UNIVERSITY OF KASHMIR, SRINAGAR
HAZRATBAL, SRINGAR-190006
NAAC, A++

NOTIFICATION

It is notified for the information of all concerned that the Vice-Chancellor, in anticipation of the approval of the Competent Bodies, has authorized prescription of syllabi for PG Diploma in Bioinformatics, 1st and 2nd Semester, as per the NEP-2020 guidelines for its implementation to the batch 2024 and onwards.

This is issued in Supersession of earlier notification vide No. F(PG-Diploma Bioinf.)Acad/KU/25 Dated 20-08-2025

Assistant Registrar
(ACADEMIC)

No F(PG-Diploma Bioinf.) Acad/KU/25
Dated:- 25-08-2025

Copy to the:-

1. Dean Academic Affairs, University of Kashmir,
2. Dean, School of Biological Science, University of Kashmir,
3. Controller of Examinations, University of Kashmir,
4. Chief Coordinator NEP Cell, University of Kashmir,
5. Coordinator, Deptt. of Bioinformatics, University of Kashmir,
6. Assistant Registrar/Controller of Examinations/Secrecy/Tabulation/ Conduct UG/ Registration/University of Kashmir, Srinagar.

BIOINFORMATICS CENTRE

University of Kashmir, Srinagar-190006

Notes

No. KU-BIC-2025-14

Dated 21/08/2025

Subject: The Syllabi for PG Diploma Bioinformatics may be considered from Batch- 2024

The Board of Studies which was ~~scheduled~~ held on 28th of April 2025 regarding the above mentioned PG Diploma Bioinformatics Syllabi may please be considered effective from Batch 2024.

This is to avoid any clash with the Batch-2025 so that the examination link for Batch 2024 may be opened.

This may be considered on priority, given the students have already completed the Ist semester syllabi a month before, and are desperately waiting for the examination.

Department committee members

Prof. Rais Qadri   Prof. Ehtishamul Haq   Prof. Firdous Khanday

Dr. Bilal Reshi   Dr. Abrar Qureshi

Coordinator

Dean Academic Affairs

UNIVERSITY OF KASHMIR, SRINAGAR
BIOINFORMATICS CENTRE
NACC Accredited Grade A++
Hazratbal, Srinagar, Kashmir-190006

Minutes of the meeting of the board of PG Diploma studies in Bioinformatics held on 28th of April 2025 at 2:00 p.m.

Agenda: Syllabus compilation for PG Diploma in Bioinformatics.

The meeting of "The board of postgraduate studies in Bioinformatics" was held on 28th of April 2025 at 2:00 p.m. under the chairmanship of Professor Mahboob Ul Hussain, Coordinator Bioinformatics Centre at the, Bioinformatics Centre, University of Kashmir.

The Chairman welcomed all the undersigned members who were present in the meeting and declared the meeting open. The agenda centered around the discussion and finalization of the syllabus for the PG Diploma in Bioinformatics. The Coordinator presented the structure as per NEP 2020 format: two semesters, each requiring 22 credits from courses in Bioinformatics.

During deliberations, the syllabus for various courses was discussed and formulated and following courses with detailed sylabbus were proposed as part of the PG diploma in bioinformatics studies.

Semester I:

- Introduction to Cell and Molecular Biology
- Introduction to Linux/Unix
- Genomics and Proteomics
- Fundamentals of Bioinformatics
- Laboratory Course

Semester II:

- Biopython Programming
- Biostatistics
- Structural Bioinformatics
- Project Dissertation

Panel of Approved Members Present in the meeting

Prof. Mahboob ul Hussain
(chairman)

Prof. Raies Ahmad Qadri
(Member)

Prof. Ehtishamul Haq
(Member)

Prof. Firdous Ahmad Khanday
(Member)

Dr. Bilal Ahmad Reshi
(Member)

Dr. Abrar Ahmad Qurashi
(Member)

Dr. Showket Ahmad Ganie
(Member)

Dr. Mushtaq A. Beigh
(Member)

Dr. Shah Ubaid ullah
(Member)

Dr. Syed Nisar Hussain Bukhari
(Member)

Dr. Basharat Ahmad Bhat
(Member)

Mudasir Manzoor Reshi
(Research Scholar)

Adan Hafiz
(Research Scholar)

BIOINFORMATICS CENTRE

UNIVERSITY OF KASHMIR

(NAAC Accredited Grade A+)

Programme Title: PG Diploma in Bioinformatics

Curriculum Based on National education policy (2020)

CURRICULUM OVERVIEW

The curriculum is based on the National education policy (2020), spanning two semesters. Students are required to obtain 22 credits in each semester. These 22 credits must be obtained from the Bioinformatics Centre of the University. Both Semester I and Semester II include class teaching, tutorials, and laboratory courses, designed to provide a comprehensive foundation in bioinformatics with practical and computational training.

Glossary of Terms Used in the Curriculum: • One Credit: 16 hours of Lectures (L) or 32 hours of Tutorials (T) or 32 hours of Practical (P) • IA: Internal Assessment • SEE: Semester End Examination • CR: Core • DCE: Discipline Centric Elective

Programme Learning Outcomes (PLOs)

PLO No.	Programme Learning Outcome
PLO 1	Demonstrate foundational knowledge in bioinformatics, including biological data types, computational biology, and sequence analysis.
PLO 2	Apply computational tools and programming languages to analyze large-scale biological datasets.
PLO 3	Understand and implement genomic and proteomic data analysis workflows.
PLO 4	Use Linux/Unix environments effectively for bioinformatics applications.
PLO 5	Analyze molecular structures and apply modeling techniques in structural bioinformatics.
PLO 6	Conduct independent research using statistical and computational approaches.
PLO 7	Communicate scientific findings effectively through reports and presentations.
PLO 8	Practice ethical standards in data handling and research.
PLO 9	Develop skills in lifelong learning and adaptability in emerging technologies.
PLO 10	Utilize digital tools and databases for data mining and interpretation in life sciences.

PROPOSED SYLLABUS FOR CHOICE-BASED CREDIT COURSES FOR PG DIPLOMA IN BIOINFORMATICS

Semester I

S.No	Course Type	Course Code	Course Title	L T P	Total Credits	IA Marks	SEE Marks	Total Marks
1	CR	PBIFCCM124	Introduction to Cell and Molecular Biology	3 1 0	4	28	72	100
2	CR	PBIFCIL124	Introduction to Linux/Unix	3 1 0	4	28	72	100
3	CR	PBIFCGP124	Genomics and Proteomics	3 1 0	4	28	72	100
4	CR	PBIFCFB124	Fundamentals of Bioinformatics	3 1 0	4	28	72	100
5	DCE	PBIFDLC124	Laboratory Course	0 0 6	6	42	108	150
Total					22	154	396	550

Semester II

S.No	Course Type	Course Code	Course Title	L	T	P	Total Credits	IA Marks	SEE Marks	Total Marks
1	CR	PBIFCBP224	Biopython Programming	3	1	0	4	28	72	100
2	CR	PBIFCBS224	Biostatistics	3	1	0	4	28	72	100
3	CR	PBIFCSB224	Structural Bioinformatics	3	1	0	4	28	72	100
4	CR	PBIFCPD224	Project Dissertation	0	0	10	10	Dissertation (200), Presentation (35), Attendance (15).		250
Total							22	84	216	550

Detailed Course Syllabus

Semester I [Core (CR)]

Course No: PBIFCCM124
Credits: 4
Course Title: Introduction to Cell and Molecular Biology
Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs)

CLO	Statement
1	Describe the structure and function of biomolecules including carbohydrates, proteins, lipids, and nucleic acids.
2	Differentiate between prokaryotic and eukaryotic cell structures and understand membrane transport mechanisms.
3	Explain processes of DNA replication, transcription, and translation in molecular detail.
4	Analyze gene regulation mechanisms at transcriptional, post-transcriptional, and epigenetic levels.

Course Contents:

Unit I: Carbohydrates – basic structure (monosaccharides, polysaccharides), roles in energy and structure; proteins – amino acid composition, primary to quaternary structure, Ramachandaran plot significance, diverse functions including enzymatic activity, transport, signaling, and structural support; lipids – phospholipid bilayer structure (brief mention of energy storage and steroid roles); nucleic acids – DNA, RNA structural variations and types.

Unit II: Prokaryotic vs. eukaryotic cells – structural/function differences; cell membrane, phospholipid bilayer with embedded proteins, passive/active transport; organelles – nucleus (chromatin, envelope), mitochondria (ATP synthesis), ribosomes (protein synthesis machinery), cytoskeleton (structure/motility).

Unit III: DNA replication – process, key enzymes (helicase, polymerase); transcription – initiation, elongation, termination, RNA processing; translation – ribosome function, genetic code, stages (initiation, elongation, termination), protein synthesis.

Unit IV: Transcriptional control – promoters, enhancers, transcription factors (DNA binding, activation/repression); epigenetics – DNA methylation, histone modification, chromatin remodeling; post-transcriptional regulation – microRNAs in protein synthesis control;Motifs and master transcriptional factors.

CLO-PLO Mapping Matrix

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCCM124.1	3	1	1	0	0	0	0	1	1	2
PBIFCCM124.2	3	1	1	0	0	0	0	1	1	2
PBIFCCM124.3	3	1	1	0	0	0	0	1	1	2
PBIFCCM124.4	2	1	1	0	0	0	0	2	1	1

Recommended Books:

1. Alberts, B., et al. Molecular Biology of the Cell. Garland Science.
2. Nelson, D.L., & Cox, M.M. Lehninger Principles of Biochemistry. W.H. Freeman.
3. "Molecular Cell Biology" by Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Anthony Bretscher, Hidde Ploegh, Angelika Amon, and Kelsey C. Martin
4. Genes XII by Benjamin Lewin

Semester I [Core (CR)]

Course No: PBIFCIL124

Credits: 4

Course Title: Introduction to Linux/Unix

Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs)

CLO	Statement
1	Navigate the Linux file system and manage files and directories using command-line tools.
2	Manage file permissions and ownership in a multi-user environment.
3	Perform text manipulation and file searching operations using grep, find, and pipes.
4	Handle basic user management and process control in Linux systems.

Course Content:

Unit I: Introduction to Linux/Unix: Operating systems – Windows vs. Linux/Unix. Concept of open-source software. Overview of Linux distributions: Ubuntu, Fedora, Debian. Graphical User Interface (GUI) in Linux – desktop environments (GNOME, KDE). Logging in and navigating the desktop environment.

Unit II: Linux/Unix File System Basics: Understanding the Linux file system hierarchy – root directory (/), home directory (/home), etc. Working with files and directories – ls, cd, mkdir, rm, cp, mv. File attributes and permissions – read/write/execute (rwx), owner/group/others.

Unit III: File Operations and Text Editing: Viewing and editing files – cat, nano. Searching for files – find, locate. Basic text manipulation – grep, head, tail. Redirection and piping – >, >>, |.

Unit IV: User Management, Processes, and Software Handling: Managing users – adding/removing users, switching users (su, sudo). Understanding processes – viewing with ps, top; stopping with kill

CLO-PLO Mapping Matrix

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCIL124.1	0	2	0	3	0	0	0	0	2	0
PBIFCIL124.2	0	2	0	3	0	0	0	0	2	0
PBIFCIL124.3	0	2	0	3	0	0	0	0	2	0
PBIFCIL124.4	0	2	0	3	0	0	0	0	2	0

Recommended Books:

1. Sobell, M. G. A Practical Guide to Linux Commands, Editors, and Shell Programming . Pearson Education.
2. Blum, R., & Bresnahan, C. LinuxCommand Line & Shell Scripting For Dummies . Wiley Publishing.
3. The Linux Command Line: A Complete Introduction by William E. Shotts Jr.
4. Linux Essentials by Roderick W. Smith

Semester I [Core (CR)]

Course No: PBIFCGP124
Credits: 4
Course Title: Genomics and Proteomics
Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs)

CLO	Statement
1	Understand Next Generation Sequencing technologies and genome assembly methods.
2	Perform gene annotation and interpret functional genomics data.
3	Analyze proteomic data using mass spectrometry-based workflows.
4	Integrate genomic, transcriptomic, and proteomic data for systems-level understanding.

Course Content:

Unit I:Introduction to genome sequencing and Next-Generation Sequencing (NGS) technologies (e.g., Illumina, PacBio, Oxford Nanopore), Principles of sequencing: Library preparation, read generation, and error correction, Genome assembly methods: De novo and reference-guided approaches, Applications of genome sequencing in genomics research and personalized medicine.

Unit II:Basics of gene annotation: Identification of coding regions, regulatory elements, and non-coding RNAs, Tools and pipelines for annotation: Importance of gene annotation in understanding genome function and disease associations, Applications in evolutionary biology and functional genomics studies.

Unit III: Introduction to proteomics and its role in studying protein expression and function, Principles of mass spectrometry: Ionization methods and fragmentation techniques, Data analysis workflows: Database searching, protein identification, and PTM analysis, Applications of proteomics in biomarker discovery, systems biology, and clinical research.

Unit IV:Overview of functional genomics: Integration of genomic, transcriptomic, and proteomic data, Computational tools for analyzing large-scale datasets: RNA-Seq, ChIP-Seq, and CRISPR screens, Role of bioinformatics databases in interpreting functional genomics data, Applications in drug discovery, precision medicine, and understanding complex biological systems.

CLO-PLO Mapping Matrix

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCGP124.1	3	3	3	0	0	0	0	1	1	2
PBIFCGP124.2	2	3	3	0	0	0	0	1	1	2
PBIFCGP124.3	2	3	3	0	0	0	0	1	1	2
PBIFCGP124.4	2	3	3	0	0	0	0	1	1	2

Recommended Books:

1. Brown, T.A. Genomes. Garland Science.
2. Liebler, D.C. Introduction to Proteomics. Humana Press.
3. Genomics: A Very Short Introduction by John M. Archibald
4. Bioinformatics for Systems Biology by Kernighan, Holmes, and Sturmfels

Semester I [Core (CR)]

Course No: PBIFCFB124
Credits: 4
Course Title: Fundamentals of Bioinformatics
Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs)

CLO	Statement
1	Identify and use major bioinformatics databases and tools for retrieving biological data.
2	Perform sequence alignment using BLAST, FASTA, ClustalW, and interpret results.
3	Construct phylogenetic trees and interpret evolutionary relationships.
4	Evaluate applications of bioinformatics in genomics, drug discovery, and personalized medicine.

Course Content:

Unit I: Introduction to Bioinformatics - Scope, Applications, and Biological Data Types,Definition and scope of bioinformatics in modern biological research,Applications in genomics, proteomics, drug discovery, and personalized medicine, Types of biological data: Nucleotide sequences, protein sequences, gene expression data, and structural data.

Unit II: Structural and Sequence Biological Databases - PDB, NCBI, EMBL, UniProt; Data Retrieval and Annotation,Overview of key Metabolic and pathway databases: KEGG, Reactome,Tools for data retrieval.

Unit III: Sequence Alignment Global and Local - Pairwise and Multiple Sequence Alignment; BLAST, FASTA,Principles of pairwise sequence alignment for comparing two sequences,Multiple sequence alignment for analyzing evolutionary relationships.

Unit IV: Phylogenetics - Tree Construction Methods and Evolutionary Analysis,Methods for constructing phylogenetic trees: Distance-based and character-based methods, Interpretation of phylogenetic trees and evolutionary relationships,Applications in biodiversity studies, genetic divergence, and evolutionary analysis.

CLO-PLO Mapping Matrix

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCFB124.1	3	3	2	0	0	0	2	1	2	3
PBIFCFB124.2	3	3	2	0	0	0	2	1	2	3
PBIFCFB124.3	2	2	2	0	0	0	2	1	1	2
PBIFCFB124.4	2	2	2	0	0	0	2	1	1	2

Recommended Books:

1. Lesk, A.M. Introduction to Bioinformatics. Oxford University Press.
2. Mount, D.W. Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press.
3. Bioinformatics: Sequence, Structure and Databanks by Des Higgins and Willie Taylor
4. Phylogenetics: The Theory and Practice of Phylogenetic Systematics by E. O. Wiley and Bruce S. Lieberman

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Semester I [Discipline Centric (DCE)]

Course No: PBIFDLC124

Credits: 6
Course Title: Laboratory Course
Maximum Marks: 150 [105 (SEE) + 45 (IA)]

Course Learning Outcomes (CLOs)

CLO	Statement
1	Retrieve and analyze biological sequences from public databases (NCBI, UniProt, PDB).
2	Perform sequence alignment and predict secondary protein structures.
3	Visualize and analyze 3D protein structures using tools like PyMOL or Chimera.
4	Design primers for PCR and perform basic scripting for automation tasks.

Practicals:

☐ Protein Primary Structure analysis
☐ Secondary structure prediction
☐ Exploring Biological Databases (NCBI, ENSEMBL, PDB, UniProt)
☐ Primer design for PCR.
☐ Navigation of PDB,NCBI,ENSEMBL database.
☐ Sequence alignment using BLAST and ClustalW.
☐ 3D-Protein structure visualization (e.g., PyMOL/Chimera/Rasmol).

CLO-PLO Mapping Matrix

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFDLC124.1	2	3	2	0	0	0	2	1	2	3
PBIFDLC124.2	2	3	2	0	1	0	2	1	2	3
PBIFDLC124.3	2	3	2	0	2	0	2	1	2	3
PBIFDLC124.4	2	3	2	0	0	0	2	1	2	3

Recommended Lab Manual:

Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins By: Andreas D. Baxevanis and B.F. Francis Ouellette Publisher: Wiley-Interscience.

Semester II [Core (CR)]

Course No: PBIFCBP224
Credits: 4
Course Title: Biopython Programming
Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs):

CLO	Statement
1	Write and execute basic Python programs for biological applications.
2	Implement loops and conditional statements to solve bioinformatics problems.
3	Read, parse, and write biological data files like FASTA and GenBank.
4	Create functions and use IDEs like Jupyter Notebook for efficient coding.

Course Content:

Unit I: Programming fundamentals: Concept of algorithms and step-by-step problem-solving. Introduction to Python: Features and advantages. Setting up the Python environment. Variables, data types (integers, floats, strings, booleans), basic operations (arithmetic, comparison, logical), and type conversion. Understanding expressions and statements.

Unit II: Control flow: Conditional execution using if, elif, and else statements. Iteration using loops: for loop for fixed iterations and while loop for conditional looping. Use of break, continue, and pass. Solving simple biological problems using control structures, such as checking sequence validity or counting nucleotides.

Unit III: Working with files: Opening, reading, writing, and closing files in Python. Handling different file formats (text, CSV). Parsing and processing biological data formats such as FASTA and GenBank.

Unit IV: Functions: Defining and calling functions, function arguments and return values. Importance of modular programming in handling complex tasks. Using built-in functions and creating user-defined functions.Overview of IDE (VS-Code Jupyter Notebook)

CLO-PLO Mapping Matrix:

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCBP224.1	2	3	2	0	0	0	2	1	2	3
PBIFCBP224.2	2	3	2	0	0	0	2	1	2	3
PBIFCBP224.3	2	3	2	0	0	0	2	1	2	3
PBIFCBP224.4	2	3	2	0	0	0	2	1	2	3

Recommended Books:

1. Downey, A.B. Think Python. O'Reilly Media.
2. Bioinformatics Programming Using Python by Mitchell L. Model
3. Python Cookbook by David Beazley and Brian K. Jones
4. Practical Computing for Biologists" by Steven H. D. Haddock and Casey W. Dunn

Semester II [Core (CR)]

Course No: PBIFCBS224
Credits: 4
Course Title: Biostatistics

Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs):

CLO	Statement
1	Calculate and interpret descriptive statistics for biological datasets.
2	Apply probability distributions to model biological phenomena.
3	Perform hypothesis testing and interpret p-values in experimental contexts.
4	Use advanced statistical methods like regression and chi-square tests in bioinformatics research.

Course Content:

Unit I: Descriptive Statistics - Measures and Interpretation
Introduction to descriptive statistics: Calculation and interpretation of mean, median, mode, variance, and standard deviation. Understanding the importance of these measures in summarizing and analyzing biological data.

Unit II: Probability and Common Distributions
Basic probability concepts: Events, outcomes, and rules of probability. Exploration of common distributions: Normal distribution for continuous data, binomial distribution for discrete success/failure events, and Poisson distribution for rare event modeling in biological contexts.

Unit III: Hypothesis Testing - Procedures and Applications
Introduction to hypothesis testing: Formulating null and alternative hypotheses, performing t-tests for comparing means, and using ANOVA for multiple group comparisons. Understanding p-values and their role in determining statistical significance in bioinformatics research.

Unit IV: Advanced Statistical Techniques and Bioinformatics Applications
Advanced statistical methods: Chi-square tests for categorical data, correlation and regression analysis for relationships between variables. Overview and use of these techniques in bioinformatics, including gene expression analysis, differential analysis, and interpreting large-scale datasets.

CLO-PLO Mapping Matrix:

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCBS224.1	2	2	3	0	0	0	2	1	2	2
PBIFCBS224.2	2	2	3	0	0	0	2	1	2	2
PBIFCBS224.3	2	2	3	0	0	0	2	1	2	2
PBIFCBS224.4	2	2	3	0	0	0	2	1	2	2

Recommended Books:

1. Zar, J.H. Biostatistical Analysis. Pearson.
2. Pagano, M., & Gauvreau, K. Principles of Biostatistics. CRC Press.
3. Statistics for Biology and Health by Richard M. Heiberger and Eric B. Holland.
4. Biostatistics: How It Works by Steve Selvin.

Semester II [Core (CR)]

Course No: PBIFCSB224
Credits: 4
Course Title: Structural Bioinformatics
Maximum Marks: 100 [72 (SEE) + 28 (IA)]

Course Learning Outcomes (CLOs):

CLO	Statement
1	Describe hierarchical protein structures and their functional significance.
2	Apply homology modeling and docking techniques for structural analysis.
3	Predict protein secondary structure using computational tools and AI models.
4	Understand drug discovery pipelines using structure-based approaches.

Course Content:

Unit I: Protein Structure -
Introduction to the hierarchical levels of protein structure: primary (amino acid sequence), secondary (alpha-helices and beta-sheets), tertiary (3D folding), and quaternary (multimeric assemblies). Idea of super secondary structures. Importance of each level in determining protein function and stability. Overview of the Protein Data Bank (PDB) as a repository for experimentally determined protein structures and its role in structural biology research.

Unit II: Molecular Modeling - Homology Modeling and Docking
Basic techniques in molecular modeling, including homology modeling Swissprot and iTasser, De-Novo methods for predicting protein structures using known templates and docking for studying protein-ligand interactions.

Unit III: Structure Prediction - Protein secondary structure prediction. Role of AI/machine learning and computational advancements in improving prediction accuracy (Alphafold), Overview of Importance of structure prediction in filling gaps in experimental data and enabling large-scale bioinformatics studies.

Unit IV: Drug Design - Structure-Based Drug Discovery
Introduction to drug design (Protein and ligand based), focusing on leveraging molecular structures of drug targets for developing small molecules or biologics. Overview of techniques like virtual screening, pharmacophore modeling.

CLO-PLO Mapping Matrix:

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCSB224.1	3	1	1	0	0	0	0	1	1	2
PBIFCSB224.2	2	2	2	0	0	0	0	1	1	2
PBIFCSB224.3	2	3	2	0	0	0	0	1	1	2
PBIFCSB224.4	2	3	2	0	0	0	0	1	1	2

Recommended Books:

1. Bourne, P.E., & Weissig, H. Structural Bioinformatics. Wiley-Liss.
2. Leach, A.R. Molecular Modelling: Principles and Applications. Pearson.
3. Structural Bioinformatics: An Algorithmic Approach by Forbes J. Burkowski.
4. Essentials of Pharmaceutical Chemistry by Catherine Roche.

Semester II [CORE (CR)]

Course No: PBIFCPD224
Credits: 10
Course Title: Project Dissertation
Maximum Marks: 250

Course Learning Outcomes (CLOs):

CLO	Statement
1	Formulate a research question and design an appropriate methodology.
2	Collect, process, and analyze relevant biological data using bioinformatics tools.
3	Interpret results and draw scientifically valid conclusions.
4	Communicate findings effectively through written dissertation and oral presentation.

Course Structure:

- Students undertake a 2-month project under faculty supervision, focusing on a bioinformatics problem (e.g., sequence analysis, structural prediction).
- Milestones: Proposal, methodology, data analysis, dissertation writing, presentation.

CLO-PLO Mapping Matrix:

CLO	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10
PBIFCPD224.1	2	2	2	0	0	0	0	2	2	2
PBIFCPD224.2	2	3	3	0	0	0	0	2	2	3
PBIFCPD224.3	2	3	3	0	0	0	0	2	2	3
PBIFCPD224.4	2	2	2	0	0	0	0	2	2	2

Assessment: Dissertation (200 Marks), Oral presentation (35 Marks), Attendance (15 Marks).