



Programme – Ph.D. (AIB – Biosciences and Biotechnology)

Course Title: ‘Omics’ in Research

Course Code: GCMB905

Credit Units: 04

L	T	P/S	SW/F W	TOTAL CREDIT UNITS
2	0	0	4	4

Course Objectives: The course grooms the students to functional investigations presented in genomic and proteomics research by acquiring methodological skills in experimental and/or computational techniques applied to research questions addressed through bioinformatics tools, overview of analytical platforms, experimental design methods and databases used to decode sequence, structure and functional data.

Pre-requisites: Graduate in Biosciences, Life Sciences

Student Learning Outcomes: On Successful completion of the course

- Students will be able to grasp the minutiae of genome / proteome organization, functioning and evolution.
- Educe the methods for gene/protein identification and ascribe potential functions to their products using computational tools.
- Recognize and validate the plans towards mapping, network modeling and engineering biology for scientific use.
- Harness their knowledge and skills to execute a novel research project aimed at the generation of new scientific knowledge.

Course Contents/Syllabus:

	Weightage (%)
Module I	20
Descriptors/Topics – Genomes – Preamble and Technologies Organization of genome structure, Variations in genome, Genome Molecular markers, First generation sequencing, High-throughput Genomic techniques – Second and third generation Sequencing techniques, De Novo Whole genome sequencing strategies	
Module II	10
Descriptors/Topics – Functional and Comparative Genomics De novo and reference based Whole genome sequencing using Next Gen sequencing, Applications - Concepts of Deep Sequencing, Resequencing; Personal genomics, Metagenomics; Genome Annotation; Genome sequence to functional	

analysis; ESTs, SAGE, QPCR, The ENCODE project; Genome-Wide Association Studies (GWAS)	
Module III	20
Descriptors/Topics Module III – Sequence Analysis Strategies and biomolecule predictive methods Biological databases and retrieval; Sequence Alignment – pairwise (Dot plot and Dynamic Programming) and multiple; Database similarity searching techniques; Concepts of motif, pattern and profile; Identification and characterization of proteins, Protein structure prediction methods: Secondary and tertiary approaches	
Module IV	15
Descriptors/Topics Module IV – Phylogenetic Analysis Concepts of evolutionary tree and phylogenetics; Evolutionary models; Types of phylogenetic trees; Phylogenetic analysis methods: UPGMA, Neighbor-Joining, maximum Parsimony, maximum likelihood. Tree evaluation methods: Bootstrapping, Randomized and jack-knifing methods, Phylogenetic analysis software: PHYLIP, MEGA	
Module V	
Descriptors/Topics – Capturing Transcriptomes and Proteomes Transcriptomics technologies; Microarray technology; Chromatin immunoprecipitation (ChIP), Chip-chip, Chip-Seq;; Gene Regulation; Proteome and Sub-proteome Analysis; Shotgun proteomics - Expression proteome analysis; Proteome Tools – Quantitative and Qualitative Analysis; Gel based analysis; HPLC; Mass Spectrometry – Concepts, Ionization and applications in proteome capturing, Proteomics in research – case studies and patterns.	20
Module VI	15
Descriptors/Topics – Interactomes and Current Explorations in Proteomics Interactomics – Proteomic Analysis of protein-protein / protein –DNA interactions - experimental and computational methods (Two-hybrid methods, Phage Display, Protein chips); Proteome-wide interaction maps and databases; Proteomics experimental workflows; Application of proteomics – Protein engineering principles, Metabolomics Technologies; Computational Proteomics - Predictive Medicine; Screening	

Pedagogy for Course Delivery:

Lectures: 27

Class Test: 1

Presentation/ Seminar: 1

Viva Voce: 1

Total: 30

Pedagogy for Self Work:

Case Studies

Review of Literature

Home Assignment

Assessment/ Examination Scheme:

Theory L/T (%)	Self Work (%)	End Term Examination
70	30	100

Theory Assessment (L&T):

Continuous Assessment/Internal Assessment					End Term Examination
Components (Drop down)	Class test	Presentation	Viva	Attendance	70
Weightage (%)	15	5	5	5	

Self Work Assessment:

Continuous Assessment/Internal Assessment					End Term Examination		
Components	Gap Analysis	Synopsis		Total	Performance	Viva	Total
Weightage (%)	15	15		30	35	35	70

Text & References:

- **Discovering Genomics, Proteomics and Bioinformatics, 2nd Edition. Campbell AM & Heyer LJ, Benjamin Cummings 2007; CSH Press, NY. ISBN-10: 8131715590**
- **Principles of Proteomics. R.M Twyman (2004). (BIOS Scientific publishers). ISBN-10: 1859962734**
- **Principles of Gene Manipulation and Genomics- Primrose S & Twyman R, 7th Edition, Blackwell, 2006. ISBN-10: 1405135441**
- **Principles of Genome Analysis and Genomics. Primrose SB & Twyman RM. 2007. Blackwell. ISBN-10: 1405101202**
- **Introduction to Genomics. A.M Lesk, Oxford University press, 2007. ISBN-10: 0199557489**
- **A Primer of Genome Science. Greg Gibson and Spencer V. Muse. 2nd ed. 2004. SINAUER Associates Inc. ISBN-10: 0878932364**
- **Introduction to Proteomics: Tools for the New Biology. Daniel C. Liebler, Humana Press Inc., 2002. ISBN-10: 0896039919**
- **Bioinformatics – Sequence and Genome Analysis – David W. Mount –Cold Spring Harbor Laboratory Press, U.S.; 2nd Revised edition, 2004. ISBN-10: 9746520709**
- **Essential Bioinformatics – Xing Xiong – Cambridge University Press, New York, 2006. ISBN-10: 0521706106**
- **Bioinformatics and Functional Genomics – Jonathan Pevsner - 2nd edition, Wiley-Blackwell, 2009. ISBN-10: 0471210048**

Any other Study Material:

- **NCBI online tutorials and Videos**
- **Genome TV – You tube videos form NIH**