



innovations from nature



acib Service Offer

BIOINFORMATICS SERVICES

acib has extensive expertise in a wide range of bioinformatics areas and can support companies to analyze data generated from high-throughput OMICS technologies.

Background

State-of-the-art next-generation sequencing, transcriptomics, proteomics, metabolomics and other high-throughput OMICS technologies enable the efficient generation of large experimental data sets. This shifted the bottleneck in biotechnological/biomedical studies from data generation to data analysis. Although the analysis of individual OMICS data sets is relatively mature, detailed understanding of the existing tools is required to analyse the data properly. Integrative analysis of data sets from the same sample applying different OMICS technologies gets more and more important and is a very active research area.

acib-Technology

We apply and develop state of the art tools for the management and bioinformatics/biostatistics analysis of data from high-throughput OMICS technologies, either individually or integratively.

acib-Offer

Data management: Management of data from fermentations (online and offline), DNA-microarrays, qPCR, proteomics (gel-based and MS/MS based). Application for SOP generation and management, experiment management and image storage. All applications are web-based and provide a sophisticated authentication and authorization system, allowing definition of fine-grained access policies to the data.

De novo genome assembly, finishing and annotation: De novo assembly of genomic sequences (bacteria, fungi, higher eukaryotes) from different sequencing technologies (Roche 454, Illumina, Ion Torrent, Pacific Biosciences). Quality checks for assemblies. Selection of the optimal sequencing strategy based on the project requirements. Scaffold ordering and orientation, gap closing. Integration of Sanger reads into the final genome assembly. Identification of rRNAs, tRNAs, ORFs, intron/exon structure and repeats; annotation via homology, visualization of genomes, creation of EMBL / Genbank files, submission to EMBL / Genbank.

Strain characterization & comparison: Identification of integration sites, characterization of position and multiplicity, identification of side effects of the integration. Characterization of strain differences, large insertions and deletions, smaller variations (SNPs, Indels) their effects on protein coding genes.

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Transcriptome sequencing, assembly and characterization: Selection of optimal sequencing strategy and sample preparation. De novo assembly of transcriptomic sequences. Isoform identification for eukaryotes. Improvement of genome assemblies and annotation based on transcriptome sequences. Annotation of transcripts, protein domain identification, clustering.

Secretome characterization: Identification of putatively secreted proteins, based on a transcriptome analysis or protein sequence data.

RNA-seq analysis: Analysis of RNA-seq gene expression data: mapping to reference genome, peak detection, identification of differentially expressed genes, clustering, gene set enrichment analysis (GO, KEGG pathways, ...), mapping of gene expression data onto pathways.

DNA-microarray analysis: Analysis of DNA-microarray gene expression data: normalization, identification of differentially expressed genes, clustering, gene set enrichment analysis (GO, KEGG pathways, ...), mapping of gene expression data onto pathways.

qPCR data analysis: Analysis of qPCR gene expression data: normalization, identification of differentially expressed genes. Identification of housekeeping genes for certain conditions to be used for normalization.

ChIP-seq analysis: Analysis of transcription factor binding or histone modification data: mapping onto reference genome, peak detection, annotation, identification of differentially bound sites, motif identification and visualization.

Methylation analysis: Analysis of DNA methylation patterns derived from bisulfite sequencing: mapping onto reference genome, methylation detection, annotation, identification of differentially methylated sites and visualization.

Microbiome analysis: Characterization of microbial communities based on amplicon sequences. Quality filtering, clustering, classification, calculation of alpha and beta diversity, rarefaction analysis, community comparison, identification of differentially abundant OTUs, visualization of results.

Metagenome analysis: Characterization and comparison of metagenomes.

Integrative -omics analysis: Integrative analysis of datasets originating from different -omics technologies applied to the same samples (e.g. transcriptome, proteome, metabolome), by applying data reduction and mapping methods.

LC-MS/MS based proteomics: Identification of peptides and proteins, clustering, comparison of the proteome of different samples. Comparison of multiple samples, annotation of individual proteins (conserved domains, GO terms, enzyme class, ...).

LC-MSⁿ based lipidomics: Identification and quantification of lipid species in a sample based on LC-MS (or LC-MS/MS) data. Data normalization, sample comparison and visualization.

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