Bio Re Inventors
New Identity of Innovation and Technology

ABOUT US

BIO RE INVENTORS (BRI) was started keeping in mind the needs of young and brilliant minds who are fascinated with the world of Bio-Technology. Gradually Bio-technology, the interdisciplinary frontier between biology, engineering, medicine, agriculture and Bio IT has grown into one of the vital fields of Science. The new discoveries and new inventions have made this field more appealing to ever growing inquisitive pool of students, researchers & professionals. Many Institutions, Research Labs & Companies have forayed into hitherto unknown territories only to be startled with unbelievable facts and extremely powerful information stored in minutest of cells. BRI is here to provide you with a platform to get acquainted with the subject matter. The platform is also designed to help interact with concerned people worldwide so as to help unravel new mysteries and cross new frontiers. Our dedicated team commits to be alongside you in this journey of learning & innovation.

Vision

To make Global innovative and adding value to India's outstanding traditional knowledge base

Mission

To help Student become inventive and creative, and to become a global leader in sustainable technologies without social and economic handicaps affecting the evolution and diffusion of grassroots innovations.

Address: Office no 206, Mayur Trade Center Phase-2, Near Chinchwad Railway Station
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TRAINING

BIOINFORMATICS

Bio Re Inventors Offers Bioinformatics training in following fields: Basic Bioinformatics, Biological Databases & Structure, Data Mining, Phylogenetic Analysis & Algorithm, Epitope Mapping, Protein Docking, Live Bioinformatics Project and Advance Perl Programming for Bioinformatics Application development.

7 days Training Modules

Module BRi-701: Sequence Analysis, Basic Bioinformatics
Module BRi-702: Protein Docking
Module BRi-703: Epitope Mapping
Module BRi-704: Basic Bioinformatics, Data Mining

15 days Training Modules

Module BRi -1501: Sequence Analysis, Basic Bioinformatics, Biological Database & Structure
Module BRi -1502: Protein Docking, Epitope Mapping
Module BRi -1503: Data Mining, Phylogenetic Analysis
Module BRi -1504: Phylogenetic Analysis, Epitope Mapping

1 month Training Modules

Module BRi -3001: Sequence Analysis, Basic Bioinformatics, Biological Database & Structure, Data Mining
Module BRi -3002: Data Mining, Phylogenetic Analysis, Epitope Mapping
Module BRi -3003: Phylogenetic Analysis, Epitope Mapping, Protein Docking

2 months Training Modules

Module BRi -2301: Sequence Analysis, Basic Bioinformatics, Biological Database, Data Mining, Phylogenetic Analysis
Module BRi -2302: Data Mining, Phylogenetic Analysis, Epitope Mapping, Protein Docking
Module BRi -2303: Small Live Project**

Module BRi-3301: Live Project**, Protein Docking
Module BRi-3302: Live Project**, Epitope Mapping

Course Module Type	Fees(INR)
7 Days Module	8,000/-
15 Days Module	10,000/-
One Month Module	15,000/-
Two Months Module	20,000/-
Three Months Module	24,000/-

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Skill Oriented Program in Bioinformatics

Next Generation Sequencing (NGS)

1. Overview of next generation sequencing technology

   i) What are NGS and Basic Concepts?
   ii) Sequencing Methods
   iii) Platform overview and Biological applications
   iv) Recent scientific breakthroughs using NGS technology
   v) Applications

2. Introduction to Sequencing

   i) Traditional Methods
   ii) Sanger sequencing
   iii) Drawbacks of Sanger's sequencing

3. NGS Data Generation

I. Generation of large scale molecular biology data. (Through Genome
II. Sequencing, Protein sequencing, Gel electrophoresis, NMR Spectroscopy, X-Ray)

4. Next Generation Sequencing Methods

   I. Roche 454
   II. Solexa/Illumine
   III. ABI SOLiD
   IV. Ion Torrent

5. Genome Databases and File Formats

8. Explore Genome databases: UCSC Browser, G Browse, ENA Archive

9. File Formats: FASTA, FastQ , SAM, BAM,VCF

6. Introduction to Galaxy

How to upload data; explore published histories; generate new history; changing dataset formats and editing attributes; to explore various NGS nodes;

7. SNP Sequence Analysis

   I. Upload Data
   II. Sequence (FastQ)
   III. Reference Genome (FASTA)
   IV. Quality Control (Grooming)
   V. Alignment with BWA
   VI. Variant Calling

8. Workflow Development for Variant Calling

Course Module Type	Fees(INR)
7 Days Module / Workshop	6,000/-
One Month Module	15,000/-
Two Month Module	21,000/-

Project Discussion & Presentation (Only applicable for 1 Month & 2 Month)

1. Project Discussion
2. Student Project Presentations

Computer Aided Drug Designing

What is CADD?

1. Lock-Key principle and induced fit theory
2. CADD and Molecular Modeling
3. Success stories of CADD

MOLECULAR MODELING AND DRUG DESIGING

MOLECULAR MECHANICS (MM)

1. The concept of the force field in MM
2. No bonded interaction potential
3. Force field energies
4. Classification of force fields
5. QM/MM methods
6. Energy minimization methods
7. Conformational Searching
8. Conformations of biomacromolucules
9. Systematic search methods
10. Random search methods
11. Genetic algorithms
12. Distance geometry

PROTEIN MODELING

1. The Protein Data Bank (PDB)
2. Relationship between sequence and 3D structure of a protein
3. Alignment of protein sequences
4. Needleman-Wunsch alignment method
5. Multiple sequence alignments (MSA)
6. Homology modeling of proteins
7. Construction of the core
8. Refinement of the homology model
9. Model verification
10. Comparison of various strategies in homology modeling
11. Drug designing
12. Molecular recognition
13. Structure-based Ligand design
14. Molecular docking
15. Virtual screening
16. Structure-based Pharmacophore generation
17. Pharmacophore representation
18. De Novo design of ligands

19. Peptides and peptide analogs as drugs: Peptidomimetics
20. Basic concepts of QSAR
21. 2D-QSAR in drug design
22. Principal component analysis (PCA)
23. Multiple linear regressions (MLR)
24. Principle component regression (PCR)
25. Partial least squares method (PLS)
26. COMFA and COMSIA
27. ADMET calculation

Course Module Type	Fees(INR)
7 Days Module / Workshop	6,000/-
One Month Module	15,000/-
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3. Project Discussion
4. Student Project Presentations

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Protein modeling and Rational drug designing

Protein modeling and rational drug designing is now a popular technique used for increasing the speed of drug designing process. This was made possible by the availability of many protein structures which helped in developing tools to understand the structure function relationships, automated docking and virtual screening.

•Basic understanding of ligand-protein interactions.

•Use Internet-based structural bioinformatics tools to analyse three-dimensional structures of a proteins and a protein-ligand complexes and perform homology-based modeling.

•Understand the general principles behind protein crystallization and X-Ray crystallography assess the requirements and take active part in the planning and the subsequent development of this type of projects.

•Be familiar with a range of ligand and structure based computational methods.

•Perform simple computational modeling tasks using state of the art software.

1. Introduction to Rational Drug Designing.
2. Molecular modeling
3. Force fields
4. Potential energy functions
5. Energy minimization Methods
6. Global and Local energy minimization
7. Conformational search methods
8. Molecular dynamics and Monte Carlo simulations
9. Sequence analysis and Applications
10. Pairwise and Multiple sequence alignment
11. Homology Modeling of Proteins
12. Ramachandranplot analysis, Procheck and Profiles3d
13. Active site Pocket identification
14. Structure based drug designing
15. Docking studies
16. Protein-Ligand docking studies
17. Protein-Protein interactions
18. Virtual screening
19. HTS
20. Hit to lead selection and validation
21. Ligand Based drug designing or QSAR studies
22. 2D and 3D QSAR (COMFA and COMSIA) studies
23. Denovo Drug Designing
24. Interaction Map generation
25. Pharmacophore studies

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26. ADME/Toxicity calculations
27. FDA in drug trials
28. Getting started to Bioperl
29. Bio Perl Benefits.
30. Bio Perl Programming
31. Sequences, strings and Arrays

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1. Project Discussion
2. Student Project Presentations

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System Biology

Advanced introduction to systems biology and the quantitative analysis of how cells Work: from gene regulation to complex networks to examples of chemotaxis, kinetic Proofreading, and collective behaviors. the aim will be to develop quantitative toolkits to analyze the complex mechanisms behind the regulation, design, and operation of biological circuits. Computer programming will be done in Matlab, though no prior experience with Matlab is necessary for the course.

Overview

1. Introduction to systems biology in the Omics-era
2. Introduction to course and discussion of format, syllabus, and grading.
3. Genomics
4. Genome-scale mutational profiling in complex disease
5. Regulation in biological systems
6. High performance genomic technologies and data analysis I: microarray
7. High performance genomic technologies and data analysis II: NGS
8. Proteomics
9. Protein complexes, Immunoprecipitation, and purification
10. Proteomic separation and peptide dissociation
11. Enrichment and identification of post-translational modifications
12. Targeted proteomics through selected reaction monitoring
13. Metabolomics
14. Protein structure and function, enzyme action
15. Metabolomics networks
16. Theory –
    1. Graph theory, mathematical modeling
    2. Exam I Collected
    3. Dynamics in network
    4. Multivariate analysis I
    5. Multivariate analysis II

    Project design, IRB review

Networks –

1. Construction: protein interaction networks
2. Construction: gene regulatory networks
3. Analysis: models, topological characteristics, robustness
4. Analysis: motifs, modules, and subnetworks
5. Tutorial: network visualization tools

Pathway –

1. Pathway-based analysis of genomic data
2. Application of gene set enrichment analysis in genomic data
3. Tutorial: pathway analysis (Ingenuity, GSEA, etc)

Application –

1. Integrative analysis: multi-dimensional genomic data analysis
2. Integrative analysis: phenotyping in complex disease
3. Neuroimaging in complex disease

Course Module Type	Fees(INR)
7 Days Module / Workshop	6,000/-
One Month Module	15,000/-
Two Month Module	21,000/-

Project Discussion & Presentation (Only applicable for 1 Month & 2 Month)

1. Project Discussion
2. Student Project Presentations

Computational Molecular Biology

This Course will deal with molecular biology. From determining the genetic sequence in a scrap of DNA to creating a 3-D virtual model of a protein, scientists use computer modeling in this field to help us better understand a world far beyond the reaches of the microscope. Study in molecular biology yields vast amounts of data that must be carefully analyzed and interconnected to construct a realistic picture of this world. Computers greatly reduce the manual workload and error associated with complex analysis. In this unit, you will learn how to use computers in order to better understand DNA sequencing, transcriptional regulation, protein structure, and protein interactions. Upon completion of this unit, you should understand each process and be able to create your own models based upon the principles and procedures studied.

Principles of Molecular Biology

DNA Sequencing

DNA Structure and Classification

Sequence Databases

- GenBank (NCBI), EMBL, DDBJ, PDB

Visualization of Macromolecules

Construction of DNA molecule

Molecules sketching

Alignment

Pair wise Alignment

Multiple Sequence Alignment

Whole Genome Alignment

Comparison with Sequence Databases

- FASTA
- BLASTA

Finding Sequence Motifs

Genome Comparison

- Molecular Phylogenetic Analysis
- Principles of Molecular Evolution
- Methods for Determining Distance
- Neighbor-Joining
- Maximum Parsimony
- Maximum Likelihood
- Bootstrap Analysis
- Transcriptional Regulation
- Transcriptional Regulation Process
- Simple Regulation
- Regulatory Networks
- Finding Regulatory Sequence in DNA
- Proteins
- Protein Structure and Classification
- Protein Preparation
- Structure Prediction
- Homology Modeling
- Fold Recognition
- Threading
- Ab Initio
- Molecular Dynamics
- Model evaluation
- Mutational studies

Structure based drug designing

- Drug targets identification
- Active site pocket detection
- Docking studies

Protein-ligand docking studies

Protein-protein docking studies

Course Module Type	Fees(INR)
7 Days Module / Workshop	6,000/-
One Month Module	15,000/-
Two Month Module	21,000/-

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Chemoinformatics

Protein modelling and rational drug designing is now a popular technique used for increasing the speed of drug designing process. This was made possible by the availability of many protein structures which helped in developing tools to understand the structure function relationships, automated docking and virtual screening. The goal is to identify a key drug target based on a thorough understanding of regulatory networks and metabolic pathways, and to design a highly specific drug based on the known three-dimensional (3D) structure of that target.

- Alignments and structure prediction tools
- Alignment methodologies, limitations, problems
- TM and secondary structure prediction
- Full structure prediction - current status
- Practical: predicting structure
- Introduction to Drug Design and Development
- Target Selection and Validation
- Lead Identification and Modification
- Computer-Aided Drug Design
- Drug Delivery
- Pre-clinical and Clinical Testing

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Pharmacoinformatics

Course covers the topics like mining of genomes of pathogenic organisms for potential targets, prediction of the structure and function of target macromolecules, Ligand and target-based in-silico screening for first hits, compound library shaping, design and optimization of lead compounds, prediction of ADMET properties and off-pharmacologies, up to selectivity. This course offers a unique blend of modern information technology and pharmaceutical sciences to the students.

- Introductory Bioinformatics
- Protein and protein physical properties
- Proteomics
- Traditional and Rational drug discovery
- Chemoinformatics databases
- Application of force fields
- Drug screening and targeting
- Active site predictors
- Binding site analysis
- Ligand design

Course Module Type	Fees(INR)
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Genomics & Proteomics

It will give a general understanding of the proteome, describe many of the different aspects of proteomics that have been developed recently, identify the technologic limitations related to proteomics. To organize the large amount of information about genomics, proteomics and bioinformatics and offer basic knowledge of genome sequencing, major differences between prokaryotic and eukaryotic genomes, basic proteomics and its applications, , comparative and evolutionary genomics and applications.

Genomics

• Large scale genome sequencing strategies
• Genome assembly and annotation
• Genome databases of Plants, animals and pathogens
• Prediction of genes, promoters, splice sites, regulatory regions:
• Identification of SNPs, SNP database (DSNP).
• Role of SNP in Pharmacogenomics, SNP arrays
• DNA microarray: database and basic tools,

Comparative genomics:

• Basic concepts and applications,
• BLAST2, Mega Blast algorithms, PipMaker, AVID, Vista, MUMmer,
• applications of suffix tree in comparative genomics,
• Comparative genomics databases: Clusters of Orthologous Groups (COGs)

Proteomics

• Protein sequence database: Swissprot, Trembl, PIR
• Sequence analysis
• Primary and secondary structure analysis
• 3D structure prediction
• Model verification
• Energy minimization methods
• Structure based drug designing
• Targets identification
• Active site pocket identification
• Molecular docking studies

Course Module Type	Fees(INR)
7 Days Module / Workshop	6,000/-
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Immunoinformatics

Immunoinformatics is using the basic bioinformatics tools such as Clustal Omega, BLAST and Tree View as well as specialized Immunoinformatics tools, such as EpiMatrix, IMGT/V-QUEST for IG and TR sequence analysis. There are also tools which are used for T and B cell Epitope mapping, proteasomal cleavage site prediction, and TAP– peptide prediction. Immunoinformatics is capable of identifying virulence genes and surface-associated proteins. We describe various information regarding classical immunology, different immunomic databases, and B-cell and T-cell Epitope prediction tools and software's.

- Introduction to Immunoinformatics Basics
- Computational Vaccinology
- Use of Bioinformatics in immunology
- Genotyping methods & Disease gene identification
- Accessing genome agencies
- Vaccine database and Data mining
- Biostatistics
- Reverse Vaccinology & Vaccine screening
- Confirmatory tools and databases.
- MHC binding & Organ Transplant and Auto Immune diseases
- Epitope prediction and Servers & Vaccine candidate design
- Relevant Tools and Soft wares

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Bioperl

Bioperl is a toolkit of Perl modules useful in building bioinformatics solutions in Perl. In india offers BioPerl it can be used to parse sequence data retrieved from local and remote databases, to transform the formats of sequence data and files, to manipulate individual sequences, to search for patterns in sequences, to assist with creating and manipulating sequence alignments, and to search for genes, transposons, and other structures in genomic data.

Getting started with Perl

- Accessing and installing Perl and BioPerl
- Running Perl programs
- Editors
- Finding help
- Using modules, like BioPerl

The Art of Programming

The Programming process

- Algorithms
- Sequences and Strings
- Variables
- Arrays
- Files

Motifs and Loops

- Flow control
- String operators
- Writing files

Subroutines

- Scoping
- Arguments
- Command line arguments
- Passing data to subroutines
- Modules and Libraries
- Debugging

Data Structures and Algorithms for Biology

Hashes

- Translating DNA into Proteins
- Working with the FASTA Format
- Reading frames

Regular Expressions

- Restriction Maps
- Restriction Enzyme Data

Topics

A Working with GenBank data
B Analyzing DNA
C Working with BLAST output

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Bio python

This course focuses on programming and the development of new software tools to solve biological problems (as opposed to simply using existing tools). Prior programming experience is desirable but not required; on the other hand, students should be prepared to demonstrate a strong commitment towards learning a Programming language. Learning the basics of Python programming: different variables, reading files, writing files, conditional statements. Being able to write a basic Python script from scratch.

- Introduction to programming and Linux
- Simple python programs: Variables, assignment statements, arithmetic expressions, input and output statements.
- Control flow statements: if statements, while statements, for statements.
- Functions: general concept, declaration and calls, parameters.
- Simple data structures: arrays (implemented as Python lists), strings
- Files: reading and writing text files.
- Using python objects.
- Writing python objects and object oriented programming.
- Using python packages: numpy, matplotlib and Biopython.
- Algorithms and problem solving techniques – the course presents at least one sorting
- Algorithm in detail and introduces students to related topics such as run-time analysis.
- Program development – the process of writing longer programs by dividing tasks into methods and classes.

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Bio java

The Biopython Project is an international association of developers of non-commercial Python tools for computational molecular biology, as well as bioinformatics. BioPython is one of a number of Bioprojects designed to reduce code duplication. Biopython allows the usage of a number of popular bioinformatics algorithms, through the web or locally. Such approach makes easier both running the algorithm and the extraction of information from its output. The goal of the biojava project is to facilitate rapid application development for bioinformatics.

- Introduction to Biojava
- Core java and Biojava concepts
- Biojava programming concepts including all packages of biojava
- BioSQL programming with JDBC
- Project work

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Sr.No.	Course Name	Duration	Course Fees
1	Bioinformatics	7 Days 15Days 1Month 2Month 3Month	8000/- 10,000/- 15,000/- 20,000/- 24,000/-
2	Next Generation Sequencing (NGS)	1 Month	15,000/-
3	Computer Aided Drug Designing	1,2 Month	15,000/-
4	Protein modeling and Rational drug designing	1 Month	15,000/-
5	System Biology	1 Month	15,000/-
6	Chemoinformatics	1 Month	15,000/-
7	Pharmacoinformatics	1 Month	15,000/-
8	Genomics & Proteomics	1 Month	15,000/-
9	Immunoinformatics	1 Month	15,000/-
10	Bio Perl	1 Month	15,000/-
11	Bio python	1 Month	15,000/-
12	Bio java	1 Month	15,000/-

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