

Basic Training:

BASIC BIOINFORMATICS & BIOLOGICAL DATA MINING & ANALYSIS [demo & hands-on]

Bioinformatics exercises for molecular cloning-Selecting genes based on disease relevance or expression patterns Gene-based data mining: Entrez Gene, Gene cards, Uniprot, HPRD, UCSC, etc., Advanced strategies in literature-based data mining and biocuration ,Case studies for selected genes, proteins and diseases, Retrieving sequences of RNA or genes , Primer designing & restriction site analysis, Concepts in sequence analysis, Basic sequence analysis exercises, Advanced sequence analysis exercises

Intermediate Training:

DATA ANALYSIS FOR FUNCTIONAL-OMICS [demo & hands-on]

Relevance of transcriptomics & proteomics: mass scale gene expression techniques and corresponding data, Introduction to protein-interactions, non-coding RNA, ontology and pathways, Case studies on molecular interactions,Case studies on pathways,An overview on functional analysis process and tools

Gene Ontology information retrieval, Gene enrichment analysis using DAVID functional

Advanced Training:

ANALYSIS OF NEXT GENERATION SEQUENCING DATA (GENOMICS, METAGENOMICS & RNA-SEQ) [demo & hands-on]

An overview of NGS technology, NGS applications to genomics & transcriptomics, and conceptual discussions, FASTQ format, depth and coverage of reads, NGS data retrieval using SRA & ENA, Quality analysis and trimming of raw reads, NGS whole-genome & exome sequencing, and reference assembly, SNP analysis concepts & resources, Reference genomes retrieval using UCSC,Reference alignment of NGS reads, SNP analysis, filtering and annotation, De-novo assembly concepts and annotation process,De-novo assembly of reads to contigs, RNA-sequencing and concepts, Identification of gene & transcript levels, and differential expression, Metagenomics, the need & approach, and resources, Metagenomics analysis of NGS reads