



L	T	P/S	SW/FW	TOTAL CREDIT UNITS
3	0	0	0	3

**Course Title: High Throughput Biology**

**Course Code: GCMB317**

**Credit Units: 3**

**Level: UG**

**Course Objectives:** The course is aimed to critically apprise the students with the concepts and tools that contribute towards understanding scientific research data analyses. Biological interpretations after the structured statistical, computational and mathematical analyses are explained thoroughly after the technical aspects of the technology involved.

**Prerequisites:** Biochemistry, Molecular Biology, Recombinant DNA technology, Bioinformatics, Genomics and Proteomics

**Course Contents / Syllabus:**

	Weightage
<b>Module I</b>	<b>25%</b>
<b>Descriptors/Topics - High-throughput sequencing technology</b>	
<ul style="list-style-type: none"><li>• Introduction to Omic's technologies, Next-generation sequencing; Genome Alignment, Genome Visualization, De Novo Assembly Genome Variation</li><li>• Quantitative transcriptomics: qRT-PCR; Advanced transcriptomics: gene expression microarrays, Next-generation sequencing in transcriptomics: RNA-seq experiments; Analysis of transcription factor binding sites</li></ul>	

<b>Module II</b>	
<b>Descriptors/Topics - High-throughput Biology: Information processing from Sequence data</b>	<b>25%</b>
<ul style="list-style-type: none"> <li>Organizing high throughput data; Analysis of Genome, Transcriptome, Metagenome, miRNA and Epigenomics data; Multiple testing and false discovery rate; Quality control of raw reads: FASTQC and fastx toolkit; Read alignment to a reference genome: Bowtie and Tophat; Peak calling: MACS, USeq and SISR</li> <li>Statistical Modeling; Hierarchical Models and the basics of Bayesian Statistics; Exploratory Data Analysis for High throughput data; Analysis of Metagenomic Data; QIIME, PICRUST; High-Throughput Sequencing Data Informatics</li> </ul>	
<b>Module III</b>	
<b>Descriptors/Topics - RNA sequencing and analysis</b>	<b>30%</b>
<ul style="list-style-type: none"> <li>Introduction to R; Informatics for RNA-seq Analysis and ChIP-seq; Experiment design for ChIP-seq and RNA-seq; Small non-coding RNA analysis: R, Reaper; Exploratory Analysis of Biological Data using R; Pathway and Network Analysis of -omic Data; Microbiome projects; Proteogenomics</li> </ul>	
<b>Module IV</b>	<b>20%</b>
<b>Descriptors/Topics - Gene Expression Analysis and Network Analysis</b>	
<ul style="list-style-type: none"> <li>Microarray Expression Analysis - Quantification of expression and differential expression analysis and differential exon usage: R, DESeq, DEXSeq; Normalisation and experimental design models for microarray data. Metabolomics - Informatics and Statistics for Metabolomics; Expression and Differential Expression, Isoform Discovery and Alternate Expression, Regulatory Network Analysis</li> </ul>	

**Pedagogy for Course Delivery:**

The class will be taught using theory and case based method. In addition to assigning the case studies, the course instructor will spend considerable time in understanding the concept of innovation through the eyes of the researcher. The instructor will cover the ways to think innovatively liberally using thinking techniques. The class will be taught through lecture, presentation and case studies. Lectures: 43

Internal Assessment: 2 Total:

45

**Student Learning Outcomes:**

- Demonstrate the ability to understand the high throughput processes and characteristics of such high throughput biological experiments.
- Evaluate the concepts of sequencing, transcriptomics and other 'omics' methods applied and deduce logical interpretations from the data analysis.
- Apply theoretical knowledge of the technologies involved to create knowledge-base for solving tactical problems in the various assignments in the subject.
- Describe the biological analytical models generated with conceptual approaches with bioinformatics and statistical approaches applied to the high throughput data.
- Critically assess the data characteristics, experimental design for efficient progress in high throughput biology.

**Assessment/ Examination Scheme:**

**Theory Assessment (L&T):**

Continuous Assessment/Internal Assessment					End Term Examination	Total
Components (Drop down)	Class Test	Home Assignment	Viva Voce	Attendance		
Weightage (75 %)	10	07	08	5	70	100

**Text:**

- **Data Mining Techniques for the Life Sciences** Oliviero Carugo (Editor), Frank Eisenhaber (Editor) Humana Press; 2010 edition. ISBN-13: 978-1603272407.
- **An Introduction To High Content Screening: Imaging Technology, Assay Development, and Data Analysis in Biology and Drug Discovery** - Steven A. Haney (Editor), Douglas Bowman (Editor), Arijit Chakravarty (Editor). Wiley-Blackwell (31 December 2014). ISBN-13: 978-0470624562.
- **High Throughput Screening: Methods and Protocols (Methods in Molecular Biology)** 29 Nov 2011 - William P. Janzen (Editor), Paul Bernasconi (Editor) ISBN-13: 978-1617794919.
- **RNA Bioinformatics (Methods in Molecular Biology) Hardcover** – 22 Jan 2015 - Ernesto Picardi (Editor) ISBN-13: 978-1493922901.