

University of North Bengal

Department of Bioinformatics



समानोमन्त्रः समितिः समानी

PhD Course work Syllabus

Course Curriculum

S l. N o	Course Code	Name of the Course	Duration	Number of Credits	Marks
1.	BICW-01	Research Methodology	First 3 Months	01	25
2.	BICW-02	Quantitative Methods and Computer Applications	First 3 Months	02	50
3.	BICW-03	Scientific Writing and Presentation	First 3 Months	01	25
4.	BICW-04	Bioinformatics	Second 3 Months	02	50
5.	BICW-05	Omics Technologies	Second 3 Months	02	50
6.	CPE-RPE	Research and Publication Ethics	Second 3 Months	02	50
		Total >>	6 Months	10	250

BICW-01 Research Methodology (01 Credit)

Research Design: Methods for defining an original research problem; Research: Definition, Importance, Meaning and Characteristics; Steps in research. Research problem: Identification, Selection and Formulation; Sampling: definition, theory, types, techniques and steps; Sample size, advantages and limitations of sampling; Data: Definition, sources and type; Data collection methods.

Biosafety Principles; Laboratory Practices and Techniques; Risk analysis and control of biohazards; Dissemination of contaminants; Safety Equipment-Biosafety cabinets; Biosafety Guidelines and regulations; Ethics of animal use in research; Reproduction of published materials; Plagiarism

BICW-02 Quantitative Methods and Computer Applications (02 Credit)

Biostatistics: Statistical concepts and Analytical methods as applied to data encountered in Bioinformatics; Basic concepts of experimental design; Quantitative analysis of data: Statistical inferences; Usage of statistical data packages; Operating system: Latest versions of WINDOWS, UNIX and LINUX; Software packages: SPSS, GraphPad, R-Statistics

BICW-03 Scientific Writing and Presentation (01 Credit)

Writing a review paper; Drafting of a proposal for research funding, Oral presentation and Submission in written form

BICW-04 Bioinformatics (02 Credits)

- **Basics and Bioinformatics databases** - history of bioinformatics, major Bioinformatics Resources, the Nucleic Acids Research database issue and the online molecular biology database collection. Protein three-dimensional databases, Protein 3D structure visualization tools, Protein sequence databases, Structure Databases, Metabolic and Signaling Pathways, Genomics Databases. Microarray Data and other Gene Expression Databases.
- **Sequence Alignment** – Sequence comparison scoring systems: PAM and BLOSUM family of matrices, Basics of Global and local alignments, Pair-wise alignment: Dot matrix analysis, Word or k-tuple methods, Multiple sequence alignment: Multiple sequence alignment as an extension of sequence pair alignment by dynamic programming.
- **Phylogeny:** Phylogenetic analysis, Definition and description of phylogenetic trees and

various types of trees, Method of construction of Phylogenetic trees [distance based method (UPGMA, NJ), Maximum Parsimony and Maximum Likelihood method]

Suggested Readings:

- N. Gautham; Bioinformatics: Databases and Algorithms; Alpha Science, 2006.
- D. W. Mount; Bioinformatics Sequence and Genome Analysis; Cold Spring Laboratory Press, 2001.
- A. M Lesk; Introduction to Bioinformatics; Oxford University Press, 2002.
- J. Bedell, I. Korf and M. Yandell; BLAST; O'Reilly Press, 2003.
- R. Durbin; Biological sequence analysis; Cambridge University Press, 1998.

BICW-05 Omics Technologies (02 Credits)

● **Genomics and transcriptomics**

History of genomics; Genome projects of model organisms; Human genome structure and comparative genomics. Principle of Sanger's di-deoxy method versus NGS and their output; shotgun sequencing method and library preparations, comparative study of standard NGS methods.

Sequence assembly concepts and challenges in assembling short reads; Algorithms for assembling short reads using graph theory such as Hamiltonian cycle and de Brjin; Types of RNAs and the respective roles in cells. Transcriptome and techniques used for transcriptomics; Gene expression analysis using RNAseq data, statistical methods; Primers design for downstream validation; Mapping algorithms such as Burrow-Wheeler.

● **Applied Genomics and Metagenomics**

Identification genetic variants from genome sequence: SNPs, SNVs, translocation, copy number variation. Concepts behind genome-wide association studies. Methylation of DNA and genetics; histone modifications, CHIPchip and CHIPseq techniques. Alternative splicing: basic concept and significance.

Overview of metagenomics principles, microbial and ecological aspects underlying metagenomic experiments; 16SrRNA data analysis, clustering/phylogenetic tree based of alignment, clustering based on composition. Concepts behind self organizing maps, principal component and other clustering tools

● **Proteomics and Chemo-informatics**

Proteome profiling methods, 2D electrophoresis image comparisons; yeast two hybrid system, protein arrays, mass spectrometry data processing and analysis; pathway analysis and identifying protein-protein interactions with mass scale expression data.

Basic concepts and application of Chemo-informatics, *In silico* representation of chemical information. Molecular Modeling and virtual screening techniques, Molecular docking: current advances and challenges.

- **Advanced Omics Technology**

Current peptidomics: Applications, purification, identification, quantification, and functional analysis; Plant Peptides: Bioactivity, Opportunities and Challenges; Lipidomics. Introduction to cell metabolism, methods of flux analysis including FBA, computational tools for whole genome metabolic model reconstruction and integrated frameworks for design of metabolic pathways such as retrosynthesis.

Suggested Readings:

- Bajorath JB (2004) “Chemo-informatics-Concepts, Methods, and Tools for Drug Discovery”, Springer
- Ramadan, E.Y.(2008). Biological Networks: Modeling and Structural Analysis.
- S. M. Brown; (2013) Next Generation DNA Sequencing Informatics; Cold Spring Harbor Laboratory Press.
- N. RodriguezEzpeleta; Bioinformatics for High Throughput Sequencing; Springer; 2012
- Y. M. Kwon and S. C. Ricke; HighThroughput Next Generation Sequencing: Methods and Applications; Humana Press; 2011

CPE-RPE Research and Publication Ethics (02 Credits)

Theory

RPE 01: Philosophy and Ethics (3 hrs)

1. Introduction to philosophy: definition, nature and scope, concept, branches
2. Ethics: definition, moral philosophy, nature of moral judgements and reactions

RPE 02: Scientific Conduct (5 hrs)

1. Ethics and respects to science and research
2. Intellectual honesty and research integrity
3. Scientific misconducts: Falsification, Fabrication and Plagiarism (FFP)
4. Redundant publications: duplicate and overlapping publications, salami slicing
5. Selective reporting and misrepresentation of data

RPE 03: Publication Ethics (7 hrs)

1. Publication ethics: definition, introduction and importance
2. Best practices/standards-setting initiatives and guidelines: COPE, WAME, etc.
3. Conflicts of interest
4. Publication misconduct: definition, concept, problems that lead to unethical behaviour and vice versa, types
5. Violation of publication ethics, authorship and contributorship

6. Identification of publication misconduct, complaints and appeals
7. Predatory publishers and Journals

Practice

RPE 04: Open Access Publishing (4 hrs)

1. Open access publications and initiatives
2. SHERPA/RoMEO online resource to check publisher copyright & self-archiving policies
3. Software tool to identify predatory publications developed by SPPU
4. Journal finder/journal suggestions tools viz. JANE, Elsevier Journal Finder, Springer Journal Suggester, etc.

RPE 05: Publication Misconduct (4 hrs)

A. Group Discussion (2 hrs)

1. Subject-specific ethical issues, FFP, authorship
2. Conflicts of interest
3. Complaints and appeals: Examples and fraud from India and abroad

B. Software tools (2 hrs)

Use of plagiarism software like Turnitin, Urkund and other open-source software tools

RPE 06: Databases and research Metrics (7 hrs)

A. Databases (4 hrs)

1. Indexing databases
2. Citation databases: Web of Science, Scopus, etc

B. research Metrics (3 hrs)

1. Impact Factor of Journal as per Journal Citation Report, SNIP, SJR, IPP, Cite Score
2. Metrics: H-index, G-index, i10 index, altmetrics