Semester	5 and 6		
Course Code:	MIBI 43774		
Course Name:	Advanced Bacterial Genetics, Bioethics and Biosafety, Bioinformatics, Molecular Biology and Gene Technology		
Credit Value:	4		
Core/Optional	Core		
Hourly Breakdown	Theory	Practical	Independent Learning
	60 hrs	-	140 hrs

Course Aim/Intended Learning Outcomes:

Upon successful completion of this course student will be able to;

- Understand and describe the molecular level interactions between eukaryotes and prokaryotes,
- Understand and explain complex genetic regulatory mechanisms in bacteria,
- Understand and describe applications of bacterial genetics,
- Explain the principles of the techniques used in recombinant DNA technologies and their applications in different fields,
- Understand the pros and cons of GM technology and related issues,
- Interpret basic biosafety and bioethics principles and their impacts on the quality of life,
- Recognize importance of biosafety practices and guidelines in scientific research,
- Understand the balanced integration between scientific research and social elements,
- Understand the need of bioinformatics tools in analyzing molecular biological data,
- Analyze biological sequences and interpret the results and
- Apply different bioinformatic tools to manipulate DNA and protein sequences.

Course Content:

Advanced Bacterial Genetics:

Differences and similarities between eukaryotic and prokaryotic chromosome structures, their gene expression and gene regulation mechanisms. DNA protein interactions. Selected human genetic disorders including cancer. Genetic basis of Bacteriotherapy, Gene therapy, Human Microbiome. Protein translocation systems in bacteria. Molecular mechanisms of bacterial resistance to extreme environments. Molecular mechanisms of bacterial pathogenesis, Pathogenicity islands, Gene flow, Genome editing, Designer bacteria. Other relevant current topics in bacterial genetics.

Molecular Biology and Gene Technology:

Recombinant DNA Technology: DNA manipulative enzymes, Restriction digestion and restriction mapping, Polymerase chain reaction. Primer designing. DNA Cloning – cloning and expression vectors, Construction of DNA libraries, Library screening, Detection of clones using hybridization (Southern blotting). *Genetically modified organisms (GMOs)*: objectives, methods used to develop GMOs, potential hazards/ risks associated with GMOs, Detection and screening of GMOs.

Sequencing Technologies: First generation of sequencing – Sanger technology, Sequence library preparation, Next generation of sequencing – 454-pyrosequencing, Illumina and Ion torrent technologies. Next-next generation of sequencing – single molecule real-time (SMRT) and PacBio sequencing.

Omic studies: Genomics - Introduction, Whole-genome sequencing projects. Transcriptomics - experimental designing, large-scale expression studies, RNA-seq, quantitative RT-PCR and other methods, designing gene expression studies with appropriate controls, DNA microarrays. Proteomics – principle, methods and approaches. Metagenomics - Principles, uses and approaches.

Bioethics and Biosafety:

Bioethics in Biotechnology: Ethical biotechnology - principles, concerns, importance, and societal and global perspectives. Morality, Ethical committees, Informed consent and Conflicts of interest. Ethical assessment of technologies – ethical issues related to human genome/ cloning projects, agricultural and animal rights and data privacy. Socio-economic impact of biotechnology. Global and local ethical policies regulations. *Biosafety:* Introduction, Biohazards and biosafety levels - classification, Biosafety guidelines. Assessment of risk associated with laboratory techniques – handling, transportation and disposal of biological materials. Bio-terrorism. National and international protocols on biosafety – Cartagena biosafety protocol.

Responsible conduct of science. Principles of good research practice.

Bioinformatics:

Introduction to bioinformatics. *Molecular biological data repositories*: Introduction, Structure and classification of databases, International Nucleotide Sequence Database Collaboration (INSDC), NCBI data model, Submitting DNA sequences to the databases, Other relevant biological databases, Retrieval of information from biological databases. *Sequence alignment and database searching*: Scoring sequence alignments – matches, mismatches, gap costs and substitution matrices. Pairwise sequence alignment – Dot-plot, Dynamic programming algorithms and k- tuple method. Multiple sequence alignments. *Database similarity searching*: Greedy Algorithms, Introduction to BLAST suite. *Genome assembly and annotations*: contig assembly, gene finding, identification of regulatory regions, gene numbers, gene ontology, functional classes and functional annotation, common tools available for genome annotations. *Molecular phylogeny*: properties of phylogenetic trees, tree construction methods, tree rooting, bootstrap method and substitution models.

Teaching /Learning Methods:
Lectures, assignments, group presentations, research paper discussions and computer-assisted assignments.

Assessment Strategy: Continuous assessment and end of the course unit examination.

Continuous Assessment 20%	Final Assessment 80%		
Details: Assignments: 20%	Theory (%) 80	Practical (%) -	Other (%) -

Recommended Reading:
- Weaver, R.F. (2011) *Molecular Biology*, 5th edition. McGraw-Hill
- Snynder, L., Peters J. E., Henkin, T. M. and Champness, W. (2013) *Molecular Genetics of Bacteria*. 4th edition. ASM press.
- Brown, T.A. (2016) *Gene Cloning and DNA Analysis*. 7th Ed. Wiley Blackwell.
- Pevsner, J. (2015) *Bioinformatics and Functional Genomics*, 3rd edition, John Wiley & Sons.
- Baxevanis, A. D, Ouellette, B. F. F. (2001) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins,* 2nd edition, John Wiley & Sons.
- Related current review and research articles from peer- reviewed journals as recommended by the lecturers.