Institute of Microbiology and Molecular Genetics
Faculty of Life Sciences
University of the Punjab, Lahore
Course Outline

Programme	BS	Course Code	MMG410	Credit Hours	3(2+1)
Course Title	BIOINFORMATICS				

COURSE INTRODUCTION

This course covers understanding biological data, using biomedical big data online resources, and analyzing genomic/transcriptomic/proteomic data. Students will be introduced to different biological databases and software tools and will be practically able to use these databases and software tools to retrieve the required data/information. Overall, students will be able to understand and explore different web-available biological data resources which is going to benefit them anytime in their research.

LEARNING OUTCOMES

On the completion of the course, the students will be able to:

1. Familiarity and working with various tools and databases used for biological data analysis.
2. Apply different types of Alignment of sequences using pairwise and multiple sequence methods to find similarity between protein or DNA sequences.
3. Develop primers and identify the restriction enzymes for restriction mapping to use latter on in diagnostic laboratories.
4. Exploration of protein 3D structures and also develop 3D structures by using online tools.

COURSE CONTENT

Introduction to Bioinformatics, Central dogma of life to understand data types, Introduction to information technology, Introduction to different primary and secondary sequence databases. Data mining in different sequence databases, Introduction to DNA and protein alignment, types of alignment and their usage, Local alignment and its programs, Primer designing, Restriction mapping, gene finding in prokaryotes and eukaryotes, Data retrieval from Biological literature databases, 3D structure database, how to analyze 3D structure of protein in software, Multiple sequence alignment and phylogenetic tree development, analyzing coting files in sequencing.

PRACTICALS

Computational analysis of various online biological primary and secondary sequence databases, data mining, downloading and retrieval of biological data from databases, how to find genes and

gene products, usage of alignment tools to find sequence similarity, primer designing, restriction mapping, how to use literature database, visualization and analysis of Protein 3D structures, construction of phylogenetic tree, computer aided drug development.

TEXTBOOKS AND READING MATERIAL

1. Loging, W. T. (Ed.). (2016). *Bioinformatics and Computational Biology in drug Discovery and Development*. Cambridge University Press.
2. Christensen, H. (Ed.). (2018). *Introduction to Bioinformatics in Microbiology*. Cham, Switzerland: Springer International Publishing.
3. Baxevanis, A. D., Bader, G. D., & Wishart, D. S. (2020). *Bioinformatics*. John Wiley & Sons.

ASSESSMENT

Sr. No.	Elements	Weightage	Details
1.	Midterm Assessment	35%	Written Assessment at the mid-point of the semester.
2.	Formative Assessment	25%	Continuous assessment includes Classroom participation, assignments, presentations, viva voce, attitude and behavior, hands-on activities, short tests, projects, practicals, quizzes etc.
3.	Final Assessment	40%	Written Examination at the end of the semester