

Training Program on Next Generation Sequencing Data Analysis, Molecular Modeling and Docking

Batch Ist: Feb 8-13, 2012

Batch IInd: March 7-12, 2012

Venue: Bio-IT Serve Tech. Pvt. Ltd., New Delhi-34



Way to Enlighten Bioinformatics...

Introduction

Next Generation Sequencing (NGS) Data Analysis

This course teaches biologists how to analyze data from Next Generation Sequencing (NGS) platforms. Topics to be covered include the description of sequencing strategies and platforms, experiment types, data formats, and command line tools for various workflows, such as quantification of transcripts, alternative splice forms, copy number variants, single nucleotide polymorphism (SNP).

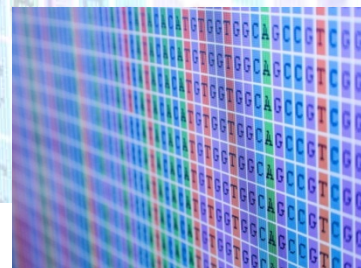
Molecular Modeling and Docking

It will cover fundamental concepts of protein structure, function and folding, with necessary mathematical background and some exposure to the practical aspects. Molecular docking aimed at giving practical experience on the basic methods of modeling of protein structures, ligands preparation and docking using bioinformatics tools.

Training Module

Module I: Whole genome sequence data analysis

- Quality control of raw reads
- Reference genome alignment
- Alignment statistics
- Genome annotation
- Variation analysis
- Comparative genome analysis
- Documentation



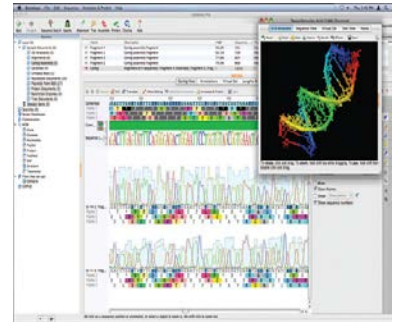
Module II: Transcriptome sequence data analysis

- Quality control of raw reads
- Sequence cleanup and filtering
- Reference genome alignment
- Alignment statistics
- Documentation



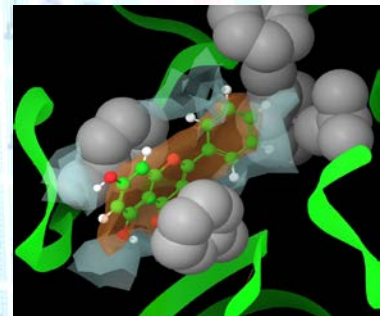
Module III: Annotation and quantification of transcriptome

- Transcriptome annotation
- AT/GC content
- Codon usage table and codon bias report
- Transcriptome quantification
- Alternative splicing events and Transcript Isoforms
- SNP discovery and UTR analysis
- *In-silico* subtraction (c-t) and (t-c) to identify difference in transcripts
- Differential expression analysis



Module IV: Molecular Modeling and Docking

- Protein structure prediction by using SWISS-MODEL
- Protein structure prediction by using MODELLER
- Protein structure optimization
- Protein structure visualization
- Protein structure preparation for docking
- Ligand preparation for docking
- Structure based drug discovery
- Ligand based drug discovery
- Protein-ligand interaction



Goal

- Understand experimental designing and analytic workflow NGS data analysis.
- Understand various NGS data formats.
- Large scale alignment and dealing with high-throughput sequencing data.
- Reads mapping and visualization in reference genome.
- Construction of protein model.
- Understand the concept of molecular docking.

Who Should Attend

Scientists, teachers and research students working in academic in various areas of Life Sciences, Microbiology, Biochemistry, Biotechnology, Pharmacy, Genetics, Plant Science, Nanotechnology, Biomedical Technology, Bioinformatics, Computer Science and Information Technology

Minimum qualification to attend this program

Post graduate or above in any discipline of life sciences

Required skills

- Basic skills with Linux command line.
- Internet browsing
- Basic programming concept

Selection Criteria

Selection will be based on first cum first basis. Preference will be given to active researchers, teachers and scientists. You will be informed by email.

Training Fees

₹ 24,983 (22, 650 +10.3 % Tax)

(To be paid only after selection)

D.D. should be drawn in favor of “Bio-IT Serve Technologies Pvt. Ltd.” payable at New Delhi.

Important Particulars

Batch Ist: **Feb 8-13, 2012**

Batch IInd: **March 7-12, 2012**

Last date of application: **31th Jan, 2012**(for batch Ist) and **29 Feb, 2012** (for batch IInd)

Intimation of selection: **1Feb, 2012**(for batch Ist) and **1 March, 2012** (for batch IInd)

Number of participants: **10**

Contact Details:

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