

B.Sc (Hons.) Biomedical Science
Discipline Specific Core (BIOMED-DSCs)
SEMESTER- VII

DISCIPLINE SPECIFIC CORE COURSE -19 (BIOMED-DSC-19)

BIOINFORMATICS AND OMICS

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		
Bioinformatics and Omics BIOMED-DSC-19	4	2	-	2	XII Passed	Basic knowledge of genetics, molecular biology

Learning Objectives

The Learning Objectives of this course are as follows:

- Students will be introduced to the field of bioinformatics and omics and their applications in biomedical research.
- Students will develop scientific and hands-on practical skills in bioinformatics that will be useful for higher studies.

Learning outcomes

The Learning Outcomes of this course are as follows:

- Students will be able to work on bioinformatics tools and databases.
- Students will be able to perform pairwise and multiple sequence alignments and construct phylogenetic trees.
- Students will learn features of genomic sequences with tools to annotate them. Various next generation sequencing technologies like the ones used for variant typing will also be taught.
- Students will be able to appreciate the role of high throughput technologies along with computational tools in deciphering the differential gene expression that is important to understand the pathogenesis and mechanism of various human diseases.
- Students will also be introduced to proteomics, epigenomics, metagenomics, and metabolomics.

SYLLABUS OF BIOMED-DSC-19

Unit-I: Biological Databases and Genome Browsers

(4 hours)

Basic description and significance of bioinformatics, Introduction to various databases and their classification (primary and secondary databases) e.g. NCBI, DDBJ, EMBL, ENSEMBL, UCSC and their use in laboratories: literature, sequence, structure, medical, enzymes and metabolic pathways databases.

Unit II: Sequence Alignment and Phylogenetic Analysis**(10 hours)**

Introduction to sequence alignment, Nucleotide and Amino acid substitution scoring matrices, local and global pairwise sequence alignments using Dynamic Programming approach (Needleman-Wunsch and Smith-Waterman algorithms), calculating the alignment score. Pairwise alignment using word/k-tuple method (BLAST). Variables in BLAST Interpretation: BLAST score, e-value, bit score, p-value.

Multiple sequence alignment and its importance, Introduction to the basics of phylogenetic analysis. Tree-building methods: character-based methods (Maximum Parsimony) and distance-based methods (UPGMA and Neighbour joining). Construction of a phylogenetic tree and identification of homologs.

Unit III: Genomics**(6 hours)**

Structural and functional features of Genome sequences, Tools for the prediction of genes and regulatory elements; Gene Ontology, Next generation sequencing analysis (ILLUMINA, Oxford), Applications in SNP typing and copy number variation detection, ChIP seq

Unit IV: Transcriptomics and other Omics Technologies**(10 hours)**

Gene expression databases, Global profiling of gene expression, Differential gene expression, analysis using microarrays and RNA-seq- Principle, design and execution, data preprocessing (Exploration, normalization, filtering), Detection of differentially expressed genes (fold change and t-test), heatmaps, classification and prediction, Functional analysis and biological interpretation of differentially expressed genes, validation using qRT PCR, Applications of expression profiling in human diseases

Overview of other omics technologies like Proteomics, Epigenomics, Metagenomics, Metabolomics and their applications in biomedical research

Practical**(60 hours)**

(Wherever wet lab experiments are not possible, the principles and concepts can be demonstrated through any other material or medium including videos/virtual labs etc.)

1. Retrieval of information from databases like NCBI, ENSEMBL, UCSC, etc.
2. Pairwise Sequence alignment using BLAST
3. Multiple Sequence alignment using tools like CLUSTAL, MUSCLE, T-Coffee, etc.
4. Phylogenetic analysis using online tools like Simple Phylogeny (EMBL-EBI), Phylogeny.fr
5. Prediction of genes and genome annotation using tools like GENEID
6. Retrieval of gene expression data from GEO or SRA
7. Differential gene expression analysis using GEO2R
8. Gene Ontology using DAVID
9. Visualization of protein interactions using tools like Cytoscape, STRING, etc.

Essential readings:

- Baxevanis, A. D., Bader, G. D., & Wishart, D. S. (Eds.). (2020). Bioinformatics. John Wiley & Sons. ISBN: 9781119335955.
- Rastogi, S. C., Rastogi, P., & Mendiratta, N. (2022). Bioinformatics: Methods and Applications-Genomics, Proteomics and Drug Discovery, Fifth Edition. PHI Learning Pvt. Ltd. ISBN: 9789354437410.
- Lesk, A. M. (2017). Introduction to genomics. Oxford University Press. ISBN: 0199557489
- Ning, K. (Ed.). (2023). Methodologies of Multi-Omics Data Integration and Data Mining: Techniques and Applications (Vol. 19). Springer Nature. ISBN: 9811982104
- Mount, D. W. (2004). Bioinformatics: Sequence and Genome Analysis. Thailand: Cold Spring Harbor Laboratory Press. ISBN: 9780879697129.
- Campbell, A.M. & Heyer, L.J. (2007) Discovering Genomics, Proteomics and Bioinformatics, 2nd Edition. Benjamin Cummings. CSH Press, New York. ISBN: 8131715590
- Metzker, M. L. (2010). Sequencing technologies-the next generation. Nature Reviews Genetics, 11(1), 31-46.
- Pevsner, J. (2015). Bioinformatics and functional genomics, 2nd Edition. John Wiley & Sons. ISBN: 0471210048

Suggested readings:

- Arivaradarajan, P., & Misra, G. (2018). Omics Approaches, Technologies And Applications. Springer, Singapore. ISBN: 9811329257.
- Ghosh, Z., Mallick, B. (2008). Bioinformatics: Principles and Applications. India: Oxford University Press. ISBN: 9780195692303.
- Latest developments in the field of bioinformatics and omics technologies through research articles.

Examination scheme and mode:

Evaluation scheme and mode will be as per the guidelines notified by the University of Delhi.