COURSE TITLE	**ADVANCES IN GENOMICS**
COURSE CODE	**01CB0506**
COURSE CREDITS	**3**

Objective:

1. Understand organization and structure of prokaryotic, eukaryotic and organellar genomes.
2. Discover modern tools and techniques involved in the analysis of genomes

Course Outcomes: After completion of this course, student will be able to:

1. Apply recombinant DNA technology to design cloning strategies using suitable vectors and host systems.
2. Analyze genomic and cDNA library construction methods, including artificial chromosomes and screening techniques.
3. Evaluate sequencing and PCR-based approaches for accuracy, efficiency, and genomic applications.
4. Apply and analyze functional genomics tools to evaluate genome-wide data and comparative genomics applications.
5. Evaluate bioinformatics pipelines to interpret complex genomic data for biological insights.

Pre-requisite of course: Basic knowledge of Bioinformatics

Teaching and Examination Scheme

Theory Hours	Tutorial Hours	Practical Hours	ESE	IA	CSE	Viva	Term Work
2	0	2	50	30	20	25	25

Contents : Unit	Topics	Contact Hours
1	**Basics of Recombinant DNA Technology** Manipulation of DNA – Restriction and Modification enzymes, Design of linkers and adaptors. Characteristics of cloning and expression vectors based on plasmid and bacteriophage, Vectors for insect, yeast and mammalian system, Prokaryotic and eukaryotic host systems, Introduction of recombinant DNA in to host cells and selection methods.	7
2	**DNA Libraries** Construction of genomic and cDNA libraries, Artificial chromosomes – BACs and YACs, Chromosomal walking, Screening of DNA libraries using nucleic acid probes and antisera.	5

Contents : Unit	Topics	Contact Hours
3	**Sequencing Basics** Maxam Gilbert's and Sanger's methods of DNA sequencing. Inverse PCR, Nested PCR, AFLP-PCR, Allele specific PCR, Assembly PCR, Asymmetric PCR, Hot start PCR, inverse PCR, Colony PCR, single cell PCR, Real-time PCR/qPCR – SYBR green assay, Taqman assay, Molecular beacons. Site directed mutagenesis.	5
4	**Next Generation Sequencing** Organization and structure of genomes, Genome sequencing methods, Conventional and shotgun genome sequencing methods, Next generation sequencing technologies (Illumina, Ion Torrent, Roche, pyro-sequencing, SOLiD), Hybridization mapping, Radiation Hybrid Maps, Optical mapping. ORF finding and functional annotation	5
5	**Advances in Genomics** Current status of genome sequencing projects, Introduction to Functional genomics, Subtractive hybridization, DIGE, Yeast Two hybrid System, Comparative Genomics, Proteogenomics, Web resources for Genomics, genome analysis and genomics applications.	6
Total Hours		**28**

Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
1	**Module1:** To perform primer designing using online tools	2
2	**Module1:** To compare the genome databases and their output formats.	2
3	**Module1:** To analyze data downloaded from online methods used for genomics	2
4	**Module2:** To analyze the SRA data using the coding language	2
5	**Module2:** To identify the Genomics data and compare using online tools	2
6	**Module3:** To perform quality check of the genomic data	2
7	**Module3:** To perform quality check of the sequenced data using the FastQC tool	2
8	**Module3:** To perform the Trimming of the adapters in sequenced data	2
9	**Module3:** To assemble the genome using free available tools	2

Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
10	**Module4:** To perform annotation using BLASTn on small sample dataset	2
11	**Module4:** To analyze offline BLAST results	2
12	**Module4:** To identify the genes from the transcripts using annotation methods	2
13	**Module4:** To perform Gene Ontology analysis on annotated transcripts	2
14	**Module5:** To compare gene using venn diagram	2
Total Hours		**28**

Textbook :

1. Next Generation Sequencing Methods and Protocols, Head, Steven R., Ordoukhanian, Phillip, Salomon, Daniel R, Springer, 2018
2. Modern Genome Annotation, Prof. Dmitrij Frishman, Alfonso Valencia, Springer, 2008

References:

1. Genome Annotation, Genome Annotation, Jung Soh, Paul M.K. Gordon, Christoph W. Sensen, Chapman and Hall/CRC, 2012
2. Annotation of the Celera Human Genome Assembly, Annotation of the Celera Human Genome Assembly, J. Craig Venter, Celera, 2000
3. Multi-genome Annotation of Genome Fragments Using Hidden Markov Model Profiles, Multi-genome Annotation of Genome Fragments Using Hidden Markov Model Profiles, Mark Menor, Hawaii, 2007

Suggested Theory Distribution:

The suggested theory distribution as per Bloom’s taxonomy is as follows. This distribution serves as guidelines for teachers and students to achieve effective teaching-learning process

Distribution of Theory for course delivery

Remember / Knowledge	Understand	Apply	Analyze	Evaluate	Higher order Thinking / Creative
20.00	30.00	20.00	10.00	10.00	10.00

Instructional Method:

1. The course delivery method will depend upon the requirement of content and need of students. The teacher in addition to conventional teaching method by black board, may also use any of tools such as demonstration, role play, Quiz, brainstorming, MOOCs etc
2. The internal evaluation will be done on the basis of continuous evaluation of students in the laboratory and class-room

Instructional Method:

3. Practical examination will be conducted at the end of semester for evaluation of performance of students in laboratory

Supplementary Resources:

1. https://omicstutorials.com/
2. https://www.ebi.ac.uk/training/
3. Students will use supplementary resources such as online videos, NPTEL videos, e-courses, Virtual Laboratory.