; Biophysical perspective of the above.

Essential readings:

a) Principles of Anatomy and Physiology with Study Guide by Gerard J. Tortora
b) Biophysics: A Physiological Approach by Professor Patrick F. Dillon (Author)

UNIT IV **(5 hours)**

Medical biophysics: Intermolecular Forces (Dipole, Polar and Nonpolar Molecules and Solubilities), Biophysics of Thermoregulation and Heat Exchange, Biophysical Principle for Biochemical Tests, Biomedical Telemetry (Biotelemetry), Patient Monitoring System, Radioactivity and ionizing radiation

Essential readings:

a) Medical Biophysics by Judit Fidy.

Practical component (30 hours)

- To prepare the blood film and identify the blood cells.
- To observe and count the lymphocytes in the blood.
- To isolate the lymphocytes from the blood.
- Effect of hypertonic/ hypotonic/isotonic on RBC membrane.

Suggested readings

Theory:

- **Books:** The latest editions of the following books are recommended:

1. Physiology, Biophysics, and Biomedical Engineering by Andrew W Wood (Taylor & Francis).
2. Textbook of Medical Physiology by Arthur C. Guyton (Elsevier Saunders).

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE07: BIOPHYSICAL METHODS: FRONTIERS

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE07: **BIOPHYSICAL METHODS: FRONTIERS**	**4**	**3**	**1**	**0**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- The major objective of this course is to delve deeper into biophysical methods and their applications in cutting-edge biological research. It emphasizes specialized and more sophisticated analytical techniques.
- Students would be provided an understanding of the historical development of these techniques and their current applications, advantages, and limitations.
- The student will be introduced to how these methods are used in modern biological research and biotechnology industry.
- The focus would be on data interpretation using these methods. The students will be motivated to analyze and discuss most appropriate methods for tackling unique research problems.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- The students will be able to apply advanced biophysical techniques for the study of complex biomolecules.
- The student will be able to understand the principles and applications of these methods.
- The students will be able to understand the design of experiments and analyse data for structural and functional analysis of biomolecular interactions.
- Student will be able to trace the history of development of these advanced techniques, making them aware of the advantages of the interdisciplinary approaches for solving complex biological problems. They will understand the current trends in biophysics and contribute to research in this field.

SYLLABUS OF BP-DSE-07

Theory component (45 hours)

UNIT I: Macromolecular Structure determination methods (10 hours)

- X-ray crystallography: History and development of X-ray crystallography, Principles of X-ray diffraction, Methods and Challenges in crystallizing biomolecules, Overview of data collection and refinement, Phase estimation through methods like Molecular replacement, Isomorphous replacement (MIR, SIR), Anamolous Dispersion (MAD, SAD), creating electron density maps, structure validation and model fitting. Introduction to Synchrotron sources. Cryo-crystallography, Advancements ex. SAXS.
- Nuclear Magnetic Resonance (NMR): Principles of 1D, 2D, 3D spectroscopy, chemical shifts and spin-spin interaction, Multidimensional NMR for protein and nucleic acid structure, Analysis of protein-ligand complexes and molecular movements.
- Electron Microscopy: Basics of cryo-EM, sample preparation, imaging, and data collection, Types (SEM, TEM), advantages and limitations of each, Combining cryo-EM and X-ray crystallography for structural determination

Essential reading:

a) Gale Rhodes (2006). Crystallography made crystal clear. Complimentary Science Series. ISBN: 0125870736
b) Bengt Nolting (2004). Methods in Modern Biophysics Springer India, ISBN: 9788181281173

UNIT II: Advances in Microscopic methods (12 hours)

- Introduction to Fluorescence microscopy: Principles, Fluorescent dyes, GFP constructs, design of experiments to study conformational changes in a model protein or nucleic acids, Monitoring binding interactions of a ligand to a protein.
- Atomic Force microscopy: Principles, topography, force spectroscopy, and imaging at the molecular level for measuring mechanical properties of biomolecules (e.g., protein-ligand interactions, DNA stretching), Force-distance curves and the study of biomolecular interactions, imaging of single-molecule conformations and surface-bound biomolecules.
- Optical Tweezers: Principles of optical tweezers, trapping and manipulating single molecules using laser beams, Measurement of force and displacement in molecular systems, Applications in studying protein unfolding, DNA/RNA mechanics, and molecular motors, Analysis of force-extension curves and thermodynamic parameters.

Essential reading:

a) Engelbert Buxbaum (2011) Biophysical Chemistry of Proteins: An Introduction to Laboratory Methods, Springer publishers ISBN 1441972501
b) Umakanta Tripathy (Editor) (2025) Biochemical and Biophysical Methods in Molecular and Cellular Biology, ISBN: 9819620872

UNIT III: Advances in Spectroscopic Methods (12 hours)

- Time resolved Spectroscopy: Overview of time-resolved absorption, fluorescence, CD, Raman techniques, Studying protein dynamics and conformational changes, Applications in enzyme kinetics, molecular mechanisms, inhibitory mechanism (competitive, non-competitive, or uncompetitive).
- Introduction to Dynamic Light scattering (DLS): Basic principles of light scattering, measuring protein size, conformational changes and heterogeneity of solution, applications in studying protein aggregation and stability
- Nanoparticle tracking Analysis (NTA): principle, method, and applications in biological context, Applications in clinical diagnostics and therapeutic industry
- Single Molecule analysis: Overview, Historical development, Impact on molecular biology, Advantages over ensemble-averaged techniques, Applications in studying biomolecular dynamics, folding, and interactions. Single-Molecule Fluorescence Spectroscopy (SmFRET): Overview, principle, experimental setup and data interpretations of Single-molecule fluorescence microscopy experiment for monitoring conformational changes and dynamic processes in real-time.

Essential reading:

a) Engelbert Buxbaum (2011) Biophysical Chemistry of Proteins: An Introduction to Laboratory Methods, Springer publishers ISBN 1441972501
b) Umakanta Tripathy (Editor) (2025) Biochemical and Biophysical Methods in Molecular and Cellular Biology, ISBN: 9819620872

UNIT IV: Advances in Protein-ligand interaction studies (11 hours)

- Surface Plasmon Resonance (SPR): Basics of SPR and its applications in studying biomolecular interactions, Interpretation of SPR sensograms, Measuring binding kinetics between proteins and ligands,
- Bio-Layer Inferometry (BLI): Overview, principle, method and working mechanism (light interference and reflection), types of sensors, and applications in biological research, use in combination with other techniques (e.g., mass spectrometry, SPR), High-throughput BLI for screening applications, and Temperature-dependent studies.
- Iso-thermal Calorimetry (ITC): Overview, principle and historical development, comparison and advantages with other biophysical techniques (e.g., surface plasmon resonance, fluorescence). Applications in studying protein-ligand binding, protein-protein interactions, and enzyme kinetics.

Essential reading:

a) Engelbert Buxbaum (2011) Biophysical Chemistry of Proteins: An Introduction to Laboratory Methods, Springer publishers ISBN 1441972501
b) Umakanta Tripathy (Editor) (2025) Biochemical and Biophysical Methods in Molecular and Cellular Biology, ISBN: 9819620872
c) Bengt Nolting (2004) Methods in Modern Biophysics Springer India, ISBN: 9788181281173

Tutorial component (15 hours)

UNIT I: Case studies related to each technique in published research papers will be discussed:

1. Understanding crystallographic data deposited in PDB and in papers, with special emphasis on case studies in protein-ligand interactions
2. Understanding data of AFM study of DNA-protein interactions in gene regulation.
3. Understanding the data and interpretation for cryo-EM in determining structures of large macromolecular complexes, and membrane proteins.
4. Understanding and analysing DLS data for interpreting heterogeneity of the sample.
5. Understanding and analysing NTA data for interpreting particles size and interactions.
6. Understanding the SPR data to analyse binding kinetics of protein-ligand interactions.
7. Understanding the BLI data to analyse binding kinetics of protein-ligand interactions.
8. Analyzing the raw data of ITC to determine thermodynamic parameters such as binding affinity (Kd), stoichiometry (n), enthalpy (ΔH), and entropy (ΔS).
9. Designing experiments for smFRET
10. Understanding use of optical tweezers to study the mechanical properties of DNA or protein folding

Suggested readings

- **Online Resources**:
  Instrumentation websites/Research Papers as discussed in class

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE08: BIOMOLECULAR INTERACTIONS

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE08: **BIOMOLECULAR INTERACTIONS**	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- Introduce the students to the essentials of Biomolecular interactions.
- The student will understand the structure of various biomolecules involved in various pathways of biological systems.
- They will be understand the interaction involve among biomolecules and its significance.
- The students will be delivered the knowledge about protein folding, denaturation and involvement of biomacromolecules among various pathological disorder

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Student will be able to evaluate the structure of amino acid and protein.
- Student will be able to correlate the role of biomolecular interactions among biological pathways.
- Student will be able to comprehend how biomolecules folded and unfolded under various environmental conditions.
- Student will be able to study different processes involve the biomolecular interactions.
- Student will be able to describe the different pathological disorders involving biomolecules.
- Student will be able to learn the therapeutics involved in disorders

SYLLABUS OF BP-DSE08

Theory component (45 hours)

UNIT I **(20 hours)**

Journey from amino acid to protein: Introduction to amino acids, partial double bond character of peptide bond; structural levels of protein, posttranslational modifications of protein, techniques to study secondary tertiary and quaternary structure of protein, Greek key motifs, leucine zippers, determination of protein structure- Sequence determination of proteins, N- and C-terminal amino acid analysis; Edman's degradation: classical and automated procedures, DNA sequencing by Maxam and Gilbert method, Sanger's method.

Essential readings

a) Lehninger; Principles of Biochemistry; W.H Freeman and Company; 8th edition, 2022

b) T. A. Brown Gene Cloning & DNA Analysis An Introduction Seventh Edition, 2016, Wiley Black well

UNIT II **(10 hours)**

Role of Cooperativity in biomolecular interactions: cooperative and non-cooperative (Sigmoidal) binding of ligands, Hill equation, Sequential and concerted model for cooperative binding. Biomolecular denaturation process, study of molecules involved in the folding pathway of proteins, and Practical aspects of binding analyses.

Essential readings

a) J.M. Berg, J.L. Tymoczko and L. Stryer; Biochemistry; W.H. Freeman and Company. 8th edition, 2021

b) T Palmer, P L Bonner (2007) Enzymes, Biochemistry, Biotechnology, Clinical Chemistry, Second edition, Woodhead Publishing

c) Irwin H. Segel (1993) Enzyme Kinetics: Behavior and Analysis of Rapid Equilibrium and Steady-State Enzyme Systems, Second edition, Wiley

UNIT III **(5 hours)**

Biomolecular interactions of Protein/DNA/lipid/carbohydrate/drugs

Essential readings

a) Arun K. Shukla (2021) Biomolecular Interactions Part A and Part B: Elsevier Science

UNIT IV **(10 hours)**

Amyloid and functions: types of amyloids, techniques to study amyloids, factors affecting protein aggregation, aggregation kinetics, and therapeutic strategies to combat neurological disorders, pathological disorders induced by protein aggregates

Essential readings

a) David Eliezer (2016) Protein Amyloid Aggregation, Methods and Protocols, Humana Press

Practical component (30 hours)

UNIT I **(20 hours)**

Molten globule study of proteins (e.g., Lysozyme), electrophoresis of proteins, molecular docking study of protein-ligand interactions, Absorption spectrum of protein and DNA.

Essential readings

a) Wilson and Walker (2018) Principles and Techniques of Biochemistry and Molecular Biology, Eighth edition.

UNIT II **(10 hours)**

Secondary and tertiary structure study of protein, aggregation kinetics study of proteins, various assays to study aggregates

Essential readings

a) Emine Ercikan Abali (2021), Biochemistry, Lippincott Illustrated Reviews

Suggested readings

Theory:

Unit I: J.M. Berg, J.L. Tymoczko and L. Stryer; Biochemistry; W.H. Freeman and Company.
Unit II: D. Whitford; Proteins, Structure and Function; John Wiley & Sons Ltd.
Unit III: Emine Ercikan Abali (2021), Biochemistry, Lippincott Illustrated Reviews
Unit IV: Simon F Campbell (2008) Protein Folding, Misfolding and Aggregation Classical Themes and Novel Approaches, RSC Publishing.

Practical:

Unit I: Freifelder, David Michael; Physical biochemistry: applications to biochemistry and molecular biology; W.H. Freeman and Company.
Unit II: David Sheehan (2009) PHYSICAL BIOCHEMISTRY: PRINCIPLES AND APPLICATIONS Second Edition,Wiley

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE09: INFECTION AND IMMUNITY

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE09: **INFECTION AND IMMUNITY**	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- To make students understand the basic concepts of infection establishment and immune activation by the host in response to such an insult.
- To make students understand the basic concepts of innate and adaptive immunity, host-pathogen interaction, and the concept of prevention of infections through vaccines.
- To make students learn the techniques used to perform research in the field of basic immunology, immunotechnology, and immunodiagnostics.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Students will understand the fundamental concepts of the human immune system and basic immunology.
- Students will be able to differentiate innate and adaptive immune systems, broadly describe how the immune systems mature in the host, and how they function in protecting the host from infections.
- Students will be able to describe the basic structures and functions of bacteria, viruses, and parasites and describe pathogenic mechanisms used by them that are important in the interaction with humans.
- Students will learn to use the information acquired during the course to hypothesize how the immune system can be used to fight pathogenic microorganisms and how antigens of pathogenic origin can be used to elicit a protective immune response against the pathogen.
- Students will become acquainted with the immunology lab techniques and immunoinformatic tools and will be able to use this knowledge for designing immunotherapeutic molecules.

SYLLABUS OF BP-DSE09

Theory component (45 hours)

UNIT I **(12 hours)**

Historic perspectives and introduction to immunology: History and scope of immunology; Types of Immunity – innate immunity, acquired immunity- natural, artificial, active and passive; Antigens, epitopes, immunogenicity, antigenicity; PAMPs, DAMPs; PRRs-toll like receptors, acute phase proteins; Myeloid and lymphoid lineage cells - granulocytes, dendritic cells, macrophages, T and B lymphocytes; Inflammatory response; Complement activation and regulation, Major Histocompatibility Complex; Primary and secondary lymphoid organs.

Introduction to infectious diseases: Definition of infectious diseases; Symptoms and signs of infection; Acute and chronic conditions; Microbial pathogens – bacteria, viruses, fungi, parasites, and non-microbial pathogen – prions; Direct and indirect person-person transmission; Animal-human transmission; Resolution of infections; Mechanisms of infection; Nomenclature of pathogens; Emerging infectious diseases.

Essential readings

a) Immunology, 6th edition, (2006), J. Kuby et al, W.H. Freeman and Company, New York. ISBN-13: 978-1429202114.
b) Janeway, C. A., Travers, P., Walport, M., & Shlomchik, M. J. (2005). Immuno Biology: the Immune System in Health and Disease. USA: Garland Science Pub.

UNIT II **(10 hours)**

Humoral and cell-mediated immunity: Immunoglobulins - basic structure, classes & subclasses of immunoglobulins, antigenic determinants; Ig genes organization; B-cell receptor; Immunoglobulin superfamily; Principles of cell signalling; Basis of self & non-self discrimination; Kinetics of immune response, memory; B cell maturation, activation and differentiation; Generation of antibody diversity; T-cell maturation, activation and differentiation and T-cell receptors; Functional T Cell subsets; Cell-mediated immune responses, ADCC; Cytokines: properties, receptors and therapeutic uses; Antigen processing and presentation; Cell-cell co-operation; Hapten-carrier system.

Essential Readings

a) Murphy, K. and Weaver, C. (2016) Janeway's Immunobiology, Garland Science, New York.
b) Immunology, 8th edition, (2012), Male, D., Brostoff, J., Roth, D.B. and Roitt, I., Elseivier Sauders. ISBN-13: 978-0323080583.

UNIT III **(9 hours)**

Clinical immunology: Immunity to infection – bacteria, viral, fungal and parasitic infections; Hypersensitivity: Type I-IV; Autoimmunity; Types of autoimmune diseases; Mechanism and role of $CD4^+$ T cells; MHC and TCR in autoimmunity; Treatment of autoimmune diseases; Transplantation – immunological basis of graft rejection; Clinical transplantation and immunosuppressive therapy; Tumor immunology – tumor antigens, immune response to tumors and tumor evasion of the immune system; Cancer immunotherapy; Immunodeficiency – primary immunodeficiencies, acquired or secondary immunodeficiencies; Autoimmune disorder; Anaphylactic shock; Immunosenescence; Immune exhaustion in chronic viral infection; Immune tolerance; NK cells in chronic viral infection and malignancy. Antibody engineering – generation of monoclonal antibodies, hybrid monoclonal antibodies; Catalytic antibodies and generation of immunoglobulin gene libraries.

Essential Readings

a) Delves, P.J., Martin, S.J., Burton, D.R., Roitt, I.M. (2017) Roitt's Essential Immunology.
b) Joanne M. Willey, Kathleen M. Sandman, Dorothy H. Wood, Prescott's Microbiology, 11th Edition, Published by McGraw-Hill Education, ISBN 978-1-260-21188-7.

UNIT IV **(14 hours)**

Immunological Techniques and Immunodiagnostics: Precipitation, agglutination and complement-mediated immune reactions; RIA, ELISA, Western blotting, ELISPOT assay, immunofluorescence microscopy, flow cytometry and immunoelectron microscopy; Surface plasmon resonance, biosensor assays; Lymphoproliferation assay, mixed lymphocyte reaction, cell cytotoxicity assays, microarrays; Immunodiagnostics based on precipitation, agglutination, haemagglutination, complement fixation test (CFT), labelled assays and *in vivo* reactions.

Vaccinology: Active and passive immunization; Introduction to live, killed, attenuated, subunit vaccines, DNA and protein-based vaccines, plant-based vaccines; Peptide vaccines; Conjugate vaccines; Role and properties of adjuvants; Reverse vaccinology; Idiotypic vaccines and marker vaccines; Viral-like particles (VLPs); Dendritic cell based vaccines; Vaccine against cancer; T cell-based vaccine; Edible vaccine and therapeutic vaccine.

Essential Readings

a) Medical Laboratory Technology Methods and Interpretations Volume 1 and 2, 6th edition (2009), Ramnik Sood; Jaypee Brothers Medical Publishers, ISBN-13: 978-8184484496.
b) Vaccinology: Principles and Practice, by Editors: W. John W. Morrow, Nadeem A. Sheikh, Clint S. Schmidt, D. Huw Davies; Wiley Blackwell, 2012.

Practical component (30 hours)

Immunoinformatics

1. Epitope Identification & Mapping

B-cell Epitopes (Linear): BepiPred 3.0 (latest version using deep learning) and ABCpred.
B-cell Epitopes (Conformational/3D): DiscoTope 3.0 and ElliPro.
T-cell Epitopes (MHC-I/CTL): NetMHCpan 4.1 and NetCTL 1.2.
T-cell Epitopes (MHC-II/HTL): NetMHCIIpan 4.0 and the IEDB Consensus Method

2. Characterization of Antigenic Potential

Antigenicity Score: VaxiJen 2.0 (alignment-independent) and ANTIGENpro.
Cytokine Inducibility: IFNepitope (for IFN-gamma) and IL4pred.
MHC Binding Affinity: The IEDB Analysis Resource for calculating IC50 values and percentile ranks.

1. **Safety & Biocompatibility**

Allergenicity: AllerTOP v2.0, AllergenFP, and Allermatch.
Toxicity: ToxinPred and its updated versions for predicting peptide toxicity.
Human Homology: NCBI BLASTp used specifically to screen for similarities against the human proteome to prevent autoimmunity.

4. Physicochemical & Structural Stability

Physicochemical Properties: ExPASy for molecular weight, pI, and instability index.
Population Coverage: IEDB Population Coverage Tool to calculate the percentage of people who can respond to selected epitopes.
Receptor Docking: AutoDock Vina, PatchDock, and ClusPro for simulating antigen interactions with TLRs or MHC molecules.
Structural Modeling: AlphaFold2 or PEP-FOLD for predicting the 3D structure of the antigen or vaccine construct.

Essential Readings

a) Immunoinformatics (Methods in Molecular Biology, Vol 2131) edited by Namrata Tomar. March 2020, Third Edition, eBook ISBN 978-1-0716-0389-5.

Suggested Readings

Theory

- **Unit I**: Robbins and Cotran Pathologic Basis of Disease, 8th edition (2009), Vinay Kumar, Abul K. Abbas, Jon C. Aster, Nelson Fausto; Saunders Publishers, ISBN-13: 978-1416031215.

- **Unit II**: Immunology: An Introduction, 4 th edition, (1994), Tizard, I.R., Saunders College Publishing, Philadelphia. ISBN-13: 978-0030041983.
- Microbiology, 7th edition, (2008), Prescott, L., John Ii Harley, Donald A. Klein, McGraw Hill. ISBN-13: 978-0071102315.

- **Unit III**: An Introduction to Immunology, Immunochemistry and Immunobiology, 5th edition, (1988), Barrett, James T., Mosby Company, St. Louis. ISBN-13: 978-0801605307.

- **Unit IV**: Kaufmann, S. H. (2004). Novel Vaccination Strategies. Weinheim: Wiley-VCH.

Practical

- Immunoinformatics: Bioinformatic Strategies for Better Understanding of Immune Function: Novartis Foundation Symposium 254, October 2003, Print ISBN:9780470853566, Online ISBN:9780470090763.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE10: PROTEIN AGGREGATION, MISFOLDING AND DISORDERS

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE10: **PROTEIN AGGREGATION, MISFOLDING AND DISORDERS**	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- To deliver the knowledge about why protein misfold and disorders related to misfolding of protein and preventive strategies.
- The student will understand formation of aggregates.
- They will be understand the difference between aggregates structures and level of toxicity.
- The students will be delivered the knowledge about mechanism of aggregation and kinetic pathways of aggregation
- The students will be motivated to learn protein misfolding disorders.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Student will be able to characterize the protein aggregates.
- Student will be able to analyse the assembly process involve in the protein misfolding.
- Student will be able to learn about factors responsible for the protein aggregation.
- Student will be able to study the various methods and protocols involve in the study of protein misfolding and also learn about the diagnostic and therapeutic against disorders

SYLLABUS OF BP-DSE10

Theory component (45 hours)

UNIT I **(20 hours)**

Protein aggregation and oligomerisation, types of aggregates, toxicity of aggregates and oligomers, Factors responsible for protein aggregation: pH, Temperature; Co-solvent; shear effect; mutation etc. ubiquitin-proteasome degradation.

Essential readings

a) Marina ramirez-alvarado, jeffery w. Kelly, christopher m. Dobson; protein misfolding diseases: Current and Emerging Principles and Therapies; John Wiley & Sons Ltd

UNIT II **(10 hours)**

Mechanism of protein aggregation, characterization of protein aggregates, kinetics of protein aggregation.

Essential readings

a) Simon F Campbell (2008) Protein Folding, Misfolding and Aggregation Classical Themes and Novel Approaches, RSC Publishing.

UNIT III **(5 hours)**

Functional amyloids, Principles of protein misfolding: oxidative stress, role of molecular chaperons, kinetic models of protein misfolding.

Essential readings

a) David Eliezer; Protein Amyloid Aggregation: Methods and Protocols; Humana Press.6.

UNIT IV **(10 hours)**

Protein misfolding disorders: Alzheimer's disease, Parkinson's disease, Prion disease, hutington disease, systemic amyloidosis, cystic fibrosis, Gaucher disese, cataract, etc., methods and protocols to study protein misfolding and aggregates, Diagnosis and therapeutic strategies.

Essential readings

a) Cláudio M. Gomes; Protein Misfolding Diseases: Methods and Protocols; Humana Press.

Practical component (30 hours)

UNIT I **(20 hours)**

Formation of aggregates by using different proteins and factors:
A. Thermally induced aggregation of bovine serum albumin.
B. pH and surfactant-induced aggregation of lysozyme.
C. effect of mechanical stress on the aggregation rate of protein.

Essential readings

a) Wilson And Walker; Principles And Techniques Of Biochemistry And Molecular Biology; CAMBRIDGE UNIVERSITY PRESS

UNIT II **(10 hours)**

Characterization of aggregates: ThT dye binding assay, Congo red dye binding assay, hydrophobicity measurement by using 8-Anilino-1-naphthalenesulfonic acid (ANS) as an extrinsic fluorophore.

Essential readings

a) Biophysics by W.HoppeW. Lohmann, H. Markl, H. Ziegler (Springer)

Suggested readings

Theory:

Unit I: Freifelder, David Michael; Physical biochemistry: applications to biochemistry and molecular biology; W.H. Freeman and Company.
Unit II: David Eliezer (2016) Protein Amyloid Aggregation, Methods and Protocols, Humana Press
Unit III: Simon F Campbell (2008) Protein Folding, Misfolding and Aggregation Classical Themes and Novel Approaches, RSC Publishing.
Unit IV: H. John Smith and Claire Simons (2019) Protein Misfolding in Neurodegenerative Diseases Mechanisms and Therapeutic Strategies, CRC Press

Practical:

Unit I: Biophysics by W.HoppeW. Lohmann, H. Markl, H. Ziegler (Springer)
Unit II: Holger Gohlke; Protein-Ligand Interactions; Willey VCH.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

SKILL BASED COURSE – BP-SBC03: SPECIALISED LABORATORY – III: Protein Chemistry

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-SBC03: **SPECIALISED LABORATORY – III: Protein Chemistry**	**2**	**0**	**0**	**2**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- To provide practical skills on basic microbiological techniques.
- To expose students to the microbiology lab environment, basic lab infrastructure, basic equipment handling, and safety guidelines.
- To develop skilled manpower capable of handling basic lab strains of bacteria e.g. *E. coli*, for future molecular biology and genetic engineering experiments.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Students will be able to isolate, characterize, and identify common bacterial organisms.
- Students will be able to calculate/determine the bacterial load of different samples.
- Students will be able to perform antimicrobial sensitivity tests.
- Students will learn about preserving bacterial cultures of short and prolonged durations.

SYLLABUS OF BP-SBC03

Practical component (60 hours)

Unit I

1. Ammonium Sulphate precipitation of protein.
2. Turbidity measurement of lysozyme by UV-Vis absorption spectroscopy.
3. Rayleigh scattering measurement of lysozyme by Fluorescence spectroscopy.
4. Demonstration of dialysis of proteins.
5. Demonstration of concentrating protein through centrifugation.
6. Scattering correction experiment to validate the concentration estimation of protein by UV-Vis spectroscopy.
7. Bacterial cell lysis by sonication.
8. Estimation of protein concentration by colorimetric methods.
9. Agarose Gel Electrophoresis of nucleic acids.
10. SDS-PAGE of proteins.
11. Case study & Group Discussion: Design of project proposals using techniques studied.

Essential readings

a) Cappuccino, J. G., & Welsh, C. (2016). Microbiology: A Laboratory Manual. Benjamin-Cummings Publishing Company.
b) Collins, C. H., Lyne, P. M., Grange, J. M., & Falkinham III, J. (2004). Collins and Lyne's Microbiological Methods (8th ed.). Arnolds.
c) Freifelder, David Michael; Physical biochemistry: applications to biochemistry and molecular biology; W.H. Freeman and Company.

Suggested readings

a) David Sheehan (2009) Physical Biochemistry: Principles And Applications Second Edition,Wiley
b) Tille, P. M., & Forbes, B. A. Bailey & Scott's Diagnostic Microbiology.
c) Green, M. R., & Sambrook, J. (2012). Molecular Cloning: A Laboratory Manual. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISSERTATION – BP-DISSERTATION:
Dissertation: DESIGN RESEARCH PROPOSAL

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DISSERTATION: **DISSERTATION: DESIGN RESEARCH PROPOSAL**	**6**	**0**	**0**	**6**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- To provide skills to students in research problem design.
- To acquaint students with the methods and process of literature review for a scientific project.
- To develop skills in formulating research problems and identify methodologies required to address the problem statement chosen.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Students will have completed Research Problem Identification.
- Students will have completed Review of Literature.
- Students will have completed Research design formulation.
- Students will have commenced experiments, fieldwork, or similar tasks

SYLLABUS OF BP-DISSERTATION: Design Research Proposal (180 hours)

The dissertation will be based on the labs assigned to the students in Sem III

UNIT1:
Design of research proposal, experiments (understanding through virtual lab), acquisition of Data, Completion of Literature Review.

Essential/recommended readings

a) William Trochim, James P. Donnelly, Kanika Arora (2023) Research Methods: The Essential Knowledge Base, Cengage
b) Saccenti E, Furlan C. Ten simple rules to complete successfully a computational MSc thesis project. PLoS Comput Biol. 2025 Jan 28;21(1):e1012756. PMID: 39874385
c) Berezin CT, Aguilera LU, Billerbeck S, Bourne PE, Densmore D, Freemont P, Gorochowski TE, Hernandez SI, Hillson NJ, King CR, KÃ¶pke M, Ma S, Miller KM, Moon TS, Moore JH, Munsky B, Myers CJ, Nicholas DA, Peccoud SJ, Zhou W, Peccoud J. Ten simple rules for managing laboratory information. PLoS Comput Biol. 2023 Dec 7;19(12):e1011652. PMID: 38060459
d) Oza VH, Whitlock JH, Wilk EJ, Uno-Antonison A, Wilk B, Gajapathy M, Howton TC, Trull A, Ianov L, Worthey EA, Lasseigne BN. Ten simple rules for using public biological data for your research. PLoS Comput Biol. 2023 Jan 5;19(1):e1010749. PMID: 36602970
e) Marai GE, Pinaud B, Bahler K, Lex A, Morris JH. Ten simple rules to create biological network figures for communication. PLoS Comput Biol. 2019 Sep 26;15(9):e1007244. PMID: 31557157.
f) Peterson TC, Kleppner SR, Botham CM. Ten simple rules for scientists: Improving your writing productivity. PLoS Comput Biol. 2018 Oct 4;14(10):e1006379. PMID: 30286072
g) Rougier NP, Droettboom M, Bourne PE. Ten simple rules for better figures. PLoS Comput Biol. 2014 Sep 11;10(9):e1003833 PMID: 25210732
h) Osborne JM, Bernabeu MO, Bruna M, Calderhead B, Cooper J, Dalchau N, Dunn SJ, Fletcher AG, Freeman R, Groen D, Knapp B, McInerny GJ, Mirams GR, Pitt-Francis J, Sengupta B, Wright DW, Yates CA, Gavaghan DJ, Emmott S, Deane C. Ten simple rules for effective computational research. PLoS Comput Biol. 2014 Mar 27;10(3):e1003506. PMID: 24675742
i) Zhang W. Ten simple rules for writing research papers. PLoS Comput Biol. 2014 Jan 30;10(1):e1003453. PMID: 24499936
j) Erren TC, Cullen P, Erren M, Bourne PE. Ten simple rules for doing your best research, according to Hamming. PLoS Compu**t** Biol. 2007 Oct;3(10):1839-40. PMID: 17967054

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

SEMESTER 4

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC CORE COURSE – BP-DSC09: HIGH-THROUGHPUT BIOLOGY

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical / Practice		
BP-DSC09: HIGH-THROUGHPUT BIOLOGY	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- select the appropriate platform for system-level understanding of cellular phenomena
- critically assess the results of a proteomics, genomics and metabolomics experiment
- understand the merits/demerits of a analysis tool employed to analyze the results of proteomics, genomics and metabolomics experiment

Learning outcomes

The Learning Outcomes of this course are as follows:

- Understanding of quantification and identification of proteins, their post-translational modifications and interactions from mass spectrometry data.
- Knowledge of commonly used technologies and bioinformatics principles for high-throughput genomics analysis.
- Know important biological databases and relevant statistics/ bioinformatics software tools to analyze microarray and NGS transcriptomics data.
- Should evaluate and apply the appropriate experimental design in a given metabolomics research question (including sample processing, choice of methods and analytical strategies).

SYLLABUS OF BP-DSC09

Theory component (45 hours)

UNIT – I **(6 hours)**

Mass spectrometry basics; Proteomics bioinformatics basics; Quantitative proteomics; Introduction to data independent acquisition approaches; MS proteomics repositories; Introduction to proteogenomics; Protein interaction data resources. Current developments and recent progress.

Essential readings:

a) Introduction to computational proteomics (first edition). Golan Yona. ISBN: 978-0367452285

UNIT – II **(27 hours)**

Advantages and disadvantages of different generations of DNA sequencers. Application-specific changes in the sample preparation methods for DNASeq, RNASeq, ChIPSeq and Metagenomics, single cell genomics.

Overview of NGS data formats – FASTQ, Single-end, Paired-end, Mate-pair. Measure of sequence read quality – Phred score; Read pre-processing and quality check assessment tools – FASTQC and Trimmomatic respectively.

Algorithm of NGS read assembly, contigs, scaffolds, assembly quality assessment using N50, total length, no. of contigs/scaffolds; Overview of read mapping, tools for read mapping – BWA, Bowtie, and their output file formats – BAM, SAM, SAMtools (Biosynthetic Gene cluster analysis); assessment of quality of read alignment; SNP and Variant Calling - Personalized medicine; variant visualisation tools – IGV.

Different methods of transcriptomic study; Quality assessment and QC of RNAseq read sequence data; Transcript identification, *de-novo* vs referenced-based transcriptome assembly; Differential gene expression analysis, Alternative splicing analysis, Visualization, Functional profiling of differentially expressed genes; Single-cell RNA-seq, spatial transcriptomics

Essential readings:

a) Next-Generation DNA Sequencing Informatics (second edition). Stuart M. Brown (Editor). ISBN 978-1-621821-23-6
b) Algorithms for Next-Generation Sequencing (first edition). Wind-Kin Sung ISBN: 978-1466565500

UNIT – III **(6 hours)**

Introduction to metagenomics, Basic methods and techniques for metagenomics study, Quality control, Community taxonomic profiling, Community diversity, metagenomic reads assembly, Taxonomic binning, metatranscriptomics, Applications of metagenomics: metagenomics of the human microbiome, bio-prospecting novel genes, metagenomics for industrial bioproducts, metagenomics for bioremediation, plant-microbe interactions, metagenomics and ecosystems biology;

Essential readings:

a) Methods in Molecular Biology (2649)- Metagenomic data analysis. Suparna Mitra (editor). ISBN: 978-1-0716-3071-6

UNIT – IV **(6 hours)**

Metabolomics: Introduction of different tools for metabolic profiling; Different tools used for metabolic data and database analysis e.g. KEGG, BioCyc, MetExplore and Cytoscape;Current developments and recent progress.

Essential readings:

a) Methods in Molecular Biology (2649)- Metagenomic data analysis. Suparna Mitra (editor). ISBN: 978-1-0716-3071-6

Practical component (30 hours)

1) Retreival, analysis and annotation of proteomics data
2) Retrieving NGS data from data sources - SRA toolkit; Aspera connect.
3) Assessment of read sequence quality using FASTQC, pre-processing of reads using Trimmomatic, Assembly of reads into genome, Determination of assembly quality and functional annotation of genes

Essential Readings:

a) Bioinformatics and Functional Genomics (third edition). Jonathan Pevsner. ISBN: 978-1-118-58176-6
b) Proteomics Data Mining - Advanced Computational Methods for Bioengineers: With R and Bioconductor (first edition). Jamie Flux. ISBN: 979-8300370244

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC CORE COURSE – BP-DSC10: MOLECULAR BIOPHYSICS

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSC10: MOLECULAR BIOPHYSICS	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- Student will understand the chemical structure of various macromolecules involved in propagation of life.
- Student will comprehend the influence of macromolecular three-dimensional structure on their function.
- Student will appreciate the relevance of physics e.g., thermodynamics, kinetics, and cooperatively to the function of biological macromolecules.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Student will be able to appreciate the effect of various forces in shaping the molecular conformation.
- Student will be able to correlate the biomolecular structure to its specific functions.
- Student will be able to comprehend the role of biomolecular conformation in function.
- Student will be able to appreciate the effect of cooperativity in protein/enzyme function

SYLLABUS OF BP-DSC10

Theory component (45 hours)

UNIT I **(15 hours)**

Nature of Chemical bonds: Forces responsible for molecular conformation, e.g., Hydrogen bonds, ionic/electrostatic interactions, Van der Waals interaction, hydrophobic interaction, and stereo-chemical factors

Macromolecular Structure

a) Protein Structure: Amino acids, peptide bond, primary, secondary, tertiary, and quaternary structure of proteins, motifs and folds, super-secondary structures.

b) Nucleic acid Structure: nucleosides and nucleotides, RNA structure, DNA structure and conformation, polymorphism of DNA

c) Other Biological Polymers: polysaccharides, associations formed among different macromolecular types

Essential readings

a) Saad Tayyab & Amru Nasrulhaq Boyce (2006) A Journey from Amino Acids to Proteins, UM press

b) Lehninger; Principles of Biochemistry; W.H Freeman and Company; 8th edition, 2022

UNIT II **(10 hours)**

Parameters defining conformation of a macromolecular chain, strategies for calculating the probable conformational status of a macromolecule, Computer simulation of macromolecular conformation, membrane protein conformation, Supercoiling of bio-macromolecules: Linking, twisting and writhing, topoisomerases

Essential readings

a) Amit Kessel, Nir Ben-Tal, Chapman and Hall (2018) Introduction to Proteins: Structure, Function, and Motion, Second Edition, CRC Press

b) T E Creighton, (1997), Protein Structure: a Practical Approach, Second Edition, Oxford University Press.

UNIT III **(5 hours)**

Special Bio-Macromolecules: Metalloproteins, nucleoproteins, ribozymes, membrane proteins, chaperons & prions.

Essential readings

a) Molecular Biophysics: Structures and Dynamics by Michel Daune (Oxford Univ. Press)

UNIT IV **(15 hours)**

Cooperativity in bio-macromolecular interactions: the phenomenon of cooperativity, DNA and protein melting, allosteric enzymes, Non-equilibrium thermodynamics in Biology: Information and Entropy, Nonequilibrium Processes, Coupling of Fluxes, Coupling of Chemical Reactions, far-from-Equilibrium Molecular Processes

Essential readings

a) Palmer T L Bonner (2007) Enzymes, Biochemistry, Biotechnology, Clinical Chemistry, Second edition, Woodhead Publishing

Practical component (30 hours)

UNIT I **(20 hours)**

- Purification of protein by using ion-exchange chromatography.
- Purity check by SDS-PAGE.
- Chemical and pH denaturation of lysozyme.

Essential readings

a) Wilson And Walker; Principles And Techniques Of Biochemistry And Molecular Biology; CAMBRIDGE UNIVERSITY PRESS

UNIT II **(10 hours)**

- Excitation and emission spectrum of lysozyme.
- Fluorescence quenching experiment of protein-ligand binding.

Essential readings

a) Freifelder, David Michael; Physical biochemistry : applications to biochemistry and molecular biology; W.H. Freeman and Company

Suggested readings:

Theory:

Unit I: Biophysics - An Introduction by Rodney Cotterill (Wiley)

Unit II: Molecular Biophysics: Structures and Dynamics by Michel Daune (Oxford Univ. Press)

Unit III: The Biophysical Chemistry of Nucleic Acids & Proteins by Thomas E. Creighton
(Helvetica Press)

Unit IV: The Physical and Chemical Basis of Molecular Biology by Thomas E. Creighton (Helvetica Press); Molecular Biophysics by MV Volkenstein (Academic press)

Practical:

Unit I: Biophysics by W.HoppeW. Lohmann, H. Markl, H. Ziegler (Springer)

Unit II: Holger Gohlke; Protein-Ligand Interactions; Willey VCH.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE11: ALGORITHMS IN COMPUTATIONAL BIOLOGY

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE11: **ALGORITHMS IN COMPUTATIONAL BIOLOGY**	**4**	**3**	**1**	**0**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- Introduce algorithmic and computational methods for biological data analysis.
- Apply classical and AI-based algorithms for sequence, genome, and protein analysis.
- Explore computational and AI-driven approaches for drug design and systems-level biology.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Apply biological, mathematical, statistical, and computational principles to analyze molecular, omics, and clinical data for solving complex biological and biomedical problems.
- Design, implement, and evaluate bioinformatics algorithms and computational tools, including sequence analysis, data integration, visualization, and machine learning–based approaches.
- Critically interpret scientific literature and data resources and communicate bioinformatics insights effectively to both specialist and non-specialist audiences.

SYLLABUS OF BP-DSE11

Theory component (45 hours)

Unit I: Introduction to Computational Biology and Algorithmic Thinking (10 hours)

Overview of biological data types (sequence, structure, network, omics); Algorithm design paradigms: dynamic programming, greedy methods, divide and conquer, graph algorithms; Complexity analysis and biological relevance.

Essential reading:

a) Gagniuc, P. A. (2021). *Algorithms in bioinformatics: Theory and implementation* (1st ed.). John Wiley & Sons. ISBN 978-1119697961.

Unit II: Algorithms for Sequence Alignment and Phylogeny (11 hours)

Pairwise sequence alignment using Needleman–Wunsch, Smith–Waterman; Index-based alignment with Burrows–Wheeler Transform (BWT) and FM-index; Progressive and consistency-based approaches of Multiple Sequence Alignment; Neighbour-Joining, Maximum Likelihood (RAxML, IQ-TREE), Bayesian algorithms for Phylogenetic reconstruction

Essential reading:

a) Gagniuc, P. A. (2021). *Algorithms in bioinformatics: Theory and implementation* (1st ed.). John Wiley & Sons. ISBN 978-1119697961.

Unit III: Algorithms for Genome Assembly and Annotation (12 hours)

Overlap–Layout–Consensus (OLC) and De Bruijn Graph algorithms; Hidden Markov Models and Neural networks for gene prediction; Transcript assembly, quantification and differential expression; Motif discovery with Gibbs Sampling and Expectation–Maximization; Leveraging AI/ML and Deep-learning methods for improving Genome Assembly and Annotation.

Essential reading:

a) Ye, S. Q. (Ed.). (2016). *Big data analysis for bioinformatics and biomedical discoveries* (1st ed.). Chapman & Hall/CRC. ISBN 978-1-4987-2452-4

Unit IV: Algorithms for Protein Structure Prediction and Drug Design (12 hours)

- **Protein Structure Prediction Algorithms:** Sequence–structure alignment algorithms for protein-structure modelling (profile–profile comparison, threading, fold recognition); *ab-initio* prediction algorithms based on energy minimisation, fragment assembly, and conformational search; deep learning–based architectures for end-to-end 3D structure prediction.
- **Molecular Docking Algorithms:** Search and scoring algorithms employing genetic algorithms, Monte Carlo sampling, simulated annealing, and gradient-based optimization for predicting ligand–receptor interactions.
- **Molecular Dynamics Algorithms:** Force field computation methods, numerical integration schemes, and enhanced sampling algorithms.

- **QSAR and Virtual Screening Algorithms:** Descriptor generation, feature extraction, and machine learning–based predictive modeling for activity prediction and similarity-based or deep-learning virtual screening.
- **Network Pharmacology and AI-driven Drug Discovery:** Graph-based algorithms for modeling drug–target interaction networks, multi-objective optimization methods, and reinforcement learning or generative deep learning frameworks for de novo molecule design.

Essential reading:

a) Algorithms in Structural Molecular Biology. Bruce R. Donald. (Donald, 2023) Edition Publisher, MIT Press, 2023 ISBN: 0262548798, 9780262548793

b) Leach, A. R. (2001). *Molecular Modelling: Principles and Applications* (2nd ed.). Prentice Hall / Pearson Education. ISBN 0-582-38210-6.

c) Haspel, N., Jagodzinski, F., & Molloy, K. (Eds.). (2022). *Algorithms and methods in structural bioinformatics* (1st ed.). Springer Cham. https://doi.org/10.1007/978-3-031-05914-8 ISBN 978-3-031-05913-1 (hardcover); ISBN 978-3-031-05916-2 (softcover).

Tutorial component (15 hours)

1. Exploration of biological data formats (FASTA, FASTQ, GFF/GTF, PDB) and basic sequence statistics using scripting.
2. Implementation of dynamic programming for global and local sequence alignment (Needleman–Wunsch and Smith–Waterman).
3. Read alignment using index-based methods (BWT / FM-index) and comparison with classical alignment approaches.
4. Multiple Sequence Alignment and phylogenetic tree construction using Neighbour-Joining and Maximum Likelihood methods.
5. Genome assembly using De Bruijn Graph–based methods and evaluation using standard assembly metrics.
6. Gene prediction and genome annotation using HMM-based and machine learning–based tools.
7. Transcriptome analysis: RNA-seq read mapping, transcript assembly, quantification, and differential expression analysis.
8. Protein structure prediction using homology modeling or deep learning–based structure prediction tools.
9. Protein–ligand molecular docking and molecular dynamics simulation with analysis of binding and stability.
10. QSAR modeling and virtual screening using molecular descriptors, machine learning, and basic network-based drug–target analysis.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE12: COMBATING DISEASES: LEVERAGING IN-SILICO APPROACHES

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE12: **COMBATING DISEASES: LEVERGING IN-SILICO APPROACHES**	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- The major objective of this course is to introduce students to classifications of diseases and their molecular basis with a focus on the use of in-silico methods to study these diseases.
- Students will learn to use computational tools that can be applied to uncover the genetic causes of diseases, identify potential biomarkers, and develop therapeutic strategies.
- The students will gain hands-on experience with publicly available data and apply in-silico methods to real-world disease data.
- The students will be motivated to critically assess scientific literature on in-silico methods in disease research.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- The students will be able to understand the molecular and genetic basis of diseases.
- The student will be able to apply in-silico methods, bioinformatics, and computational biology approaches to study diseases.
- The students will be able to analyze and interpret data from biological databases related to diseases.

SYLLABUS OF BP-DSE12

Theory component (45 hours)

UNIT – I

a. Introduction to Diseases (12 hours)

- Definition, prevalence, classification types.
- Overview of infectious, metabolic, genetic and life-style-related diseases.
- Overview of rare/orphan diseases.
- Current challenges in diagnosing and treating complex diseases.

b. Genetic Basis of Diseases

- Types of mutations involved, Genetic variants, and their identification.
- Role of epigenetics and gene regulation in disease manifestation.
- Techniques for rare disease gene discovery: exome sequencing, genome sequencing, and linkage analysis.

Essential Readings:

a) RUNGE M.S. (Author) (2006) Principles of molecular medicine. Humana Press. ISBN: 9781588292025

b) Jules J. Berman (2014). Rare Diseases and Orphan Drugs: Keys to Understanding and Treating the Common Diseases, Academic Press.

UNIT – II

a. Data sources and Biomedical databases (20 hours)

- Introduction to Disease Ontology and Phenotype Ontology
- Overview of public databases: OMIM, Orphanet, ClinVar,
- Genetic and Rare Diseases Information Center (GARD).

b. In-silico tools useful for studying Diseases

- Principles of Genone-wide association studies (GWAS), application in identifying genetic variants.
- Introduction to computational tools like PLINK, SNPedia, and HapMap for variant analysis.
- Identifying disease-causing mutations using SIFT, PolyPhen, CADD.

Essential Readings:

a) Jonathan Pevsner (2015) Bioinformatics and Functional Genomics, Wiley-Backwell ISBN: 1118581784

b) Alon Uri (2018) Introduction to systems biology, Boca Raton CRC Press, ISBN:9781498770903

UNIT – III Identifying Therapeutic targets and pathways (8 hours)

- Network analysis of biological pathways through KEGG, Reactome, and BioGRID.
- Understanding protein-protein interactions (PPIs) in the context of diseases, (STRING, BioGRID, and Reactome).
- Visualization of networks and Identifying key regulatory nodes as molecular targets.

Essential Readings:

- a) Jonathan Pevsner (2015) Bioinformatics and Functional Genomics, Wiley-Backwell ISBN: 1118581784

UNIT – IV Frontiers in Diseases research (5 hours)

- Drug repurposing through pathway analysis in disease studies.
- The role of big data in understanding diseases, Introduction to AI/ML techniques in disease diagnosis.
- The future of in-silico drug discovery for diseases and personalized medicine.

Essential Readings:

a) RUNGE M.S. (Author) (2006) Principles of molecular medicine. Humana Press. ISBN: 9781588292025

Practical component (30 hours)

UNIT I: Databases/Webservers for analysing the following:

1. Analyzing examples of disease mutations at the molecular level (e.g., Cystic fibrosis, Duchenne muscular dystrophy).
2. Accessing and analysing data present in OMIM
3. Accessing and analysing data present in Orphanet
4. Accessing and analysing data present in ClinVar
5. Accessing and analysing data present in the Genetic and Rare Diseases Information Center (GARD).
6. Learning to mine and use data from PLINK
7. Learning to mine and use data from HapMap
8. Learning to mine and use data from SIFT
9. Learning to mine and use data from CADD
10. Understanding and extracting information from databases like KEGG
11. Understanding and extracting information from databases like Reactome
12. Understanding and extracting information from databases like BioGRID
13. Case study: Structural analysis of a protein linked to a disease.
14. Case study: Pathway analysis through PPI networks for metabolic disorder.
15. Case study: Drug repurposing

Essential readings

- **Online Resources**:

1. Databases, as discussed in the practical component.
2. https://ojrd.biomedcentral.com/articles/10.1186/s13023-024-03286-8

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE13: PROTEIN ENGINEERING AND APPLICATIONS

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE13: **PROTEIN ENGINEERING AND APPLICATIONS**	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- The major objective of the course is to give the students an in-depth understanding and the skills necessary for independent target selection and protein engineering to develop novel products for society, with problem-solving.
- Another objective is to show the steps necessary for performing such protein engineering for a biotechnology invention.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- The student will be able to analyze the structure of proteins with databases.
- They will be able to analyze and compare the amino acid sequences and structures of proteins and relate this information to function.
- Students will learn the function of individual amino acids and their influence on the solubility, structure, and function of proteins, and understand the major factors for protein folding.
- Students will be able to construct bacterial expression plasmids for natural and modified genes and analyze the DNA sequence of proteins for factors that can affect the expression and properties of the protein.
- Based on the above analysis, be able to construct modifications to change the protein's properties.

SYLLABUS OF BP-DSE13

Theory Component (45 hours)

UNIT I **(8 hours)**

Concepts of protein structure and stability: Introduction to protein engineering; Protein structure and function; Protein folding and misfolding; Protein activity-stability-flexibility relationships (enzymatic, thermodynamic and kinetic); Forces stabilizing proteins – van der Waals, electrostatic, hydrogen bonding, covalent and weakly polar interactions, hydrophobic effects; Entropy – enthalpy compensation; Correlation between structural features governing protein specificity-and-affinity and biophysical parameters like – pH, temperature, ionic strength, amino acid sequence.

Essential readings:

a) Introduction to Proteins: Structure, Function, and Motion, Second Edition By Amit Kessel, Nir Ben-Tal, Chapman and Hall/CRC, 2018.
b) Edited by T E Creighton, (1997), *Protein Structure: a Practical Approach*, 2nd Edition, Oxford University Press.

UNIT II **(8 hours)**

Protein engineering concepts, approaches, and applications: Structural features of thermostable, cryostable, and halotolerant proteins. Creation of novel or altered structural proteins, enzymes, antibodies, antigens, transporters, receptors, and transcription factors; Redesign of structure, function, stability, and aggregation; Creation of designer and chimeric/fusion proteins; Combinatorial approaches to protein engineering; Rational approaches to protein engineering; Applications: enzyme engineering, protein allostery, biocatalysis, enzyme immobilization, protein production, antibody therapeutics, natural product biosynthesis.

Essential Readings:

a) Molecular Biology and Biotechnology, Edited by Ralph Rapley, PDF ISBN: 978-1-83916-896-3, EPUB ISBN: 978-1-78801-939-2, 17 May 2021.
b) Recent reviews from *Nature Biotechnology, Protein Science, PNAS*.

UNIT III **(9 hours)**

Tools and methods: Recombinant DNA technology-based strategies; Constructs, vectors, strains, affinity fusion tags; Chemical modification strategies; Site-directed mutagenesis – PCR-based and primer extension methods, Use of labels; Heterologous protein expression; Protein purification approaches; Protein handling; Protein biochemical and physico-chemical characterization using - ELISA, BLI, far-UV and near-UV CD, Fluorescence spectroscopy, UV absorbance, ORD, FTIR. **Computational tools:** Molecular visualization (PyMOL, UCSF Chimera) molecular modelling, Ab initio protein structure prediction, molecular docking, molecular dynamics simulations, energy functions and scoring**.**

Essential readings:

a) Mueller and Arndt, *Protein Engineering Protocols*, 1st Edition, Humana Press.
b) Recent reviews from *Nature Biotechnology, Protein Science, PNAS*.

UNIT IV **(8 hours)**

Protein Engineering- Combinatorial: Chemical mutagenesis; Error-prone PCR; Synthetic peptide combinatorial libraries; V_H-V_L combinatorial scFv libraries, Principles and applications of phage, ribosome, yeast and bacterial display; Module shuffling; Gene site saturation mutagenesis; Selection and screening approaches for folding and function - high throughput screening methodologies like GigaMetrix, High throughput microplate screens.

(12 hours)

Protein Engineering- Rational: Guided protein recombination; Domain fusion; Backbone Reversal; Global conservative mutagenesis; Excision of super-secondary structures; Substructure shuffling with symmetric structures; Surface reengineering; Disulphide bond introduction; Loop redesign; Active surface transplants between homologous beta-sheet proteins; Whole surface transplants; Enzyme active site transplants; Loop transplants on beta/alpha barrels; Site-directed mutagenesis for kinetic or thermodynamic stability; Protein core and surface electrostatics reengineering; Thermostability and cryostability engineering; Industrial/ Biotechnological/ Medical/ Pharmaceutical Applications.

Essential Readings:

a) Stefan Lutz, Uwe Theo Bornscheuer (Editors), Protein Engineering Handbook, 2008, Wiley VCH, ISBN-10: 352731850X; ISBN-13: 978-3527318506.
b) Mallorie N. Sheehan Protein Engineering: Design, Selection, and Applications, Nova Science Publishers, Inc. (2011).

Practical component (30 hours)

1. Selection of target proteins for engineering using various databases.
2. Identification of possible sites for mutagenesis, combining the literature information and molecular visualization of the structure of the target protein.
3. Generation of mutant sequences and model generation.
4. Validation of the models using the Ramachandran plot, using online software.
5. Structural comparison of the mutant protein models with the wild-type protein for selection of the stable mutant.
6. Molecular dynamic simulation studies with the mutant and wild-type proteins.
7. Molecular docking studies with the selected mutant(s) and the ligand for the prediction of the functional characteristics of the mutants.

Essential Readings:

a) Baxevanis, A. D., Bader, G. D., & Wishart, D. S. (Editors). Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 4th Edition. Wiley-Blackwell, Hoboken, NJ, 2020. ISBN-13: 978-1119335580; ISBN-10: 1119335582.
b) Latest manuals, handbooks, and workflow guides available online for each tool.

Suggested readings:

Theory:

- **Unit I:** J Kyte; (2006), *Structure in Protein Chemistry*, 2nd Edition, Garland publishers.
- **Unit II:** Jeffrey L. Cleland & Charles S. Craik (Eds), Protein Engineering: Principles and Practice, Wiley (1996).
- **Unit III:** Ed. Robertson DE, Noel JP, (2004), Protein Engineering Methods in Enzymology, 388, Elsevier Academic Press.
- **Unit IV:** Sheldon J. Park & Jennifer R. Cochran (Eds) Protein Engineering and Design, CRC Press (2009).

Practical:

- Lesk, A. M. Introduction to Bioinformatics. 5th Edition, Oxford University Press, Oxford/New York, 2019. ISBN-13: 978-0198794141; ISBN-10: 0198794142.

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISCIPLINE SPECIFIC ELECTIVE COURSE – BP-DSE14: CELLULAR AND MOLECULAR NEUROPHYSIOLOGY

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DSE14: **CELLULAR AND MOLECULAR NEUROPHYSIOLOGY**	**4**	**3**	**0**	**1**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

● Students will be able to understand the physical principles involved in the functioning of the cell & organelle membranes, ion channels, receptors & cell signaling.

● Students will be able to understand the biophysical basis of the functioning of neurons & other brain cells, their electrical behavior & communication mechanisms.

● Students will be able to understand the biophysics of perception, cognition & memory formation and the related neuronal disorders.

Learning Outcomes

The Learning Outcomes of this course are as follows.

- Should achieve conceptual understanding of the structure & function of biological membranes including ion channels, receptors & other components.
- Should understand the functioning of the nervous system, electrical behavior of neurons & other brain cells.
- Should be able to make a comparison between the functioning of the natural brain & artificial (computer) brain.
- Should understand the biophysical principle of learning & memory.
- Should understand newer mechanisms of learning.

SYLLABUS OF BP-DSE14

Theory component (45 hours)

Unit I **(8 hours)**

Overview of the Nervous System: Introduction to neurons; The Neuron Doctrine; Components and classification of neurons; Types of neurons; Cytology of neurons; Dendrites structure and function; Axons structure and functional aspects; Ultrastructure; Myelination and synapses. impregnation method; Structure and function of glial cells; Different types of glial cells: astrocytes, oligo dendrocytes and Schwann cells; Overview of glial and neuronal relationship in the CNS; Importance of astrocytes in glutamate metabolism and blood brain barrier; Microglial phenotypes; Glial –neuronal interplay in the CNS; Principles of fixation and staining of nervous tissue; Methods of tissue processing for microtomy and cryotomy.

Essential readings

a) Squire, Fundamental Neuroscience (4th Edition), Elsevier,2013
b) Bear, Neuroscience-Exploring the Brain (3rd Edition), Lippincott, 2007

Unit II **(20 hours)**

Biophysical basis of Neurophysiology : **Electrical behavior of the biological membrane**: Model membranes; Biological membranes and Dynamics; Membrane Capacitance; Transport across cell and organelle membranes; Ion Channels; Experimental methods to study Ion Channels.

Electrical properties of excitable membranes: Membrane conductance, linear and nonlinear membrane, ionic conductance, current-voltage relations; Ion movement in excitable cells: Physical laws, Nernst-Planck Equation, active transport of ions, movement of ions across biological membranes; Membrane potential and role of sodium and potassium pumps

Neural Signals: Physicochemical principles; Resting potential; Action Potential; Membrane theory of action potential; Hodgkin-Huxley's (HH) model

Sensory Receptors and Perception.

Special Senses: Vision: Photochemistry of vision, Neural pathways of vision, accommodation, light & accommodation reflexes, modern concept of color vision,

Audition: Organ and Pathways of audition

Olfaction: Olfactory organ, olfactory transduction, pathways

Gustation: Gustatory organ, pathways, transduction.

Pathophysiological conditions related to Sensory system

Essential readings

a) The Structure of Biological Membranes by Philip L. Yeagle, (CRC Press).
b) Duchene E. Haines, Fundamental Neuroscience for Basic & Clinical Applications (3rd Edition), Churchill Livingstone, 2006
c) Bear, Neuroscience-Exploring the Brain (3rd Edition), Lippincott, 2007

Unit III **(10 hours)**

Synaptic transmission & Neurotransmission Synaptic vesicles; Principles of synaptic transmission: Electrical and chemical synapses; Calcium hypothesis: Control of transmitter release; Synthesis and trafficking of neuronal proteins. Synaptic transmission at nerve-muscle synapses; Synaptic transmission at central synapses; Ligand-gated channels; Second messengers and synaptic transmission. Sodium/ potassium pump – Role of calcium. Chemical transmission

Essential readings

a) Kandel, Principles of Neural Science (5th edition), McGraw Hill,2013

Unit IV **(7 hours)**

Neurotransmitters & Neuromuscular Coordination Neurotransmitters – types, synthesis and secretion of neurotransmitters, Receptors–adrenergic receptors and cholinergic receptors. Regulation of transmission, Neurotoxins. Forces involved in ligand–receptor interaction, neuromuscular transmission, reflex action, and reflex arc. Regulation of body temperature. Interaction between sense organs and neurons. Artificial neurons; Neural Basis of Cognition and Behavior, Prediction of membrane protein types from sequences, voltage-sensing elements in any membrane protein.

Essential readings

a) Elements of. Molecular. Neurobiology. Third Edition. C. U. M. Smith. Copyright © 2002 John Wiley & Sons, Ltd

Practical component (30 hours)

- Basic concepts of microscopy, stereology, and image analysis; Principles and applications of confocal microscopy.
- Study of the nerve cell: cresyl violet staining.
- Study of permanent slides.
- Acquisition of data for various physiological parameters using various computational data acquisition systems.

Essential/Recommended readings

Theory:

Suggested Books:

The latest editions of the following books are recommended:

1. Neuroscience: A Mathematical Primer by Scott, A. (Springer)
2. Cognitive Neuroscience: The Biology of the Mind by Gazzaniga, M.S. et al. (W.W.Norton & Co)
3. Membrane Biophysics by Mohammad Ashrafuzzaman, Jack A. Tuszynski, (Springer Science & Business Media)
4. Methods in Membrane Lipids by Alex DoPico (Humana Press)

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

SKILL BASED COURSE – BP-SBC04: SPECIALISED LABORATORY – IV: Advanced Analytical Methods

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-SBC04: SPECIALISED LABORATORY- IV: Advanced Analytical Methods	**2**	**0**	**0**	**2**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- The objective of this skill enhancement laboratory course is to provide analytical skills of advanced protein related experiments.
- Student will be taught various types of chromatography for protein purification
- To expose students to the software related to analysis of analytical ultra-centrifugation

Learning Outcomes

The Learning Outcomes of this course are as follows:

- To students will be able to execute the affinity chromatography experiment.
- Students will be able to perform experiment of size exclusion chromatography.
- Students will be able to perform analysis by using software related to analytical ultra-centrifugation.

SYLLABUS OF BP-SBC04

Practical component (60 hours)

Unit I

1. Affinity purification of proteins (HIS-Tag).
2. Demonstration of Gel filtration.
3. Crystallization setup of proteins
4. Data analysis of Analytical Ultracentrifuge: SEDFIT software
5. Data analysis of Analytical Ultracentrifuge: SEDPHAT software
6. Data analysis of Analytical Ultracentrifuge: GUSSI software
7. Case study/Group Discussion of data analysis and results.

Essential readings

a) Schuck, P., Zhao, H., Brautigam, A. C., Ghirlando, R., BASIC PRINCIPLES OF ANALYTICAL ULTRACENTRIFUGATION. CRC Press.
b) Schuck, P., Zhao, H., SEDIMENTATION VELOCITY ANALYTICAL ULTRACENTRIFUGATION: Interacting Systems. CRC Press. Arnolds.
c) Freifelder, David Michael; PHYSICAL BIOCHEMISTRY : APPLICATIONS TO BIOCHEMISTRY AND MOLECULAR BIOLOGY; W.H. Freeman and Company.

Suggested readings:

a) David Sheehan; PHYSICAL BIOCHEMISTRY: PRINCIPLES AND APPLICATIONS; John Wiley & Sons Ltd
b) Freifelder, David Michael; Physical biochemistry: applications to biochemistry and molecular biology; W.H. Freeman and Company.
c) Wilson And Walker; Principles And Techniques Of Biochemistry And Molecular Biology; CAMBRIDGE UNIVERSITY PRESS

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.

M.Sc. Biophysics and Bioinformatics

DISSERTATION – BP-DISSERTATION: DISSERTATION: ANALYSIS, INTERPRETATION & PRESENTATION

CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
BP-DISSERTATION: **DISSERTATION: ANALYSIS, INTERPRETATION & PRESENTATION**	**6**	**0**	**0**	**6**	**NIL**	**NA**

Learning Objectives

The Learning Objectives of this course are as follows:

- The objective of this course is to provide skills to students design experiments, analyse the results.
- To develop skills in tackling research problems and compiling their study as publishable material or product development.

Learning Outcomes

The Learning Outcomes of this course are as follows:

- Students will have completed Experimentation/fieldwork.
- Students will have completed the submission of the dissertation.
- Students will have completed a Research output in any of the 3 forms
    b) Prototype or product development/patent.
    c) Any other scholastic work as recommended by the BRS ad approved by Research Council
    d) Publication in a reputed Journals such as Scopus Indexed journals or other similar quality journals
    e) Book/book chapter in a publication by a reputed publisher

SYLLABUS OF BP-DISSERTATION: Analysis, Interpretation and Presentation

(180 hours)

The dissertation will be based on the labs assigned to the students in Sem III

UNIT1:
Analysis of data, interpretation and presentation of work

Essential/recommended readings

a) William Trochim, James P. Donnelly, Kanika Arora (2023) Research Methods: The Essential Knowledge Base, Cengage
b) Saccenti E, Furlan C. Ten simple rules to complete successfully a computational MSc thesis project. PLoS Comput Biol. 2025 Jan 28;21(1):e1012756. PMID: 39874385
c) Berezin CT, Aguilera LU, Billerbeck S, Bourne PE, Densmore D, Freemont P, Gorochowski TE, Hernandez SI, Hillson NJ, King CR, KÃ¶pke M, Ma S, Miller KM, Moon TS, Moore JH, Munsky B, Myers CJ, Nicholas DA, Peccoud SJ, Zhou W, Peccoud J. Ten simple rules for managing laboratory information. PLoS Comput Biol. 2023 Dec 7;19(12):e1011652. PMID: 38060459
d) Oza VH, Whitlock JH, Wilk EJ, Uno-Antonison A, Wilk B, Gajapathy M, Howton TC, Trull A, Ianov L, Worthey EA, Lasseigne BN. Ten simple rules for using public biological data for your research. PLoS Comput Biol. 2023 Jan 5;19(1):e1010749. PMID: 36602970
e) Marai GE, Pinaud B, Bahler K, Lex A, Morris JH. Ten simple rules to create biological network figures for communication. PLoS Comput Biol. 2019 Sep 26;15(9):e1007244. PMID: 31557157.
f) Peterson TC, Kleppner SR, Botham CM. Ten simple rules for scientists: Improving your writing productivity. PLoS Comput Biol. 2018 Oct 4;14(10):e1006379. PMID: 30286072
g) Rougier NP, Droettboom M, Bourne PE. Ten simple rules for better figures. PLoS Comput Biol. 2014 Sep 11;10(9):e1003833 PMID: 25210732
h) Osborne JM, Bernabeu MO, Bruna M, Calderhead B, Cooper J, Dalchau N, Dunn SJ, Fletcher AG, Freeman R, Groen D, Knapp B, McInerny GJ, Mirams GR, Pitt-Francis J, Sengupta B, Wright DW, Yates CA, Gavaghan DJ, Emmott S, Deane C. Ten simple rules for effective computational research. PLoS Comput Biol. 2014 Mar 27;10(3):e1003506. PMID: 24675742
i) Zhang W. Ten simple rules for writing research papers. PLoS Comput Biol. 2014 Jan 30;10(1):e1003453. PMID: 24499936
j) Erren TC, Cullen P, Erren M, Bourne PE. Ten simple rules for doing your best research, according to Hamming. PLoS Compu**t** Biol. 2007 Oct;3(10):1839-40. PMID: 17967054

The dissertation will be based on the labs assigned to the students in Sem III

Note: Examination scheme and mode shall be as prescribed by the Examination Branch, University of Delhi, from time to time.