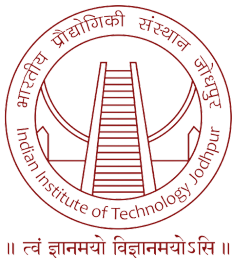
Postgraduate Diploma

in

Next Generation OMICS Technologies and Applications

2023



Program Structure

Certificate and Diploma Course in Next Generation OMICS Technologies and Applications

1. Introduction

The certificate and diploma course in next generation OMICS technologies and applications is a holistic training program designed to meet the requirements of people from different backgrounds such as healthcare professional, post-graduate students, people from industry or academia as well as a service provider. The program would cater to the needs of upskilling, training and orientation of different multi-omics based techniques, and the analysis of data and their applications towards healthcare, pathogens, clinical, nutrition and agriculture. Recent advancements and wide use of high-throughput technology are producing an explosion of biological datasets that serve as a source for computational and statistical modeling of diseases and biological processes. The analysis of various omics datasets can provide better understanding of the underlying disease mechanism, prevention and prediction. Moreover, high-throughput sequencing data analysis helps medical professionals in clinical applications as well as enable advanced understanding of basic biological problems. This program provides an overview of the high-throughput technologies for massively parallel (so-called next-generation) sequencing & multi-omics technologies for addressing different biological questions. Moreover, this program will focus on concepts for developing and implementing computational methods for learning from omics data, managing those data, and using the data for biological research to improve human health.

2. Objective of the Programme

The objective of this programme is to cultivate an understanding of multi-omics studies, technologies and state-of-the-art computational methods for analysis of multi-omics datasets. The course aims to provide the cutting edge skill sets to efficiently plan for multi-omics experiments, generate the different layers of biological data, analyze and interpret the outcomes.

3. Expected Attributes

- Ability to understand different next-generation multi-omics technologies.
- Capability to design the experiment for conducting OMICS studies.
- Gain an aptitude to apply the knowledge for different OMICS applications.
- Ability to apply machine learning, statistics and computational methods for analysis of the different OMICS data.

4. Learning Outcome

- Knowledge of available high-throughput multi-omics technologies, including their comparison in terms of advantages and disadvantages for specific applications.
- Design a multi-omics study efficiently, including effective budget planning.
- Knowledge of different NGS and microarray experiments and their possible applications.
- Knowledge of computational and statistical concepts for analysis of OMICS datasets.
- Develop skills to interpret the analysis results for biological inference.
- Efficiently plan and manage technical projects in different OMICS domains.

5. Offered for:

- Working professionals from pharma, sports, nutrition and health and wellness, diagnostic industries

- Researchers from R&D and academic institutions
- Clinicians and service providers
- PhD, Medical graduates, BTech or Master's in any sciences.

5.1 Eligibility:

<table>
<tr><td colspan="3">Eligibility</td></tr>
<tr><td colspan="3">(i) The applicant must have a bachelor’s degree in engineering or science or medicine (minimum 4-year program) or a master’s degree in bioengineering or bioscience or in a related field.

(ii) A minimum of 60% marks in UG/PG or a minimum CGPA of 6.0 on a scale of 10 with corresponding proportional requirements when the scales are other than 10.

(iii) Preference will be given to working professionals in industry/R&D laboratories/Academic Institutions.

(iv) The applicant must qualify for the written test and /or interview conducted by IIT Jodhpur or its appointed partner.</td></tr>
<tr><td colspan="3">Prerequisites</td></tr>
<tr><td>Certificate 1</td><td>Certificate 2 (ONLY)</td><td>Diploma</td></tr>
<tr><td>NIL</td><td>Should have completed 13 credits (or ~150 hours) of coursework or equivalent in these topics:
● Experiment design approaches for OMICS study
● Multi-OMICS Resources and Technologies
● Basics of OMICS Data Analysis</td><td>Entry through Certificate 1: NIL

Entry through Certificate 2: Prerequisites same as for Certificate 2 (ONLY)</td></tr>
<tr><td colspan="3">Credit Requirements</td></tr>
<tr><td>Certificate 1</td><td>Certificate 2 (ONLY)</td><td>Diploma</td></tr>
<tr><td>13 credits</td><td>15 credits</td><td>28 credits

Option 1 (entry through Certificate 1) : 13 credits from Certificate 1 and 15 from Certificate 2</td></tr>
</table>

		Option 2 (entry through Certificate 2): 15 credits from Certificate 2 and additional 13 credits from elective courses

6. Program Modules

i. OMICS experiments and technologies
   a. Basics of experiment design
   b. OMICS study design
   c. Next generation sequencing technologies
   d. Microarrays & SNP typing
   e. Single cell technologies
   f. Spatial transcriptomics

ii. OMICS data science
   a. Basic of data science
   b. NGS data analysis
   c. OMICS data types
   d. Data science methods for OMICS datasets
   e. AI & ML applications in OMICS

iii. OMICS applications
   a. Modern approaches of drug designing
   b. Precision medicine
   c. Drug target and drug discovery
   d. Clinical genomics

7. Topics Cloud for Compulsory Courses

Topic	**Content**
Experimental Design	Basic principles of experiment design, steps for planning, conducting and analyzing an experiment, simple comparative experiments, sample size and power determination, blocking scenarios, factorial designs, foldover designs, crossed array design, random effects models, nested and split plot designs
OMICS Technologies	Introduction to NGS technology, NGS run setup, NGS run monitoring, microarray and SNP typing technology, sample QC and call rate identification, introduction to single cell technologies and spatial transcriptomics, sample preparation, for single cell gene expression, single cell immune profiling, fixed RNA profiling, Single Cell Assay for transposase-accessible chromatin using sequencing (ATAC -seq), single cell multiome ATAC + Gene Expression, spatial gene expression for FFPE, spatial gene expression for as well as fresh and frozen, introduction to proteomics, Mass spectrometry, 2D gel electrophoresis, DNA-Protein interaction studies, proteomics and drug designing platforms
OMICS Data Science	Introduction to bioinformatics, data driven discovery with examples in healthcare, Introduction to genomic variations & mutations, data

	formats, data repositories, data extraction, file preparation, bioinformatics tools and algorithms for pre-processing, alignment, variant calling, multiple sequence alignment and phylogenetic analysis, introduction to metagenomics, metagenomic sequencing & applications of metagenomics, metagenomics pipeline, introduction to transcriptomics, introduction to machine learning, unsupervised machine learning methods, dimensionality reduction, GUI server, clustering, supervised, classification & feature selection

8. Program Structure

Course name	Credit	Category	Course name	Credit	Category
Semester 1			**Semester 2**		
Design of OMICS Experiments	3-0-0 [3]	C	Sample QC and Processing Techniques for NGS	2-0-2 [3]	C
Next Generation OMICS Technologies	3-0-0 [3]	C	Advanced OMICS Data Analysis	2-0-2 [3]	C
Basics of OMICS Data Analysis	2-0-2 [3]	C	Multi-omics Research Applications	3-0-0 [3]	C
OMICS Databases	1-0-0 [1]	C	Mini Project	3	C
Elective I	3	E	Elective II	3	E
Total Credits = 13			**Total Credits =15**		

9. Elective courses

9.1 Elective courses for semester 1:

Note: elective courses listed in below table are available for both certificate and diploma participants.

S.NO.	Course name	L-T-P	Hours	Credits
1	Introduction to Non-Clinical NGS Applications and Genomics Analysis Tools	3-0-0	42	3
2	Statistics for Clinical Interpretation from Omics Data	2-0-2	56	3
3	Microbial Genomes & Microbiomes	3-0-0	42	3
4	Principles of Drug Discovery	3-0-0	42	3
5.	Transcriptome Data Analysis	3-0-0	42	3
6	Proteomics and Metabolomics	3-0-0	42	3

9.2 Elective courses for semester 2:

Note: elective courses listed in below table are available for Certificate 2 / diploma participants.

S.NO.	Course name	L-T-P	Hours	Credits
1	Protocols for Clinical Next Generation Sequencing ApplicationsBBL7140	2-0-2	56	3
2	OMICS-Based Precision Medicine	2-0-2	56	3
3	Computational Personal Genomics	2-0-2	56	3
4	Artificial Intelligence (AI) in Healthcare	2-0-2	56	3
5	AI/ML based Rational Drug Discovery	2-0-2	56	3
6	Computational Structural Bioinformatics	2-0-2	56	3
7	Applications of OMICS in Plant Science	3-0-0	42	3

9.3 Mini project for semester 2:

Participants will complete a mini project co-supervised by IIT Jodhpur Faculty and partners, or can opt for any of these courses as a part of their mini project:

S.NO.	Course name	L-T-P	Hours	Credits
1	Protocols for Clinical Next Generation Sequencing Applications	2-0-2	56	3
2	OMICS-Based Precision Medicine	2-0-2	56	3
3	Computational Personal Genomics	2-0-2	56	3
4	Artificial Intelligence (AI) in Healthcare	2-0-2	56	3
5	AI/ML based Rational Drug Discovery	2-0-2	56	3
6	Computational Structural Bioinformatics	2-0-2	56	3

10. Summary of courses

S.N.	Course Name	Type
1	Design of OMICS Experiments	Compulsory
2	Next Generation OMICS Technologies	Compulsory
3	Basics of OMICS Data Analysis	Compulsory

4	Sample QC and Processing Techniques in OMICS	Compulsory
5	Advanced OMICS Data Analysis	Compulsory
6	Multi-omics Research Applications	Compulsory
7	Introduction to Non-Clinical NGS Applications and Genomics Analysis Tools	Elective
8	Statistics for Clinical Interpretation from Omics Data	Elective
9	Protocols for Clinical Next Generation Sequencing Applications	Elective
10	OMICS-based Precision Medicine	Elective
11	Computational Personal Genomics	Elective
12	Computational Structural Bioinformatics	Elective
13	Applications of OMICS in Plant Science	Elective
14	AI/ML based Rational Drug Discovery	Elective
15	OMICS Databases	Compulsory
16	Microbial Genomes & Microbiomes	Elective
17	Principles of Drug Discovery	Elective
18	Artificial Intelligence (AI) in Healthcare	Elective
19	Transcriptome Data Analysis	Elective
20	Proteomics and Metabolomics	Elective

11. Detailed courses contents

11.1 Compulsory courses for semester 1

Title	Design of OMICS Experiments	Number	BBL6340
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory
Prerequisite	None		

Objectives
The Instructor will:
1. Provide an understanding of how OMICS experiments should be designed so that when the data are collected, these shortcomings are avoided.
2. focus on the design of the experiment and not on the analysis.

Learning Outcomes
The students are expected to have the ability to:
1. understand the issues and principles of design of experiments for multi-omics studies
2. understand experimentation designs and follow the guidelines for designing experiments

Contents
Basic Design Principles [14 lectures]: steps in planning of an experiment, exploratory *vs.* hypothesis driven studies, deductive, inductive and abductive reasoning, biological and analytical variance, study design considerations for discovery and validation studies, data driven discovery with examples from different domains e.g. predictive, preventive, personalised and participatory (P4) and precision medicine, overview of molecular diagnostics and treatment development, design issues in omics experiments, randomization in omics experiments, multi-level replication in omics experiments, sample size and power determination, resource allocation, pooling biological samples

Designs for Multi-omics Experiments [14 lectures]: experiments with one factor and multiple levels, two sample experiments, completely randomized design (CRD), complete block design, randomized complete block design (RCBD), blocking scenarios in multi-omics experiments, incomplete block design, reference design, loop design, crossover designs, factorial designs with two treatment factors, unreplicated factorial designs, confounding and blocking in factorial designs, blocking in unreplicated design, 2-level fractional factorial designs

Study designs [7 lectures]: family-based designs, population-based designs, case-studies, descriptive studies, ecological studies, case-control design, case-only design, cross-sectional studies, cohort studies

Multi-omics data modelling [7 lectures]: types of variables, modelling process, model assumptions, simple linear regression, multiple linear regression, ANOVA, interpreting the coefficients, inferences about the population slope, examples from multi-omics studies

Textbook
1. Montgomery, D. C. (2020). Design and Analysis of Experiments, 10th Edition, John Wiley & Sons

Reference Books
1. Kaltenbach H.M., (2021), Statistical Design and Analysis of Biological Experiments, Springer

Online Course Material
https://online.stat.psu.edu/statprogram/stat503

Title	Next Generation OMICS Technologies	Number	BBL6400
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory

Prerequisite	NIL		

Objectives:

The instructor will:

1. Introduce various technologies and relevant instrumentation applicable in multi-omics research.

Learning Outcomes

The students are expected to have the ability to:

1. Identify the right technology and method to be used in biological experiment design involving omics approaches for systems biology

Contents

Omics approaches for systems biology [6]: Fundamentals of systems biology; Integrative omics approaches for systems biology, Model systems, Treatments, Measurements, case studies

Technologies for Genomics & Transcriptomics [12 lectures]: Sanger vs Next Generation Sequencing Technologies; Introduction to microarrays; Microarray workflow; Limitations; Next-generation sequencing workflow - Preliminary sample quality control, Sample Preparation, Sequencing chemistries; Instrumentation; Multiplexing strategies; Strategies for aiding in analyses of data

Technologies for Proteomics & Metabolomics [10 lectures]: Separation technologies for proteins - Gel based & gel independent; Instrumentation; Fundamentals of metabolomics - Quenching; Separation technologies - Basics of gas chromatography; Detection & identification of proteins & metabolites - Basics of Mass spectrometry

Introduction to single cell technology [8 lectures]: Overview; single cell isolation & sequencing and its applications, advances in and limitations of single-cell omics, use of single-cell omics in the study of cellular heterogeneity and cellular functions. Single cell technologies; single cell isolation technologies, Sample Preparation recommendation, Single Cell Gene Expression. Single Cell Immune Profiling,, Single Cell ATAC, Single Cell Multiome ATAC + Gene Expression. Introduction to Spatial technologies, fixed RNA profiling.

Introduction to Structural Genomics [6 lectures]: Fundamentals- Structure of macromolecules, polypeptide conformation, secondary structures, folds, protein-protein interactions, structure modelling, Data resources- PDB, PISA, QSalignWeb, PPI databases (Biogrid, STRING), pfam.

Textbooks

1. Arthur L., (2017) Introduction to Genomics, Oxford University Press
2. Zhao S. and Shirley L., (2019). Single Cell Technologies and Applications" Springer
3. Brown T.A., (2017). Genomes 4, Garland Science
4. Arthur L., (2019). Introduction to Bioinformatics, Oxford University Press
5. Twyman R., (2013), Principles of Proteomics, 2nd Edition, CRC Press

Reference Books

1. Manuel J. Tavares R. S. and Tapia J.C., (2018). Next Generation Sequencing: Applications and Challenges. Elsevier.
2. Calogero R.A. and Benes V., (2023) Single cell Transcriptomics: Methods and Protocols. Springer ISBN: 978-1-0716-2756-3
3. Mount D.W., (2004) Bioinformatics: Sequence and Genome Analysis. CSHL Press,

Online Course Material

1. Vikash Kumar Dubey, Proteomics & Genomics, NPTEL Course Material, Department of Biosciences & Bioengineering, Indian Institute of Technology Guwahati, https://nptel.ac.in/courses/102103017/
2. S. Ganesh, Functional Genomics, NPTEL Course Material, Indian Institute of Technology Kanpur, https://nptel.ac.in/courses/102104056/
3. Sanjeeva Srivastava, Proteomics: Principles and Techniques, NPTEL Course Material, Department of Biosciences & Bioengineering, Indian Institute of Technology Bombay, https://nptel.ac.in/courses/102101007/6

Title	Basics of OMICS Data Analysis	Number	BBL6410
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory
Prerequisite	NIL		

Objectives
The Instructor will:

1. Introduce omics data types which includes genomics, metagenomics, epigenomics, transcriptomics and single cell transcriptomics.
2. Discuss specialization tracks which includes infectious diseases, oncology, precision medicine, neurosciences, agriculture, space-omics & metabolic disorders

Learning Outcomes

The students are expected to have the ability to:

1. Understand the difference between data types of each omics study.
2. Perform basic analysis for different specialization track in omics research

Contents
Introduction to Genomic Data Analysis [6 Lectures]: read quality assessment, raw and aligned genomics file formats, read alignment, genetic variants, variant calling for SNVs, CNVs, SVs, Functional Analysis of Variants, genomic data types, visualization using genome browser tool, functional annotation of genetic variants, comparative genomics

Introduction to Metagenomic Data Analysis [3 Lectures]: data preprocessing and quality control, metagenomic data analysis workflow, taxonomic profiling and community composition analysis

Introduction to Transcriptomic Data Analysis [4 Lectures]: gene expression profiling, tools for preprocessing and quality control, assembly and annotation, differential gene expression analysis, pathway analysis, functional enrichment analysis

Introduction to Proteomic and Metabolomic Data Analysis [5 Lectures]: Analysis of Mass Spec data - peptide mass fingerprinting, NMR data analysis, differential proteomics/metabolomics, qualitative proteomics/metabolomics, detecting post-translational modifications

Introduction to OMICS Data Integration [10 Lectures]: multi-omics data examples, challenges with high-throughput data, batch effect correction, normalization and transformation, horizontal integration schemes, meta-analysis methods, vertical integration schemes including parallel integration and hierarchical integration, example case-studies on multi-omics data integration

Laboratory Experiments [14 sessions]:
Introduction to R Programming, genomic data analysis using R: variant calling, functional annotation, sequence alignment, phylogenetic analysis, visualization tools for the phylogenetic composition of microbial communities based on 16S rRNA, Transcriptomic Data Analysis: quantification of gene expression, generation and interpretation of multiQC report, differential gene expression analysis, pathway analysis

Textbook

1. 1. Tseng G, Ghosh D, Zhou XJ (2015), Integrating Omics Data, Cambridge University Press
   2. Barh D, Azevedo V (2017), Omics Technologies and Bio-engineering, Elsevier

Reference Books:

1. Nardini C, Dent JE, Tieri P (2019), Multi-omic Data Integration, Frontiers Media SA
2. Arivaradarajan P. and Gauri M. G., (2018), Omics Approaches, Technologies and Applications: Integrative Approaches For Understanding OMICS Data, Springer
3. Schneider M.V. and Orchard S, (2016), Bioinformatics for Omics Data: Methods and Protocol., Humana Press

Online Course Material

1. BigOmics Analytics, https://bigomics.ch/tutorials/
2. Omics Data Analysis and Integration, https://www.altexsoft.com/blog/omics-data-analysis/
3. Computational Genomics with R, https://compgenomr.github.io/book/

Title	Omics Databases	Number	BBL7121
Department	Bioscience and Bioengineering	L-T-P [C]	1-0-0 [1]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory

Prerequisite	NIL		

Objectives

The Instructor will:

1. Introduce the biological databases commonly encountered in omics research and will highlight how different data types are used across biology

Learning Outcomes

The students are expected to have the ability to:

1. Store / retrieve biological data in / from relevant databases and process it for analyses

Contents

Biological Databases: [14 lectures] Sequence databases, gene expression databases, sequence read archives, peptide databases, metabolite libraries, Phenomic databases, data file formats, conversion between formats, considerations for data submission to databases, considerations for using data retrieved from databases, data quality control.

Textbook

1. Byron K., Herbert K.G., Wang J.T.L, (2016), Bioinformatics Database Systems, CRC Press
2. Srivastava C., (2019), Informatics in Proteomics, CRC Press

Reference Books

1. Bergeron B., (2016), Bioinformatics Computing, Pearson
2. Mount D.W., (2004) Bioinformatics: Sequence and Genome Analysis. CSHL Press

11.2 Compulsory courses for semester 2

Title	Sample QC and Processing Techniques for NGS	Number	BBL7140
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory
Prerequisite	NIL		

Objectives

The instructor will:

1. Provide an overview sampling approaches and methods to be considered while planning an NGS experiment.
2. Discuss various aspects of sample collection, storage, shipment, risk assessment and appropriate handling of biological samples
3. Provide insights into the importance of sample processing and quality control in NGS studies

Learning Outcomes

The students are expected to have the ability to:

1. Plan and execute NGS experiments following proper sample collection, extraction and quality control protocols
2. Follow all safety protocols when handling biological samples to minimize exposure and loss of sample integrity

Contents

Introduction to biological sample collection [10 lectures]: Types of biological samples - Simple, complex, mixed; Appropriate controls; Replications, Documentation, metadata collection, record maintenance & anonymization; Ethics of biological sample collection; Biosafety regulations, equipment & practices; Stabilization and preservation of samples; Transportation; Short-term & long-term storage; Effects of preservation & storage; Waste management; Standards (ISO/NABL etc.)

Sample processing & Quality Control [10 lectures]: Avoiding biases during sample processing; Nucleic acid extraction - Lysis methods; Nucleic acid quantification & quality assessment for next generation sequencing - Spectrophotometry, electrophoresis based approaches, fluorescence based approaches, relevant instrumentation, strengths & limitations of various quality control methods, Automation of sample processing.

Designing a sample collection and processing workflow seminar series [8]: Presentations by the class on a comprehensive pipeline for sample collection, processing and quality control

Laboratory Experiments [14 sessions]:

1. General lab safety, Biosafety equipment and practices
2. Sample collection, documentation, storage, stabilization, packaging & shipping
3. Nucleic acid extraction from
    a. Simple - Gram-negative bacteria
    b. Complex - Tissue / Yeast
    c. Mixed samples - Soil / Stool
4. Nucleic acid quality control - Differences between stored, fresh & stabilized samples
    a. Spectrophotometry & agarose gel electrophoresis
    b. Fluorescence-based assays
5. Nucleic acid fragmentation & assessing size distribution of fragmented DNA
6. Size selection of fragmented DNA
    a. Left sided selection
    b. Right sided selection

Textbook

1. Barker K., (2004). At the Bench, Cold Spring Harbor Laboratory Press.

2. Kappelmann-Fenzl E.M., (2021). Next Generation Sequencing and Data Analysis, Springer,

Reference Books

1. Pahuja M.,(2021) ICMR Guidelines for Good Clinical Laboratory Practices (GCLP), ICMR
2. Centers for Disease Control and Prevention (2009). Biosafety in Microbiological and Biomedical Laboratories. U.S. Government Printing Office.

Online Course Material

1. Research / review articles provided by the Instructor
2. https://apps.who.int/iris/rest/bitstreams/51002/retrieve

Title	Advanced OMICS Data Analysis	Number	BBL7150
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory
Prerequisite	Basics of OMICS data analysis		

Objectives

The Instructor will:

1. Provide an understanding on different omics data analysis, data extraction, file preparation and pipeline processing for biological interpretation.
2. Demonstrate the workflow for omics data analysis pipelines.

Learning Outcomes

The students are expected to have the ability to:

1. Analyze omics data analysis and interpret Biological insights while applying statistical tests and data visualization techniques.
2. Work on real life studies with the knowledge gained.

Contents

Machine Learning for OMICS Data Analysis [7 Lectures]: Ridge penalty, Lasso penalty, SVM, Decision Trees, Random Forest, Bagging, principal component analysis (PCA), K-means, K-NN

Single-OMICS Data Analysis [14 Lectures]: mutability analysis and interpretation, differential mutation analysis, copy number variation (CNV) analysis, genome-wide association studies (GWAS)**,** hypervariable

regions of ribosomal RNA, microbiome variability and composition analysis, functional metagenomics, single-cell RNA-seq analysis, case-studies

OMICS Data Integration [7 Lectures]: matrix factorisation, factorisation with components and loading vectors, Canonical Correlation Analysis (CCA), network-based methods of integration

Laboratory Experiments [14 sessions]:
Perform genomics data retrieval from public repositories, perform pre-processing and quality assessment using Trimmomatic tool, annotation of vcf file using R, QIIME2 pipeline for taxonomy classification, perform alpha & beta diversity analysis, perform genome-wide association analysis, perform functional enrichment analysis, perform single cell transcriptomic data analysis, perform N-integration of two or more datasets that are measured across the same N samples using mixOmics package.

Textbook

2. 1. Tseng G, Ghosh D, Zhou XJ (2015), Integrating Omics Data, Cambridge University Press
   2. Lê Cao KA, Welham ZM (2022), Multivariate Data Integration Using R Methods and Applications with the mixOmics Package, CRC Press

Reference Books:

1. Nardini C, Dent JE, Tieri P (2019), Multi-omic Data Integration, Frontiers Media SA
2. Arivaradarajan P. and Gauri M. G., (2018), Omics Approaches, Technologies and Applications: Integrative Approaches For Understanding OMICS Data, Springer
3. Schneider M.V. and Orchard S, (2016), Bioinformatics for Omics Data: Methods and Protocol., Humana Press

Online Course Material

1. BigOmics Analytics, https://bigomics.ch/tutorials/
2. Omics Data Analysis and Integration, http://mixomics.org/
3. Computational Genomics with R, https://compgenomr.github.io/book/
4. Vahabi N, Michailidis G. Unsupervised Multi-Omics Data Integration Methods: A Comprehensive Review. Front Genet. 2022 Mar 22;13:854752. doi: 10.3389/fgene.2022.854752. PMID: 35391796; PMCID: PMC8981526.

Title	Multi-OMICS Research Applications	Number	BBL7160
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Compulsory
Prerequisite	None		

Objectives
The Instructor will:
1. Provide an overview of the broader application of multi-omics in the scientific research specialization tracks like oncology, neurosciences, infectious diseases, metabolic disorders, and agriculture

Learning Outcomes
The students are expected to have the ability to:
1. understand the various applications of multi-omics technologies
2. explores applications of omics in bioinformatics, cancer research and therapy, molecular biology, and neurosciences

Contents
Application areas of NGS sequencing: Functional Genomics (4 lectures), Epigenomics (2 lectures), Hereditary diseases, Diagnostics and Prenatal testing (5 lectures), Plant Genomics (3 lectures), Population genomics (4 lectures), Complex diseases (6 lectures), Metagenomics (4 lectures), Gene x Environment interaction (4 lectures), Nutrigenomics (2 lectures), Pharmacogenomics (2 lectures), Sociogenomics (2 lectures), Ayurgenomics (2 lectures), Structural genomics and drug discovery (2 lectures)

Textbook
1. Barh D., Blum K., and Madigan M.A. (2012). OMICS Biomedical Perspectives and Applications. Taylor & Francis

Reference Books
1. Barh D., Azevedo V., Zambare V., (2013). OMICS Applications in Biomedical, Agricultural, and Environmental Sciences. Taylor & Francis
2. Romualdi C., Calura E., Risso D., Hautaniemi S, Finotello F. (2020) Multi-Omic Data Integration in Oncology. Frontiers Media SA.

Online Course Material
3. Morales J., (2022). Multi-omics for Health and Disease: https://youtu.be/Orr_qez58ZE. Open session of the 95th annual meeting of the National Advisory Council for Human Genome Research (NACHGR)
4. Hu, C., and Weiping J. (2021). Multi-Omics Profiling: The Way toward Precision Medicine in Metabolic. Journal of Molecular Cell Biology. Oxford Academic.

11.3 Elective courses for semester 1

Title	Introduction to Non-Clinical NGS Applications and Genomic Analysis Tools	Number	BBL7170
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	NIL		

Objectives:
The instructor will:
1. Provide an in-depth foundation on the NGS library construction and introduce various NGS library solutions within the domains of research, agriculture, and microbiology portfolio.

Learning Outcomes:

The students are expected to have the ability to:

1. Independently choose the appropriate NGS experiments for their specific research applications
2. Perform appropriate library preparation protocols that are required to address different research objectives.

Contents

Fundamentals of NGS library construction [12 Lectures]: Features of NGS libraries, Library preparation technologies, Indexing and multiplexing, Library validation, and quality control, Library normalization and pooling, Common challenges in library preparation, Best practices for library construction.

Non-clinical library preparation methods [14 Lectures]: Ligation-based workflow, Tagmentation based workflow, Target enrichment workflow, Whole genome sequencing for large and small genome, Whole Exome sequencing, Whole transcriptome sequencing, Small RNA sequencing, Gene expression profiling, RNA exome enrichment, Ribosome profiling, Protein-DNA interactions, Protein-Protein interaction, RNA-Protein interaction.

NGS Experimental Design [10 Lectures]: Case Study 1 - Metagenomics Experiment Design, Case Study 2 - Transcriptomics Experiment Design, Case Study 3 - Whole Genome Sequencing Experiment Design, Experimental Design Challenges, and Troubleshooting.

Insights on onboard Instrument analysis solutions [6 Lectures]: Benchtop sequencer local manager introduction, Analysis modules, Dashboard introduction, Result folder file structure, Analysis files details.

Textbook

1. Wang X. (2016). Next generation sequencing and data analysis. CRC Press.
2. Woyke T. and Fierer N, (2021). Metagenomics: Methods and Protocols, Springer Protocols.

Reference Book:

1. Richards J.E. and Hawley R.S. (2010). The Human Genome: A User's Guide, Academic Press
2. Lesk M. (2018). Introduction to Genomics, Oxford University Press.

Online Course Material

1. Hess, J., Kohl, T., et.al. (2020). Library preparation for next generation sequencing: A review of automation strategies. *Biotechnology Advances*, https://doi.org/10.1016/j.biotechadv.2020.107537.

2. Ho, C.K., Cui, X., etal.(2016). Whole-genome sequencing analysis using next-generation sequencing data. Current Protocol. Essential Lab. Tech. https://doi.org/10.1002/cpet.2.

Title	Statistics for Clinical Interpretation from OMICS data	Number	BBL7180
Department	Bioscience & Bioengineering	L-T-P [C]	2–0–2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective

Prerequisite	Basics of OMICS Data Analysis		

Objectives

The Instructor will:

1. introduce to medical statistics and evidence-based medicine
2. introduce to basic knowledge of computational and statistical methods in clinical research

Learning Outcomes

The students are expected to have the ability to:

1. explain the appropriateness of statistical approaches in research
2. make biological inference from the analyzed data

Contents

Statistical methods in clinical research [8 lectures]: gold standard of scientific inference, population and sample, type of variables, measure of location, Apgar score, Box-Whisker plot, random variables, Binomial distribution, Law of large numbers, variance, standardization, likelihood and probability, maximum likelihood principle, parameter estimation, confidence interval, student's t distribution

Epidemiology and Diagnostic testing [6 lectures]: morbidity measures, prevalence and incidence, relative risk, types of epidemiological studies, odds ratios, attributable risk, Bayes theorem, positive predictive value, negative predictive value, likelihood ratio, sensitivity, specificity, ROC curve, Youden's index, differential diagnostics

Statistical testing and modeling [12 lectures]: null hypothesis, statistical testing procedure, significance level, statistical testing errors, p-value, binomial proportion tests, One sample t-test, one-sided versus two-sided testing, two-sample t-test, parametric and non-parametric tests, multiple testing, effect size and power, measures of concordance, covariance, correlation coefficients, simple linear regression, multiple linear regression, logistic regression

Survival analysis [2 lectures]: definitions, censoring, survival functions, log-rank test, hazard function, hazard ratio, Cox regression analysis

Laboratory Experiments [14 sessions]

Calculate the mean and standard deviation for given data, perform sorting and find median and quartiles, Draw a box-whisker plot of the selected columns in given dataset and write conclusions, Calculate the values of the probability function of the random variable, estimate the respective effect measure and calculate confidence interval, Calculate the positive and negative predictive value of the ELISA test for given subpopulations, Plot the two ROC curves, perform statistical tests on given dataset, find model equations, perform Kaplan-Meier estimation and log-rank test

Textbooks

1. PezzulloJ. 2013. Biostatistics For Dummies. Wiley

Reference Books

1. Petrie A., Sabin C., 2019. Medical Statistics at a Glance. Wiley

Self-Learning Material

1. https://online.stat.psu.edu/stat500/

Title	Microbial Genomes & Microbiomes	Number	BBL7370
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	NIL		

The Instructor will:

1. Illustrate the various methods applicable in the generation, analysis and interpretation of microbial genome sequencing data

2. Outline the methods involved in determining the microbiome and assessing its importance in health, environment and agriculture

Learning Outcomes

The students are expected to have the ability to:

1. Determine the best possible methods to determine the sequence of bacterial genomes with naturally varying properties.

2. Be acquainted with the microbiomes associated with specific niches, methods to study them and infer what it means to have a specific microbiome in a given environment

Contents

Introduction to microbial genomes [4 lectures]: Prokaryotic genome anatomy, Extrachromosomal elements, Separation

Genome sequencing [8 lectures]: Timeline of DNA sequencing technologies, Explosive abundance of Genomic Data, Problems with genome assembly and solutions, Coding sequence prediction, Methods of gene prediction, Pathways and metabolic models

Functional & Comparative Genomics [10 lectures]: Experimental annotation, Gene expression profiling, Interactome,Genome alignment, Genomic phylogeny, Pan-genomics

Genome evolution [10 lectures]: Genomic islands, Genome plasticity, Resistome, Molecular epidemiology, Minimal genome concept, Synthetic genomes, Genomic alterations

Microbiomes [10 lectures]: Introducing metagenomics, detecting unculturable microbes, the human microbiome project, 16S based microbiome analysis, metagenome shotgun sequencing, importance of the microbiome in health, applications of microbiome sequencing in agriculture & the environment

Textbook

1. Brown T.A. (2007) Genomes 3, Blackwell publications

2. Fraser C.M., Read T.D., Nelson K.E., (2004), Microbial Genomes, Humana Press

Reference Books

Review & Research articles as prescribed by the Instructor

Online Course Material

Ganesh S., Functional Genomics, NPTEL Course Material, Department of Biological Sciences and Bioengineering, Indian Institute of Technology, Kanpur, http://nptel.ac.in/courses/102104056/

Title	Principles of Drug Discovery	Number	BBL7140 CSL7XX1 CSL7XX2
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	NIL		

Objectives

The Instructor will:

1. focus on route of drug design and discovery

Learning Outcomes

The students are expected to have the ability to:

1. understand the principles of drug design and development

Contents

BBL7XX1: Principles of Drug Discovery [1-0-0] (fractal 1)drug targets, pharmacokinetics, administration and dosing, drug testing: in vivo and in vitro, drug discovery: natural lead, synthetic lead, combinatorial synthesis, pharmacokinetics based drug design, chemical development, process development, toxicology, pharmacology, drug metabolism, clinical trials, commercialization (14 lectures)

CSL7XX0: Machine Learning-1 [2-0-0] (fractal 2) introduction, gradient descent, support vector machines, decision trees, neural networks (14 lectures)

(fractal 3) nearest neighbour, clustering, dimensionality reduction, generative models, feature selection and generation (14 lectures)

Text Books

1. Stromgaard,K., Krogsgaard-Larsen,P., Madsen,U., (2016) Drug Design and Discovery, 5 CRC Press

Self-Learning Materials

1. Department of Computer Science, Stanford University

https://see.stanford.edu/Course/CS229

Title	Transcriptome Data Analysis	Number	BBL7150
Department	Bioscience & Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	Nil		

Objectives

The Instructor will:

1. Illustrate the intricacies involved in choosing the right transcriptomic platform and will highlight the key steps of data analysis

Learning Outcomes

The students are expected to have the ability to:

1. Analyse various types of transcriptomic dataset and draw biological meaning from the data

Contents

Fractal 1:

Introduction to Microarray Data: Gene expression biology, The technical foundations, Types of microarrays- two-channel cDNA arrays, single-channel Affymetrix genechips, microarray platforms, Designing a microarray experiment-The basic steps (4 lectures)

Pre-processing steps: Importance of microarray data pre-processing, Background correction, Data normalization (5 lectures)

Analysis: Identification of differentially expressed genes, Classifying samples from two populations, grouping co-expressed genes (3 lectures).

Fractal 2:

Introduction to RNA Sequencing Data: Sequencing chemistries, choosing the right method for an application, principal considerations while designing an RNA sequencing experiment (2 lectures)

Quality Control: Sequence quality scores, pre-processing steps & considerations, FastQC, filtering & trimming of low-quality reads, detecting contaminants, removing adapters, red flags & troubleshooting (3 lectures)

Reference mapping: Alignment tools, assessment of alignment statistics, manipulating alignments, visualizing alignments (2 lectures)

De novo assembly: Transcriptome reconstruction & inherent complexities (3 lectures), pre-processing considerations for de novo assembly (2 lectures), de Bruijn graph, assembly tools, R & bioconductor for data analysis (4 lectures)

Fractal 3:

Gene expression analysis: Annotation, counting reads per transcript (2 lectures), differential gene expression, importance of biological & technical replicates, graphical representation (5 lectures)

Detecting Non-coding RNAs: Methods for detecting non-coding RNAs (2 lectures)

Applications of RNA sequencing: Transcriptome response profiling, finding splice variants, detecting allele specific expression in disease (5 lectures)

Textbook

1. Simon R. M., Korn E. L., McShane L. M., Radmacher M. D., Wright G. W., Zhao Y.

(2003), Design and Analysis of DNA Microarray Investigations, Springer-Verlag New York.
2. Korpelainen E., Tuimala J., Somervuo P., Huss M., Wong G., (2015), RNA-Seq Data Analysis: A Practical Approach, CRC Press
3. Wang X., (2016), Next-Generation Sequencing Data Analysis, CRC Press

Reference Books

Hackenberg M. And Aransay A. M. (2011), Bioinformatics for High Throughput Sequencing, Springer New York

Self-learning Material

1. Microarray based DNA Detection---- http://nptel.ac.in/ courses/104103018/41
2.RNA-Seq Analysis tutorial by University of Minnesota: https://www.youtube.com/watch?v=PHU8haU_Glo

Title	Metabolomics and Proteomics	Number	BBL7160
Department	Bioscience & Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	Nil		

Objectives

The Instructor will:

1. Introduce metabolomics as a discipline highlighting some methods for data generation, analysis and interpretation
2. Introduce the biological databases commonly encountered in proteomics research and will highlight how different data types are used across biology

Learning Outcomes

The students are expected to have the ability to:

1. Choose the appropriate method to qualitatively or quantitatively analyze the metabolome and proteome from different biological samples
2. Store / retrieve biological data in / from relevant databases and process it for analyses

Contents

Metabolomics Technologies & Data analysis [16 lectures]: Mass spectrometry for metabolite profiling (3 lectures), liquid & gas chromatography separation technologies (3 lectures); capillary electrophoresis based separation technology (2 lectures); nuclear magnetic resonance in profiling (2 lectures); single cell metabolomics (2 lectures), processing of data for analysis, statistical analysis (2 lectures), lifestyle disease biomarker identification, lipidomics (2 lectures)

Mass spectrometry for proteomics [14 lectures]: Basic principles (2 lectures), ionization methods (2 lectures), mass analyzers & mass spectrometers (4 lectures), analysis of MS data, analysis of MS/MS data (4 lectures), simple vs complex samples (2 lectures)

Applications [6 lectures]: Clinical samples, extraction methods, sample preparation, metabolic markers of disease, comparative metabolomics, metabonomics

Case studies [6 lectures]: Qualitative proteomics, differential proteomics, detecting post-translational modifications, interactomics

Textbook

1. Lovric, J., (2011), Introducing Proteomics: From Concepts to Sample Separation, Mass Spectrometry and Data Analysis. 11th Edition, Wiley-Blackwell.
2. Fan T.W.M., Lane A.N., Higashi R.M., [Eds], (2012), The Handbook of Metabolomics, Springer

Reference Books

1. Twyman R., (2013), Principles of Proteomics, 2nd Edition, CRC Press
2. Conn P.M., [Ed.] (2003), Handbook of Proteomic Methods, Springer
3. Sussulini A., [Ed] (2017), Metabolomics: From Fundamentals to Clinical Applications,

Springer

Online Course Material

1. Sanjeeva Srivastava, Proteomics: Principles and Techniques, NPTEL Course Material, Department of Biosciences & Bioengineering

11.4 Elective courses for semester 2

Title	Protocols for Clinical Next Generation Sequencing Applications	Number	BBL7190
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	Nil		

Objectives

The instructor will:

1. Provide an overview on the various library preparation protocols for clinical applications of Next Generation Sequencing

Learning Outcomes

The students are expected to have the ability to:

1. Process clinical samples and obtain high-quality starting material required for NGS
2. Understand and independently select and apply NGS sample preparation pipelines for multiple clinical NGS applications.

Contents

Emerging technologies and trends in clinical genomics [14 Lectures]: Diagnostic Genomics and Rare Diseases, Cancer Genomics and Precision Oncology, Pharmacogenomics, Non-Invasive Prenatal Testing (NIPT) and Reproductive Genomics, Infectious Disease Genomics and Pathogen Identification, Inherited Genetic Disorders and Carrier Screening.

Clinical Library Preparation solutions [14 Lectures]: Hereditary testing for complex diseases, Histocompatibility testing, Targeted approach for clinical testing, Tumor profiling, Exome and enrichment panels, clinical panels targeting disease-associated regions of the exome, mRNA profiling, Preimplantation genetic screening, Screening gene fusion and screening for germline variants

Laboratory Experiments [14 sessions]

HLA panel library preparation: DNA isolation, purification & QC, Amplification Setup, Amplicon Quantification, Amplicon Pooling, Fragmentation & End Repair, Ligation DNA Cleanup & Size Selection,

Indexing PCR DNA Cleanup & Size Selection, Library Pooling, Library QC, denaturation, and dilution, NGS run set up, Onboard data analysis.

Exome Library preparation: DNA isolation, purification & QC, Library preparation for targeted enrichment,, Library QC, Denaturation and dilution, Sequencing run set up, Onboard data analysis.

Textbook

1. Sivasubbu S, Scaria V. (2015), Exome sequencing analysis and interpretation: Handbook for clinicians. J Pract Cardiovasc Sci.
2. Kulkarni S, Pfeifer J. (2015), Clinical Genomics. A Guide to Clinical Next Generation Sequencing. Elsevier Inc., Academic Press.

Reference book:

1. Wong L. (2015), Next Generation Sequencing, translation to Clinical Diagnostics, Springer
2. Boegel S. (2018), HLA typing, Methods and Protocols, Springer.

Online Course Materia

1. Melton R. and Spirk,T. (2016). Obtaining high quality DNA from diverse clinical samples. Current. Protocol. Microbiol. https://doi.org/10.1002/9780471729259.mc01e09s40

2. Wolf, K. (2016). Next-generation sequencing library preparation from FFPE tissue samples. Current. Protocol. Mol. Biol. https://doi.org/10.1002/0471142727.mb0724s113

Title	OMIC-Based Precision Medicine	Number	BBL7200
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	Basics of OMICS data analysis		

Objectives

The Instructor will:

1. Provide an understanding on how genomics and data analysis could be utilized for a personalized therapeutic approach.
2. Discuss the social, ethical and legal implications associated with personalized medicines along with possible research applications.
3. Introduce to the pipeline of personalized medicine for health, prevention and monitoring adverse effects

Learning Outcomes

1. Apply genomics data analysis approach to determine treatment response.
2. Leverage public repositories to explore data to apply personalized technologies for precision treatment.
3. Learn about translational precision medicine

Contents

Fundamentals of Precision Medicine [7 Lectures]: Understanding human genome variability and phenotype consequences, Germline and Somatic Mutations, Clinical Relevance of Mutations, ACMG and AMP guidelines for variant classification, ethical, legal and social implications, precision approaches for oncology, infectious diseases, metabolic disorders and neurosciences, objectives of precision oncology, variability in drug response.

Genomics for Precision Medicine [7 Lectures]:
Monogenic disease diagnosis, molecular classification of tumors, drug response prediction and selecting optimal treatments, Drug-target identification, Disease Classification, Pathway analysis, Monitoring disease progression, predicting disease risk

Practice of genomic medicine in clinic [5 Lectures]:
Basics of genetics and genomics, from variants affecting health and disease to medicine. Pharmacology, mechanism of action,clinical decision making, research and advancements in the field, population health, introduction to integrative clinical and multi-omics data analysis

Targeted Drug Discovery and Development: [5 Lectures]
Introduction to cheminformatics, Target identification, Structure Prediction & variant analysis, Chemical & Protein Databases, Virtual and targeted screening, precision docking and downstream analysis.

Pharmacovigilance: [4 Lectures]
Identification of target population, data collection on the use of precision medicine with reported effects, monitoring adverse effects, data analysis, identification of potential safety concerns, risk benefit profile, reporting of findings to regulatory agencies, mitigating risk associated with the use of precision medicine, medicine withdrawal, need of continuous monitoring of precision medicine usage.

Laboratory Experiments [14 sessions]:
Perform molecular biology techniques in a simulated environment, such as RT-PCR, Next Generation Sequencing, expression of therapeutic proteins. Explore big data repositories for multi omics data, variant analysis, patient drug response based on genetic profile, clinical interpretation, Application of tools for 3D structure analysis

Textbook

1. Jain K.K., 2021. Textbook of Personalized Medicine, Springer
2. McCarthy J.J. and Mendelsohn B.A., (2017) Precision Medicine: A Guide to Genomics in Clinical Practice, McGraw Hill

Reference Textbook

1. Aydogan B. and Radosevich J.A., 2020. Precision Medicine in Oncology, Wiley
2. Hariharan R., 2018. Genomic Quirks, IISc Press and Strand Life Sciences

Online Course Material

1. Kosorok, Michael R., and Eric B. Laber. “Precision Medicine.” Annual Review of Statistics and

Its Application, vol. 6, no. 1, Mar. 2019, pp. 263–86. DOI.org (Crossref),
2. https://doi.org/10.1146/annurev-statistics-030718-105251.
3. https://youtu.be/A22GGEQWagc; https://portal.gdc.cancer.gov/.
4. https://www.youtube.com/@cbioportal9876 ; https://www.cbioportal.org/
5. Modeling Cancer Precision Medicine
6. TCGA Liver Cancer - Precision Oncology

Title	Computational Personal Genomics	Number	BBL7210
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	NIL		

Objectives
The Instructor will enable:
1. understanding what can be learned computationally from a personal genome and
2. understanding how sequence differences between individuals lead to phenotypic differences in gene expression, disease predisposition, or response to treatment.

Learning Outcomes
The students are expected to have the ability to:
1.Gain basic bioinformatics skills needed to analyze a personal genome.
2.Gain the ability to critically read and interpret basic science and translational literature relevant to personal genomics.
3. Gain skills and experience necessary to carry out original research related to personal genomics.

Contents
Introduction to Personal Genomics [2 lectures]: overview of course, central dogma, personal genomics revolution, genome projects

Population Genomics [10 lectures]: genome evolution, mutation, genetic drift, natural selection, gene flow, linkage disequilibrium, Hardy-Weinberg equilibrium, genetic variation, phasing, imputation, HMMs, relative finding, ancestry analysis, Identity by decent (IBD), Identity by state (IBS), crowd genomics, Y-STRs, TMRCA, genome privacy concerns, mtDNA analysis

Risk Prediction [10 lectures]: Mendelian traits, complex traits, genome-wide association studies, multiple testing problem, Locus Zoom plot, eQTL study, odds ratio, polygenic risk scores, population stratification, heritability estimation, linear mixed models, LD score regression, gene-environment interactions

Cancer genomics [6 lectures]: cancer driver gene identification, mining data from somatic mutation databases, mutation signature analysis, differential analysis of multi-omics data for normal-tumor context with expression or methylation datasets.

Laboratory Experiments [14 sessions]
Perform global ancestry analysis, Perform local ancestry analysis in admixed genomes, calculate LD using 1000 genome dataset, Carry out a genome-wide association analysis, ExAC mining and Polyphen

interpretation, Confounder correction and imputed association, PRS calculation, estimate heritability using LD-score regression

Textbook
1. Hartl D. and Clark A.G., 2006. Principles of Population Genetics. Sinauer Associates. ISBN: 978-0878933082

Reference Books
1. Foulkes A.S., 2009. Applied Statistical Genetics with R: For Population-based association studies. Springer, ISBN: 978-0387895536 (available as an E-Book)

Self learning materials
1. https://canvas.ucsd.edu/courses/27425/modules

Title	Artificial Intelligence (AI) in Healthcare	Number	SHL7140
Department	Bioscience & Bioengineering	L-T-P [C]	2–0–2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	NIL		

Objectives
1. To acquaint the students with recent advances in AI in healthcare, focusing in particular on deep learning approaches for healthcare problems.

Learning Outcomes
The students are expected to have the ability to:
1. Apply cutting-edge deep learning models in the context of a variety of healthcare data including image, text, multimodal and time-series data
2. Design and program efficient algorithms related to deep learning, train models, conduct experiments, and deliver artificial intelligence-based applications

Contents
Fractal 1: AI Applications in Genomics and Proteomics [1-0-0]
New models in healthcare, big data types and data accumulation (2 lectures);
Identification of functional units in DNA sequences, cancer diagnosis (3 lectures);
RNA types, RNA sequences structure (3 lectures);
Protein structure prediction, protein classification, protein interactions (4 lectures);
Graph convolutional network for gene expression data analysis (3 lectures)

Fractal 2: AI Applications in Bio-imaging and Biomedical [1-0-0]
Introduction to medical imaging modalities, biomedical signals (3 lectures);
Applications in anomaly classification using imaging and signal data (3 lectures);
Medical image alignment, motion analysis, tracking (4 Lectures);
Partitioning specific cellular structures (segmentation), detection of cell nuclei (4 lectures)

Laboratory Experiments [14 sessions]

study gene expression regulation using DNN (3 labs); protein classification using DNN/RNN (3 labs); design and implement algorithm for protein structure prediction (2 labs); apply DNN/CNN to classify cancer subtypes using imaging or signal data (3 labs)

Textbook

1. Wu, G., (2016), Machine Learning and Medical Imaging, Elsevier.
2. Shortliffe E.H., James J. Cimino, (2013) Biomedical Informatics, 4th Edition,

Reference Books

1. Arjun P., (2019). Machine Learning and AI for Healthcare: Big Data for Improved Health Outcomes,
2. Eric Topol (2019). Deep Medicine: How Artificial Intelligence Can Make Healthcare Human Again, Basic Books, NY .

Self-Learning Material

1. AI in Healthcare Specialization: https://www.coursera.org/specializations/ai-healthcare

Title	AI/ML based Rational Drug Discovery	Number	BBL7220
Department	Bioscience & Bioengineering	L-T-P [C]	2–0–2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	Nil		

Objectives:

This course will involve a deep dive into recent advances in AI in healthcare, focusing in particular on deep learning approaches for drug discovery problems.

Learning outcomes:

The students are expected to:

1. Understand various methods for representation of a molecule, molecular descriptors, and structure computation software.
2. Select/Develop appropriate DL/ML techniques to perform a particular drug discovery related analysis.

Contents:

Fractal 1 [14 lectures]: Introduction, Chemical formats: Key features of SDL, MDL and PDB files, SMILES systems (3 lectures), Canonical Smile, CML file, Conversion of file formats (3 lectures), Molecular descriptor (0-4D descriptors), molecular interaction field (MIF) (2 lectures) and comparative molecular field analysis (CoMFA) (1 lecture), descriptor to data matrix conversion(2 lectures) Graph Neural Networks (GNNs), Generative Models for Molecule Design (2 lectures), Molecular docking based virtual screening, Pharmacokinetics assessment (1 lecture).

Fractal 2 [14 lectures]: Explainable AI in Drug Discovery, Identification of relevant molecular descriptors using feature selection techniques and deep learning (3 lectures), application of supervised learning and deep learning for predictive modeling of QSAR (3 lectures), ligand based virtual screening (1 lecture), ADME and drug sensitivity prediction (2 lectures), unsupervised learning for denovo drug molecule design, drug repurposing, and meta data based analysis of target-disease-drug association, Drug-likeness, In-silico toxicity assessment.(5 lectures)

Laboratory Experiments [14 sessions]

PDB, AlphaFold Db, ZINC, PubChem, ChEMBL, UCSF Chimera, for Biomolecular Visualization, Open Targets Genetics, Cheminformatics using R: SMILES Notation, SMARTS: Highlight substructural patterns/Pharmacophores bold text, Highlight atoms based on attributes, Substructure/pharmacophore search, Chemical databases, In-silico toxicity prediction/assessment using pkCMS, Molecular docking using Autodock/Autodock vina, Drug likeness and ADMET analysis using SwissADME,Toxicity Drug-Target Interaction Prediction

Textbook

1. N. Brown, (2020) Artificial Intelligence in Drug Discovery, Royal Society of Chemistry, 1st edition.
2. M. Chang,(2020) Artificial Intelligence for Drug Development, Precision Medicine, and Healthcare, Taylor & Francis Group, 1st edition.

Reference Books

1. A.R R. Leach, (2001) Molecular Modelling: Principles and Applications, Prentice Hall, , 2nd edition.
2. B. Ramsundar, P. Eastman, P. Walters, V. Pande, (2019) Deep Learning for the Life Sciences: Applying Deep Learning to Genomics, Microscopy, Drug Discovery, and More, "O'Reilly Media, Inc. , 1st edition.

Self-Learning Material

1. AI in Drug Discovery Decision Support, IBM Watson Health, https://www.youtube.com/watch?v=SWd7ehX0rus
2. Deep Learning for Drug Discovery, BayesGroup.ru, https://www.youtube.com/watch?v=Xf2uI4S9IMo

Course Title	Computational Structural Bioinformatics	Number	BBL7230
Department	Bioscience and Bioengineering	L-T-P [C]	2-0-2 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective
Prerequisite	NIL		

Objectives:

To develop an understanding of the structure of biomolecules (DNA/RNA/proteins), their interactions, evolution, dynamics, and structure-function relationship, and acquire knowledge on computational approaches to access and analyze biomolecular structure data

Learning outcomes:

The students are expected to:

1. Acquire an In-depth understanding of the three-dimensional structure of bio-macromolecules and the latest bioinformatics resources and methods to study the structure-function relationship

2. Get acquainted with the *state-of-the-art* tools and computational methods related to macromolecule structure visualization, modeling, interaction, and dynamics.

Contents

Introduction to Structural Biology and related resources [6 lectures]: Fundamentals- Structure of macromolecules (protein/DNA/RNA), RNA structural diversity, polypeptide conformation, secondary structures, folds, interactions, and stability. *State-of-the-art* structure determination methods. Macromolecule structure data resources- PDB, PISA, EPPIC, QSalignWeb, PFam, RFam.

Structure modeling, interactions, and docking [10 lectures]: Computational structure prediction methods/ algorithms- Homology modeling, threading, de-novo (AlphaFold), diversity of protein-protein interactions, docking (protein-protein/DNA/ligand), PPI databases (Biogrid, STRING)

Structure Analysis and Dynamics [12 lectures]: Structure comparison/alignment (MMalign, KPAX), evolutionary studies (sequence and structure conservation) (*6 lectures*). Protein/DNA structure dynamics and flexibility, Simulating biomacromolecules- predicting suitable *in-silico* conformations of proteins/DNA/protein-protein/protein-DNA complexes (6 lectures).

Laboratory Experiments [14 sessions]

1. Accessing Macromolecular Structure data from PDB and Visualizing in PYMOL/ MOL*
2. Prediction of protein 3D structure model from amino acid sequence
3. Docking and analysis – Protein-protein/DNA/small molecule docking and analysis
4. Analysis of the effect of mutation(s) in protein interactions / mutation modeling
5. Structure alignment and comparison
6. Protein/DNA structure flexibility
7. Predicting suitable in-silico conformations of protein-peptide complexes

Textbook

1. Mount D.W.,(2004). Bioinformatics: Sequence and Genome Analysis. CSHL Press,
2. Lesk A., (2019). Introduction to Bioinformatics, Oxford University Press,
3. Leach A.R., (2001). Molecular Modelling: Principles and Applications, Prentice Hall,

Reference Books

1. Encyclopedia of Bioinformatics and Computational Biology, Elsevier, 2019

Title	Applications of OMICS in Plant Science	Number	BBL7240
Department	Bioscience and Bioengineering	L-T-P [C]	3-0-0 [3]
Offered for	PG Diploma in Next Generation OMICS Technologies and Applications	Type	Elective

Prerequisite	NIL		

Objectives

To familiarize students with OMICS applications in plant science

Learning Outcomes

The students are expected to have:

1. a thorough understanding of the principles of gene manipulation for genetic improvement of cultivated plants for yield and environmental stress management and production of biofuel and biopharmaceuticals

2. develop inquisitiveness to explore unknown gene functions and molecular mechanisms in plants for

future applications

Contents

Fractal 1. Introduction to plant genomes (14 lectures)

Plant nuclear and organelle genomes. Gene families and paralogs. Plant genome surveillance

RNAi and gene silencing. siRNA, lncRNA and miRNA, RNA-directed DNA methylation in higher plants.

Bioinformatic analysis and target validation of small RNAs

Fractal 2. Plant functional genomics (14 lectures)

Forward and reverse genetics, Overexpression, Knockout, knockdown, Constitutive, Inducible and tissue-specific promoters. Virus-induced gene silencing. Transposon tagging.

Genotyping and epigenome profiling

Genome-wide association study (GWAS), transcriptome-wide association study (TWAS) and epigenome-wide association study (EpiWAS) in plants for gene discovery

Plant chemical genomics

Fractal 3. Plant transcriptome analysis and applications of plant OMICS (14 lectures)

Microarrays, Next-Generation sequencing., Application of plant OMICS for crop improvement towards abiotic stress tolerance, disease resilience, better quality and shelf life

Text Books

1. Kahl G. and Meksem K., 2008. The Handbook of Plant Functional Genomics: Concepts and Protocols, WileyVCH..

Self-Learning Materials

1. https://archive.nptel.ac.in/courses/102/106/102106080/

2. https://nptel.ac.in/courses/102103016

12. Program fee structure

Certificate 1: Basics of Next Generation OMICS Technologies and Applications

Certificate 2: Advanced Next Generation OMICS Technologies and Applications

SNO.		**Certificate 1**	**Certificate 2**	**Diploma (Certificate 1 & Certificate 2 together)**
1	Fee (for Indian)	1.20 lakhs	1.50 lakhs	2.50 lakhs

Notes:

1. Fee for a foreigner participant will be 20% higher than that for Indian participant
2. Immersion fee of INR 10,000 will be charged. Immersion fee covers administrative costs. It does not include students' lodging and food costs. Immersion is mandatory for Certificate 2 and diploma students.

********** **End** **********