CREDIT DISTRIBUTION, ELIGIBILITY AND PRE-REQUISITES OF THE COURSE

Course title & Code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Lecture	Tutorial	Practical/ Practice		
Genomics, Proteomics and Bioinformatics DSE-16	4	2	0	2	Semester VII	Nil

Learning Objectives:

- Introduce students to fundamental and emerging concepts in genomics, proteomics, and bioinformatics.
- Familiarize students with analytical tools and real-world applications of omics technologies across agriculture, health, and environmental sectors.
- Explore interdisciplinary fields such as metagenomics, epigenomics, and single-cell genomics and their significance in global problem-solving.
- Develop basic computational skills to utilize bioinformatics databases and tools for data interpretation in genomics and proteomics.

Learning Outcomes:

By the end of the course, students will be able to:

- Explain the principles and applications of genomics in agriculture, human health, and environmental science.
- Understand the concepts of epigenetics and demonstrate familiarity with tools used to study epigenetic modifications.
- Describe metagenomics and single-cell genomics, and their relevance in microbiome analysis and environmental monitoring.
- Understand core techniques and tools in proteomics, including post-MS data analysis, and their translational value.

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- Demonstrate knowledge of bioinformatics concepts, databases, and software tools for sequence, structure, and functional analysis of biological data.

Theory :   **30 Hours**

Unit 1: Genomics and Epigenetics   **10 Hours**
Genomic concepts: genomes, genes, and non-coding regions, Structure of complexity of eukaryotic genome, Applications in agriculture, health, and the environment, CRISPR-Cas9: A beginner-friendly introduction to genome editing, Genomics ethics: privacy, data sharing, and equity. Epigenomics. DNA methylation and histone modifications, Overview of Bisulfite sequencing and ChIP-Seq, Role of epigenetics in stress adaptation in plants.

Unit 2: Metagenomics and Single-Cell Genomics   **5 Hours**
Metagenomics: concept and applications, Human Microbiome Project (HMP), Environmental metagenomics: Role in pollution control and ecosystem management. Single-cell genomics: its concept and importance.

Unit 3: Proteomics   **7 hours**
Overview of Proteomics, Complexity of protein structure (primary, secondary and tertiary), Post translational modifications (phosphorylation, glycosylation), Proteome analysis by 2-D gel electrophoresis, Edman sequencing (Methodology and limitations in protein sequencing) and MALDI-ToF (Matrix-Assisted Laser Desorption/Ionization – Time of Flight), nLC-MS/MS (nano-Liquid Chromatography coupled with Tandem Mass Spectrometry), X-ray crystallography.

Unit 4. Bioinformatics   **8 hours**
Introduction to bioinformatics: definition and scope, Nucleotide and Protein databases (GenBank, UniProt, PDB), metabolic pathway database (KEGG), Search engines for databases (Entrez and PubMed), File format (FASTA), BLAST, Concept of sequence alignment, molecular phylogeny

PRACTICALS :   **60 Hours**
1. Virtual Exploration of Plant Genomes:

    1a. Access a plant-specific genome database (e.g., *Oryza sativa* in Gramene or

    Arabidopsis thaliana in TAIR).

    1b. Search for a gene of interest (e.g., drought resistance or photosynthesis-related

    genes).

    1c. Record details such as gene location, sequence, function, and related pathways.

1d. Compare homologous genes between two plant species using BLAST.

2. Study of GenBank and UniProt for the retrieval of nucleic acid and amino acid sequences

3. Sequence homology and gene annotation through BLAST tool.

4. Illumina sequencing through photographs.

5. Explore single nucleotide polymorphisms (SNPs) in plants and their role in trait variation.
6. Predict the structure of protein from its amino acid sequence. (Phyre 2/ Modweb/ CPH model/ Swiss Model).

7. Analysis of protein (s) on 2-D Gels, X-ray crystallography and protein microarray through photographs.

8. *In silico* analysis for PTM, Localization, and functions using the above-mentioned software.

9. Basic handling of data, transcriptome assembly, batch blast, batch primer design, setting up a local blast, basic of genome assembly, and isolation of microsatellites using MISA.

Suggested Readings (Books and Articles):
- Brown, T.A. (2017). *Genomes 4*. Garland Science. *A student-friendly introduction to genomics with clear explanations and examples.*
- Dale, J.W., & Park, S.F. (2010). *Molecular Genetics of Bacteria*. Wiley-Blackwell. *Covers foundational concepts in bacterial genomics and applications.*
- Allis, C.D., Caparros, M.-L., Jenuwein, T., & Reinberg, D. (2015). *Epigenetics*. Cold Spring Harbor Laboratory Press. *(Focus on the introductory sections for basics of DNA methylation and histone modifications.)*
- Pevsner, J. (2015). *Bioinformatics and Functional Genomics*. Wiley-Blackwell. *(Chapters on metagenomics provide a straightforward introduction with practical applications.)*
- Handelsman, J. (2004). *Metagenomics: Application in Microbial Ecology*. ASM Press. *(Focuses on simple and engaging content about microbial diversity studies.)*
- Doudna, J.A., & Sternberg, S.H. (2017). *A Crack in Creation: Gene Editing and the Unthinkable Power to Control Evolution*. Houghton Mifflin Harcourt. *(Written for a general audience, this book explains CRISPR in simple terms.)*
- Regev, A. et al. (2017). "The Human Cell Atlas." *eLife*. *(Overview of single-cell genomics and its goals in mapping human cells.)*
- Varshney, R.K., Roorkiwal, M., & Sorrells, M.E. (2017). *Genomic Selection for Crop Improvement*. Springer. *(Readable sections on GWAS and genomic applications in crop breeding.)*
- Sandel, M.J. (2009). *The Case Against Perfection: Ethics in the Age of Genetic Engineering*. Harvard University Press. *(Simplifies the ethical dilemmas posed by genomics and genome editing.)*