SATHYABAMA
INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)
Accredited "A" Grade by NAAC | 12B Status by UGC | Approved by AICTE
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SCHOOL OF BIO AND CHEMICAL ENGINEERING

DEPARTMENT OF BIOINFORMATICS

BOARD OF STUDIES - MINUTES OF MEETING

Subject: Board of Studies- Department of Bioinformatics
Venue: Molecular Modelling Lab
Date: 03/07/2021
Agenda: Opinion/suggestion for improvement of syllabus

The following members were present
Chairperson

Dr. Wilson Aruni, Pro-VC, Sathyabama Institute of Science and Technology

External Member

1. **Dr. C Elizabeth Rani Junius**, HoD, Department of Biotechnology, Hindustan College of arts & science, Chennai

Department Members

1. Dr. Jemmy Christy, Assistant Professor
2. Dr. D. Alex Anand, Assistant Professor
3. Dr. Swetha Sunkar, Assistant Professor

Internal members

1. Dr. Ramesh Kumar, Associate Professor and head, Biotechnology Department
2. Dr. Valli Nachiyar, Associate Professor, Biotechnology Department.
3. Dr. Jayshree Nellore, Associate Professor, Biotechnology Department.

A Meeting of the Board of Studies for the Department of Bioinformatics with external member was held on 03-07-21 at 11.00 a.m. virtually to discuss about the content revision for The following two papers of B.Sc Bioinformatics and Data science and one paper for M.Sc Bioinformatics and Data science have been put forth for revision

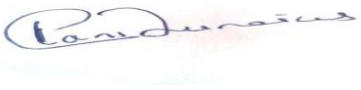
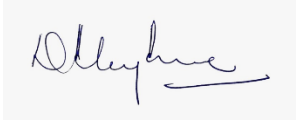
Minutes of the BOS meeting

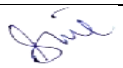
- The Chairperson Dr. Wilson Aruni, Pro Vice-chancellor welcomed the External and Internal members for the Board of Studies meeting held on 3rd July 2021 at 11 AM.
- The theory paper modeling of molecules, Next generation sequencing, Structural and Functional genomics has been modified and put forth for BOS approval.
- A copy of the syllabi framed by the Internal BOS members was sent a week in advance to the External Member according to their specialization and field of expertise for their review. Their valuable suggestions and comments were received well before the meeting and modifications have been carried out and kept before the members today for further discussions.
- The revisions have been carried out in such a way that a make it more coherent for the current application
- Revised curriculum was discussed and approved.

Meeting ended with vote of thanks.

Minutes approved.

Members:

Dr. Wilson Aruni	
Dr. C. Elizabeth Rani Juneius	
Dr. Alex Anand	
Dr. Jemmy Christy	

Dr. Swetha Sunkar	

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SCHOOL OF BIO AND CHEMICAL ENGINEERING

DEPARTMENT OF BIOINFORMATICS

BOARD OF STUDIES - MINUTES OF MEETING

Subject: Board of Studies- Department of Bioinformatics
Venue: Molecular Modelling Lab
Date: 29/11/2021
Agenda: Opinion/suggestion for improvement of syllabus

The following members were present
Chairperson

1. Dr. Wilson Aruni, Pro-VC, Sathyabama Institute of Science and Technology

External Member

2. Dr. C Elizabeth Rani Junius, HoD, Department of Biotechnology,
   Hindustan College of arts & science, Chennai

Department Members

4. Dr. Jemmy Christy, Assistant Professor
5. Dr. D. Alex Anand, Assistant Professor
6. Dr. Swetha Sunkar, Assistant Professor

Internal members

4. Dr. Ramesh Kumar, Associate Professor and head, Biotechnology Department
5. Dr. Valli Nachiyar, Associate Professor, Biotechnology Department.
6. Dr. Jayshree Nellore, Associate Professor, Biotechnology Department.

A Meeting of the Board of Studies for the Department of Bioinformatics with external member was held on 29/11/2021 at 11.00 a.m. virtually to discuss about the content revision for The following two papers of B. Sc Bioinformatics and Data science and one paper for M.Sc Bioinformatics and Data science have been put forth for revision

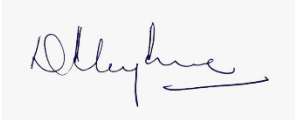
Minutes of the BOS meeting

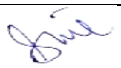
- The Chairperson Dr. Wilson Aruni, Pro Vice-chancellor welcomed the External and Internal members for the Board of Studies meeting held on 29/11/2021 at 11 AM.
- In the theory paper SBIA1401, Structural Biology for the BSc course the last unit is devoid of tools for research. This was proposed to be included. The proposed tools were COOT and MAIN for model building and Dino, CueMol, ENDscript, ESPrip and GRASP for molecular graphics.
- In the PG curriculum of SBIA7409, Health informatics, updated databases such as access medicine, clinical key, embase and trip database were suggested to be included in the final unit.
- The revisions have been carried out in such a way that a make it more coherent for the current application
- Revised curriculum was discussed and approved.

Meeting ended with vote of thanks.

Minutes approved.

Members:

Dr. Wilson Aruni	
Dr. C. Elizabeth Rani Juneius	
Dr. Alex Anand	
Dr. Jemmy Christy	

Dr. Swetha Sunkar	

Department of Bioinformatics
BOS – July 3rd 2021
Syllabus revision

The following two papers of B. Sc Bioinformatics and Datascience and two papers for M. Sc Bioinformatics and Datascience have been put forth for revision.

List of Papers for which revisions are suggested

B. Sc (Bioinformatics and Datascience)		
S.No	Subject Code	Subject name
1	SBIA1501	Modelling Of Molecules (Semester 5)
2	SBIA3004	Next Generation Sequencing (Elective)
M.Sc (Bioinformatics and Data science)		
3	SBIA5101	Structural And Functional Genomics (Semester 1)
4	SBIA7408	Next Generation Sequence Data Analysis (Elective)

2019 regulation Syllabus

SBIA1501	MODELLING OF MOLECULES	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

The course intends to impart knowledge on the various concepts of molecular modelling and its application in drug designing with a focus on identification of lead molecules and the concept of pharmacophore.

Unit I INTRODUCTION TO QUANTUM MECHANICS 9hrs

Basic Concepts in Molecular Modelling: Introduction, Coordinate systems, Energy surfaces. Introduction to Quantum mechanics - Schrodinger wave equation, Time dependent and time independent forms.

Unit II BASICS OF MOLECULAR MECHANICS 9hrs

Features of molecular mechanics, force fields; Bond structure and bending angles – electrostatic, van der Waals and non –bonded interactions, hydrogen bonding; Energy minimization; Application of energy minimization.

Unit III MOLECULAR MECHANICS 9hrs

Molecular Mechanics Introduction, Vander Waals and Dipole-Dipole Interaction, Types of Potential- Lennard- Jones, Truncated Lennard – Jones, Ionic and Polar potentials, Types of force field- AMBER, CHARMM, Merck Molecular Force Field, Consistent Force Field, MM2, MM3 and MM4 Force Field.

Unit IV MOLECULAR DYNAMICS 9hrs

Molecular Dynamics using simple models; Molecular Dynamics with continuous potentials and at constant temperature and pressure; Time-dependent properties; Solvent effects in Molecular Dynamics; Conformational changes from Molecular Dynamics simulation. Introduction, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, duration of the MD run.

Unit V SIMULATION AND MODELLING 9hrs

Methods of computer aided drug design, ligand design methods, drug design approaches, Target identification and validation, lead optimization and validation, Structure and ligand-based drug design, modelling of target-small molecule interactions.

COURSE OUTCOMES

At the end of the course the students will

CO1 –Be able to apply and understand the modelling on the basis of quantum mechanical aspects.

CO2 –To discuss the various types of interactions possible between the macromolecule and the ligand.

CO3 –Identify the lead molecule by virtual screening.

CO4 –Design the strategy towards drug design.

CO5 –Design the strategy towards drug design based on the structural aspects of the macromolecule.

CO6 –Adopt and implement the concepts of modelling to derive structures for molecules

TEXT / REFERENCE BOOKS:

1. Andrew Leach - Molecular Modelling: Principles and Applications, 2nd Edition. Pearson Education EMA, 2001.
2. R.K. Prasad - Quantum Chemistry, 3rd Edition, 2006.

Syllabus after revision

SBIA1501	MODELLING OF MOLECULES	L	T	P	Credits	Total Marks
		3	1	0	4	100

COURSE OBJECTIVES

The course intends to impart knowledge on the various concepts of molecular modelling and its application in drug designing with a focus on identification of lead molecules and the concept of pharmacophore.

Unit I Introduction to quantum mechanics

Basic Concepts in Molecular Modelling: Introduction, Coordinate systems, Energy surfaces. Introduction to Quantum mechanics - Schrodinger wave equation, Time dependent and time independent forms. Born-Oppenheimer approximation

Unit II Molecular mechanics

Features of molecular mechanics, force fields; Bond structure and bending angles – electrostatic, van der Waals and non –bonded interactions, hydrogen bonding; Commonly used forcefields – AMBER, CHARMM, GROMOS. Energy minimization – Potential energy surface, algorithms. Application of energy minimization.

Unit III Conformational analysis and simulation

Conformational analysis – introduction, conformational search methods. Computer Simulation: Basics, Uses. Molecular dynamics simulation – Time and ensemble averages, analysis of MD simulations. Monte Carlo simulation method.

Unit IV Biological Thermodynamics

Basics of thermodynamics: entropy, enthalpy, Gibbs free energy. Energy transformation in biological systems, Laws of thermodynamics. Boltzmann rule. Thermodynamic models of binding.

Unit V Applications of molecular modelling

Molecular modelling in drug design - CADD, Docking and QSAR studies, Protein 3D modelling. Modeling interactions, Organic–Inorganic Interface Simulations for Smart Novel Material Discoveries, Modeling of Nanopores for DNA Sequencing Applications

Color ash represents the syllabus to be changed; Color orange represents the changed content

Justification

- The theory paper SBIA1501 - Modeling of molecules has been modified and put forth for BOS approval. The changes carried out are
- Unit 3 4 and 5 have been changed to encompass all the important concepts in modelling.
- Conformational analysis which was initially not included is included in unit 3 and simulation concepts provided in unit 4 has been included in unit 3.
- The concept of thermodynamics is included in unit 4 as this is the basis for the functioning and stability of a system.
- Unit 5 is modified to include the applications of molecular modelling from drug design to novel material discovery and also nanopore modelling as this would give an insight into the latest research utility of molecular modelling

2019 regulations - syllabus

SBIA3004	NEXT GENERATION SEQUENCING	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

This course will provide an introduction to the technology, data analysis, tools and resources for next generation sequencing data. The content is intended to provide a broad overview of the subject areas, and to highlight key resources, approaches and methodologies.

Unit I INTRODUCTION TO NGS

9hrs

NGS Platforms: Introduction to NGS, Roche/454 FLX, Illumina/Solexa Genome Analyzer, Applied Biosystems SOLiD system, Helicos Heliscope, Pacific Biosciences/single molecule real time (SMRT) sequencing.

Unit II SEQUENCE DATA **9hrs**

Genome assembly algorithms: Alignment of short-reads to reference genome using spaced seed (ELAND, SOAP), index-filtering algorithm (SeqMap), quality-score (RMAP), q-filter algorithm (SHRiMP), FM-index (Bowtie, BWA, SOAP2), suffix tree (MUMmer). Sequence Alignment formats: Sequence Alignment/Map (SAM) format, Binary Alignment/Map (BAM) format, Tools for conversion (SAMtools), Alignment viewers (IGV, MGAviewer).

Unit III SEQUENCE DATA ASSEMBLY

9hrs

De-novo assembly: Overlap-layout-consensus (OLC) approach (Arachne, Phusion), de Bruijn and Euler path approach (Euler, SOAPdenovo), string graph assembler (SGA). Scaffolding: Supercontig, contig orientation, contig ordering, contig distancing and gap closing using SOAPdenovo, ABySS, OPERA and RACA.

Unit IV SOFTWARES IN NGS ANALYSIS

9hrs

Application of R in NGS analysis: Introduction to Bioconductor, Reading of RNA-seq data (ShortRead, Rsamtools, GenomicRanges), annotation (biomaRt, genome Intervals), reads coverage and assign counts (IRanges, Genomic Features), differential expression (DESeq).

Unit V APPLICATIONS **9hrs**

Biological applications of NGS: Whole-genome sequencing, Exome sequencing, Transcriptome sequencing, Epigenome sequencing, Interactome sequencing, methylome sequencing.

COURSE OUTCOMES

At the end of the course the students will

CO1 –Describe the applications of the different NGS technologies, including the weakness and strengths of the approaches.

CO2 –Explain the steps involved in a general NGS data analysis.

CO3 –Explain key theoretical concepts of alignment and de novo assembly.

CO4 –Synthesize and formulate a project and relevant question within the field.

CO5 –ndependently perform a basic NGS data analysis.

CO6 –Apply analytical and reflective skills in analyzing results from individual steps and the final project.

TEXT / REFERENCE BOOKS:

1. Next-generation DNA sequencing Informatics by Stuart M. Brown, Cold Spring Harbor Laboratory, 2013.
2. RNA-seq Data Analysis: A Practical Approach by Eija Korpelainen, Jarno Tuimala, Panu Somervuo, Mikael Huss, Garry Wong. Chapman & Hall/CRC, 2014.
3. Next generation sequencing: Translation to Clinical Diagnostics by Wong Lee-Jun C. (ed.), Springer, 2013.
4. Next-generation genome sequencing: Towards Personalized Medicine by Michal Janitz, WileyVCH, 2008

Syllabus after revision

SBIA3004	NEXT GENERATION SEQUENCING	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

This course will provide an introduction to the technology, data analysis, tools and resources for next generation sequencing data. The content is intended to provide a broad overview of the subject areas, and to highlight key resources, approaches and methodologies.

Unit 1 Introduction to sequencing

Over view of sequencing, Need and applications. Generations in sequencing – first generation sequencing – Sangers method and Maxam Gilbert method. Second generation sequencing – NGS platforms - Roche/454, Illumina/Solexa, Ion torrent, SOLiD system. Third generation sequencing

Unit 2 NGS workflow

Library preparation – Template enrichment – Emulsion and Bridge PCR, Sequencing: NGS platforms; Comparison of NGS platforms. Data analysis- Data acquisition - Reads and quality check, Base calling. Read alignment and refinement, Sequence assembly. Variant calling. File formats used in NGS.

Unit 3 RNA SEQUENCING

Data acquisition- Read alignment – Transcriptome assembly - Differential expression analysis – Alternative splicing - Allele-specific expression - RNA editing – smRNA

Unit 4 Chip Seq

Basics on immune precipitation, Types of Chips Seq – XchIP and NChIP. Workflow – isolation, mapping, peak finding – functional analysis and annotation

Unit 5 Applications of NGS

Whole-genome sequencing, Exome sequencing, Targeted sequencing, Pooled sequencing, methylome sequencing. Next generation sequencing applications in Agri-Biotech, health care, metagenomics, GWAS.

Color ash represents the syllabus to be changed; Color orange represents the changed content

Justification

- The revisions have been carried out in such a way that a complete overview of NGS and its types have been incorporated.
- Introduction to the need of sequencing has been added in unit 1 to refresh the basics of sequencing.
- Unit 2 has been reframed in such a way that it includes the entire process of NGS
- RNA seq has been included in Unit 3 as working on transcriptome is focused currently
- Chip seq has been included in unit 4 as this topic deals with the overall interactions between proteins and DNA.
- Unit 5 has been retained as that includes the different applications of NGS in various fields of research

SBIA5101	STRUCTURAL AND FUNCTIONAL GENOMICS	L	T	P	Credits	Total Marks
		3	*	0	3	100

COURSE OBJECTIVES

To have a knowledge on the conformational parameters and their influence on the structure of the macromolecule and to acquire a knowledge on the structure and activity relationship.

UNIT I INTRODUCTION

Structure & Organization of Prokaryotic & Eukaryotic genome - Nucleotide and protein sequencing methods –Chemical, Enzymatic, high through put method – Automated sequencing methods – shotgun – chromosome walking, Contig assembly - Levels of structures in biological macromolecules.

UNIT II CONFORMATIONAL ANALYSIS

Biomolecules and their interactions - Forces that determine protein and nucleic acid structure, basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions and ionic interactions, disulphide bonds - Prediction of proteins structure - Nucleic acids, general characteristics of nucleic acid structure, geometrics, glycosidic bond rotational isomers - Ribose puckering - forces stabilizing ordered forms, base pairing, base stacking- tertiary structure of nucleic acids.

UNIT III STRUCTURAL ANALYSIS OF MACROMOLECULES

Size and shape of macromolecules - methods of direct visualization - X-ray crystallography – X–ray diffraction, determination of molecular structures, electron microscopy, NMR. Protein structure databases - Protein Data Bank - SCOP - CATH - structure superposition - RMSD - TM-score- structure alignment - Different structure alignment algorithms - DALI, CE, VAST, TM-align - protein folds in PDB.

UNIT IV STRUCTURE-FUNCTIONS RELATIONSHIP

DNA binding proteins, Prokaryotic and Eukaryotic transcription factors - DNA polymerases, Helix-turn-Helix motif in DNA binding, Trp repressor, Zn fingers, helix-turn helix motifs in homeodomain, Leucine zippers - DNA polymerases, Membrane proteins and receptors, Trans-membrane segments, bacterio-rhodopsin, photosynthetic centers, epidermal growth factor, insulin and PGDGF receptors and their interaction with effectors, protein phosphorylation, immunoglobulins, Serine proteases, ribonuclease, lysozyme.

UNIT V FUNCTIONAL GENOMICS

Introduction to Functional Genomics - cytological maps - Hap Map - SNPs and variation-Genotyping, microarray- analysis and applications. Microarray oligo sets and fabrication - integrative genomics and Meta genomics. Quantitative Proteomics. Fluorescent imaging techniques. Quantitative RT-PCR analysis. High-throughput cloning and expression strategies. Next Generation Sequencing applications.

COURSE OUTCOMES

On completion of the course the student will be able to

CO1: The student will acquire a basic knowledge on the basics of genomics.

CO2: They will be able to appreciate the influence of conformational parameters on the structure of the macromolecule.
CO3: Will be able to select the particular method of structural analysis methodology, given the protein.
CO4: Assess the structure and activity relationship of the macromolecule.
CO5: Acquire knowledge on the functional aspects of genomics.
CO6: Explore the strategies used in high throughput screening of biological data

TEXT / REFERENCE BOOKS

1. Cantor R., Schimmel P.R., Biophysical Chemistry, Vol. I, II, W.H. Freeman & Co., 1985.
2. Kensal E. van Holde, W. Curtis Johnson and P. Shing Ho, Principle of Physical Biochemistry, Prentice Hall, New York, 1998.
3. Pennington SR, Dunn MJ, Proteomics from Protein Sequence to Function, Viva Books Ltd, 2002.
4. G. Gibson and M. V. Muse. A primer of Genome Science. Sinauer Associates Inc; 2 edition, December 2004.

Syllabus after revision

SBIA5101	STRUCTURAL AND FUNCTIONAL GENOMICS	L	T	P	Credits	Total Marks
		3	*	0	3	100

COURSE OBJECTIVES

To have a knowledge on the conformational parameters and their influence on the structure of the macromolecule and to acquire a knowledge on the structure and activity relationship.

UNIT I INTRODUCTION

Structure & Organization of Prokaryotic & Eukaryotic genome - Nucleotide and protein sequencing methods –Chemical, Enzymatic, high through put method – Automated sequencing methods – shotgun –, Contig assembly - Levels of structures in biological macromolecules.

UNIT II CONFORMATIONAL ANALYSIS

Biomolecules and their interactions - Forces that determine protein and nucleic acid structure, hydrogen bonding, hydrophobic interactions and ionic interactions, disulphide bonds. Nucleic acids, general characteristics of nucleic acid structure, geometrics, glycosidic bond rotational isomers - Ribose puckering - forces stabilizing ordered forms, base pairing, base stacking-tertiary structure of nucleic acids.

UNIT III STRUCTURAL ANALYSIS OF MACROMOLECULES

Size and shape of macromolecules - methods of direct visualization - X-ray crystallography – X–ray diffraction, determination of molecular structures, electron microscopy, NMR. Protein structure databases - Protein Data Bank - SCOP - CATH - structure superposition - RMSD - TM-score- structure alignment - Different structure alignment algorithms - DALI, TM-align.

UNIT IV STRUCTURE-FUNCTIONS RELATIONSHIP

DNA binding proteins, Prokaryotic and Eukaryotic transcription factors - DNA polymerases, Helix-turn-Helix motif in DNA binding, Trp repressor, Zn fingers, helix-turn helix motifs in homeodomain, Leucine zippers - DNA polymerases, Membrane proteins and receptors, Trans-membrane segments, bacterio-rhodopsin, photosynthetic centers, epidermal growth factor, protein phosphorylation, Serine proteases, ribonuclease, lysozyme.

UNIT V FUNCTIONAL GENOMICS

Introduction to Functional Genomics - cytological maps - Hap Map - SNPs and variation-Genotyping, microarray- analysis and applications. Meta genomics. Quantitative Proteomics. Fluorescent imaging techniques. Quantitative RT-PCR analysis.

Color ash represents the syllabus to be changed; Color orange represents the changed content

Justification

- The following “basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles,” has been removed from unit 3 as it comes under geometry
- CE, Folds in PDB are removed from unit 3 as it is shown in structure classification databases
- Insulin and PGDGF receptors and their interaction with effectors, immunoglobulins have been removed from unit 4 as there are too many examples.
- Microarray oligo sets and fabrication - integrative genomics and High-throughput cloning and expression strategies. Next Generation Sequencing applications have been removed from unit 5 to justify the title of the unit

2019 Regulation syllabus

SBIA7408	NEXT GENERATION SEQUENCE DATA ANALYSIS	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

- NGS bioinformatics workflow steps following sequence generation
- NGS for transcriptomics; QC, mapping, visualization tools
- NGS for genomics; assembly, alignment, QC and variant calling tools
- Exploring EMBL-EBI resources

UNIT I DNA SEQUENCING

9hrs

DNA Sequencing, first generation DNA sequences, Drawbacks of the first-generation sequencing method- Emergence of Next generation sequencing -Platform overview- Biological applications- Basic concepts- Recent scientific breakthroughs using NGS technology

UNIT II OVERVIEW OF NGS TECHNOLOGY

9hrs

Pyro-sequencing, Illumina Genome Analyzer, Applied Biosystems Sequencing, Ion Torrent Sequencing, Polonator Technology, Nanopore Sequencing, Single Molecule Real Time DNA sequencing- Comparison of Next generation sequencing techniques, & applications- Drawbacks of NGS, NGS File formats- FASTA, FASTQ, FNA, CSFASTA, GFF, SAM and BAM

UNIT III NGS DATABASES AND ANALYSIS OF NGS DATA

9hrs

NGS databases, Sequence Analysis: Pairwise and multiple sequence alignment methods and tools-Sample data processing with annotation

UNIT IV ALIGNMENT AND ANALYSIS

9hrs

Genome alignment and analysis tools-BWA (Burrows-Wheeler Aligner), SAMtools, GATK (The Genome Analysis Toolkit), IGV (Integrative Genomics Viewer), HISAT, StringTie, Cuffcompare, Velvet, Oases, Trinity

UNIT V TRANSCPTOMICS ANALYSIS **9hrs**

Transcriptome (RNA) sequencing, Exome sequencing, Genome Annotation, Using NGS to detect sequence variants, ChIP-sequence, biological theories on ChIP-sequence analysis, Understanding the non – coding genome, Disease gene identification, DNA fragment evaluation, Peak identification, two condition comparison, Saturation analysis, Motif finding and related theories

Max 45 hrs

COURSE OUTCOMES

After this course the students will be able to

CO 1: Discuss a variety of applications and workflow approaches for NGS technologies

CO 2: Use a range of bioinformatics software and tools to undertake basic analysis of NGS data

CO 3: Understand the advantages and limitations of NGS analyses

CO 4: Submit, browse and access a range of NGS data available in public repositories using EBI resources

CO 5: Comprehend the different areas of NGS analysis utility

CO 6: Apply the knowledge of NGS technology in transcriptome data analysis

TEXT BOOKS /REFERENCES

1. Ali Masoudi-Nejad, Zahra Narimani, Nazanin Hosseinkhan; "Next Generation Sequencing and Sequence Assembly", Methodologies and Algorithms, Springer; 2013.
2. Stuart M. Brown, "Next-Generation DNA Sequencing Informatics", Cold Spring Harbor Laboratory Press, 2013.
3. Mark I. Rees, "Challenges and Opportunities of Next-generation Sequencing for Biomedical Research", Academic Press, 2012.

Syllabus after revision

2019 Regulation syllabus

SBIA7408	NEXT GENERATION SEQUENCE DATA ANALYSIS	L	T	P	Credits	Total Marks
		3	0	0	3	100

COURSE OBJECTIVES

- NGS bioinformatics workflow steps following sequence generation
- NGS for transcriptomics; QC, mapping, visualization tools
- NGS for genomics; assembly, alignment, QC and variant calling tools
- Exploring EMBL-EBI resources

UNIT I DNA SEQUENCING

DNA Sequencing, first generation DNA sequencing, Drawbacks of the first-generation sequencing method- Emergence of Next generation sequencing -Platform overview- Biological applications- Basic concepts- Recent scientific breakthroughs using NGS technology

UNIT II OVERVIEW OF NGS TECHNOLOGY

Pyro-sequencing, Illumina Genome Analyzer, Applied Biosystems Sequencing, Ion Torrent Sequencing, Polonator Technology, Nanopore Sequencing, Single Molecule Real Time DNA sequencing- Comparison of Next generation sequencing techniques, & applications- Drawbacks of NGS, NGS File formats- FASTA, FASTQ, FNA, CSFASTA, GFF, SAM and BAM

UNIT III NGS DATABASES AND ANALYSIS OF NGS DATA

NGS databases. Data analysis work flow: Library preparation, Sequencing, Data analysis: reads, Alignment and assembly, variant calling

UNIT IV Transcriptome analysis

Transcriptome (RNA) sequencing**,** Data acquisition- Read alignment – Transcriptome assembly - Differential expression analysis – Allele-specific expression - RNA editing.

UNIT V NGS applications

Exome sequencing, Targeted sequencing, Whole-genome sequencing, Pooled sequencing, methylome sequencing. Role of NGS in Agri-Biotech, health care, metagenomics, GWAS.

Color ash represents the syllabus to be changed; Color orange represents the changed content

Justification

- The syllabus of NGS has been reframed to make it more coherent
- Details on NGS workflow has been incorporated in unit 3 to provide more clarity
- Unit 4 focuses on RNA seq which is shifted from unit 5
- Unit 5 includes all the applications of NGS.