

Course	Discipline Specific Core
Semester	VI
Paper Number	MBTCR6141T
Paper Title	GENOMICS AND PROTEOMICS
No. of Credits	6
Theory/Composite	Theory
No. of periods assigned	5 Theory + 1Tutorial
Course description/objective	<p>The course aims to</p> <ul style="list-style-type: none"> · impart theoretical knowledge and information about computational tools of genomics. · impart theoretical knowledge and provide information about computational tools of proteomics. · introduce students to structural and functional genomics and DNA sequencing methods. · introduce students to proteomics and techniques for analysis of proteomes. · to provide knowledge about computational tools for highthroughput handling of gene and protein sequences · provide students with information about web based servers and software for genome analysis by means of projects/ tutorials.
Syllabus	<p>Module A: (40 Marks)</p> <p>UNIT I Introduction to Genomics, DNA sequencing methods - Insights into Long Read and Short Read sequencing. Data output formats, Sequence Assembly, Genome Annotation, genome analysis, Gene prediction, Promoter prediction, Repeat Masking. Degradome Sequencing and applications. Insights into single cell genomics.</p> <p>Unit II The human genome project. Concepts of draft and whole genome, Controversies associated with the human genome project and recent developments. Structural, Functional and Comparative Genomics. Concept of Pangenome and use of graphs, applications of genome data in forensics, disease diagnosis and genetic counselling.</p> <p>UNIT III (5 Periods): Tutorial Managing and Distributing Genome Data: Web based servers and softwares for genome analysis: ENSEMBL, VISTA, UCSC Genome Browser, NCBI genome. Selected Model Organisms' Genomes and Databases.</p> <p>No. of Classes: 3 /week.</p> <p>Module B: (40 Marks)</p> <p>UNIT IV: Proteomics: Chemical properties of proteins. Physical interactions that determine the property of proteins, Short-range interactions, electrostatic forces, van der Waals interactions, hydrogen bonds, Hydrophobic interactions. Determination of sizes gel filtration, Introduction to Proteomics, Top-down and Bottom-up proteomics. Analysis of proteomes tools. 2D-PAGE. Sample preparation, solubilization, reduction, resolution, 2D-DIGE, Reproducibility of 2D-PAGE, Mass spectrometry based methods for protein identification: MALDI, ESI- MS, <i>Denovo</i> sequencing using mass spectrometric data.</p>

	No. of Classes: 3 / week.
Readings	<p>1. Genes IX by Benjamin Lewin, Johns and Bartlett Publisher, 2006.</p> <p>Modern Biotechnology, 2nd Edition, S.B. Primrose, Blackwell Publishing, 1987.</p> <p>Molecular Cloning: A Laboratory Manual (3rd Edition) Sambrook and Russell Vol. I to III, 1989.</p> <p>Principles of Gene Manipulation 6th Edition, S.B. Primrose, R.M. Twyman and R.W. Old. Blackwell Science, 2001.</p> <p>Pevsner, J. (2009). Bioinformatics and Functional Genomics. II Edition. John Wiley & Sons.</p>
Evaluation	<p>Continuous Internal Assessment (Genomics Project): 20 marks</p> <p>End-Semester Theory Examination: 80 marks</p>
Paper Structure for End Sem Theory	<p>Module A (40 Marks)</p> <p>Q.1. Five objective type questions each of 2 Marks, i.e. 5 x 2 = 10 marks.</p> <p>Q.2, Q.3 and Q.4 are compulsory, each of 10 marks, i.e. 3 x 10 = 30 marks</p> <p>Module B (40 Marks)</p> <p>Q.5.: compulsory question of 10 marks containing objective questions</p> <p>Any 3 questions of 10 marks each from Q.6-Q.9.</p> <p>No part will be more than 5 marks.</p>