GUJARAT TECHNOLOGICAL UNIVERSITY

Syllabus for M.Sc. in Industrial Biotechnology, Semester - 3

Subject Name: Elective -Introduction to Omics Based Technologies

Subject Code: 1330108 W.E.F 2021-22

1. Learning Outcomes

Learning Outcome Component	Learning Outcome (Learner will be able to)
Theoretical and practical understanding of Introduction to Omics Based Technologies	● Understand how high throughput DNA sequencing (HTS) can be used to identify disease causing genetic variants in monogenic diseases. ● Understand how Genome Wide Association studies (GWAS) can detect disease associated markers in multifactorial diseases.
Value applications of Introduction to Omics Based Technologies in biological research as well as in biotech-industries	● Understand how HTS technologies can be used to explore changes in gene expression. ● Understand application of various OMICS technologies.
Effective Communication	● Communicate concepts and ideas effectively.
Professional & Ethical Behaviour	● Transparency, honesty and ethical reasoning in handling genomic DNA for research work.

LO – PO Mapping: Correlation Levels:

1 = Slight (Low); 2 = Moderate (Medium); 3 = Substantial (High), "-"= no correlation

Sub Code:	PO1	PO2	PO3	PO4	PO5	PO6	PO7
LO1:Theoretical and practical understanding of Introduction to Omics Based Technologies	3	2	2	2	3	2	2
LO2:Value applications of Introduction to Omics Based Technologies in biological research as well as in biotech-industries	2	3	2	2	3	3	2
LO3: Effective communication	2	2	3	2	2	3	2
LO4: Professional & Ethical Behaviour	3	2	2	2	2	2	3

2. Course Duration: The course duration is 45 sessions of 60 minutes each.

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3. Course Contents:

Module No:	Module Content	No. of Sessions	70 Marks (External Evaluation)
1	**Genome Mapping** Structure and organization of prokaryotic and eukaryotic genomes- nuclear, mitochondrial and chloroplast genomes; Computational analysis, Databases, Finding genes and regulatory regions; Tools for genome analysis– PCR, RFLP, DNA fingerprinting, RAPD, SNP detection, SSCP, FISH to identify chromosome landmarks; Human Genome Project- landmarks on chromosomes generated by various mapping methods, BAC libraries and shotgun libraries preparation, Physical map, Cytogenetic map, Contig map, Restriction map, UCSC browser.	9	14
2	**Microarray technology** Basic principles and design, cDNA and oligonucleotide arrays, DNA microarray, Instrumentation and structure; Designing a microarray experiment. Comparative Genomic Hybridization (CGH) arrays, Resequencing arrays; Different platforms (Affymetrix, Agilent etc.); Data Processing and Normalization - Algorithms of data processing and Normalization; Tools used to normalize; Microarray databases – NCBI; GEO (Gene Expression Omnibus), ArrayExpres (EBI); Functional Analysis: Differential gene expression; Gene Ontology functional enrichment tools, Pathway analysis (KEGG Database); Applications of Microarray technology;Case studies - Application of expression profiling in human disease; Comparison of Microarray technology and High throughput sequencing technology.	10	14
3	**Sequencing technologies**	10	14

	Introduction to sequencing, Maxam and Gilbert method, Sanger Sequencing techniques and applications; Next Generation sequencing (NGS), quality check, Library, Preparations, Platform overview and comparison (Illumina, 454 (Roche), SOLiD (Life technology), Specific Biosciences, Ion Torrent, Nanopore, PacBio; Types of NGS, DNAsequencing - Whole genome sequencing, exome sequencing, Deep sequencing, ChIP sequencing, RNA-sequencing and types (small RNA sequencing, non coding RNA sequencing), Whole transcriptome sequencing; Data Processing and Analysis: Data Quality Check, filtering and Genome assembly and mapping to reference genomes, mapping tools (bowtie, maq etc.), Sequence Alignment formats: Sequence Alignment/Map (SAM) format, Binary Alignment/Map (BAM) format, Functional Analysis: Pathway analysis, Gene Ontology analysis; Application of different sequencing technique, methylomics, in vivo protein binding, genome wide association studies (GWAS), Histone modification, microbial sequencing.		
4	**Proteomics** Relationship between protein structure and function; Outline of a typical proteomics experiment, One- and two-dimensional gel electrophoresis (IEF and 2D electrophoresis), Alternatives to electrophoresis; Multiplexed protein analysis, Spot visualization and picking; Tryptic digestion of protein and peptide fingerprinting, Mass spectrometry : ion source (MALDI, spray sources), analyzer (ToF, quadrupole, quadruple ion trap) and detector; Post translational Modifications: Quantitative proteomics, clinical proteomics and disease biomarkers, mass spectral tissue imaging and profiling; Protein-protein interactions: Surfaceomes and Secretomes, Solid phase ELISA, pull-down assays (using GST-tagged protein) tandem affinity	8	14

	purification, western analysis, surface plasmon resonance technique; Yeast two hybrid system, Phage display, Protein interaction maps, Protein arrays-definition; Types of protein arrays, Applications- diagnostics, expression profiling. Protein databases, Protein databank.		
5	**Metabolomics** Introduction and overview of metabolites, sample collection and processing, Non tracer and tracer (radio labelled)-based techniques in metabolomics (HPLC, NMR, LC-MS and GC-MS); Metabolome data processing derived by various techniques, analysis of databases (MetaboLight, MetaCyc, MMCD etc.), Analysis tools, Metabolic pathways and network analysis; Metabolic flux analysis (TCA, Amino acids, fatty acids, intermediary metabolites), Stoichiometric metabolic flux analysis, ^{13}C metabolic flux analysis (MFA), Metabolic control analysis (MCA); Applications of metabolomics; Integration of metabolomics data sets with other data (eg. Transcriptomics, enzyme activity etc.).	8	14

4. Pedagogy:

- ICT enabled Classroom teaching
- Practical / live assignment
- Interactive classroom discussions

5. Evaluation:

Students shall be evaluated on the following components:

A	**Mid-Semester Examination**	**(Internal assessment-30 Marks)**
B	**End-Semester Examination**	**(External assessment-70 Marks)**

6. Reference Books:

No	Author	Name of the Book	Publisher	Year of Publication / Edition
1	Brown TA	Genomes	Garland Science	3rd Edition

2	Campbell AM and Heyer LJ	Discovering Genomics, Proteomics and Bioinformatics	Benjamin Cummings	Latest Edition
3	Primrose S and Twyman R	Principles of Gene Manipulation and Genomics	Blackwell	7th Edition
4	Rehm H	Protein Biochemistry and Proteomics	Academic Press	4th Edition
5	Twyman RM.	Principles of Proteomics	Garland Science Taylor & Francis Group	2nd Edition
6	Liebler DC	Introduction to Proteomics Tools for the New Biology	Humana Press	Latest Edition
7	Teresa Whei-Mei Fan, Andrew M. Lane, Richard M. Higashi	Handbook of Metabolomics	Springer	Latest Edition
8	John C. Lindon, Jeremy K. Nicholson, Elaine Holmes	The Handbook of Metabonomics and Metabolomics	Elsevier	Latest Edition

Note: Wherever the standard books are not available for the topic appropriate print and online resources, journals and books published by different authors may be prescribed.

7. List of Journals/Periodicals/Magazines/Newspapers / Web resources, etc

- https://www.rsc.org/journals-books-databases/about-journals/molecular-omics/

Course Outcomes:

On completion of this course, students should be able to:

- On completion of the course, students should have:
- Overview of genome variation in population including technologies to detect these variations;
- Understand how high throughput DNA sequencing (HTS) can be used to identify disease causing genetic variants in monogenic diseases;
- Understand how Genome Wide Association studies (GWAS) can detect disease associated markers in multifactorial diseases;
- Understand how HTS technologies can be used to explore changes in gene expression;
- Understand application of various OMICS technologies.