USC Libraries Bioinformatics Service

About Our Service

The USC Libraries Bioinformatics Service helps USC faculty, staff and students with their bioinformatics needs and facilitates interdisciplinary collaboration on 'omics research.

Free Access

All software and resources are available to USC users at no cost. You can find access request forms on our website: nml.usc.edu/bioinformatics/software

User Training

Both in-house developed and vendor training workshops are offered. Tutorials, materials and recording of previous training workshops can be found on the individual software page. nml.usc.edu/bioinformatics/workshop

Premium Bioinformatics Tools

We license and provide free access to a comprehensive collection of premium bioinformatics software to USC faculty, staff and students.

Literature Search & Study

Quickly locate relevant literature as well as expert-curated findings on genes, proteins, diseases, drugs, etc.

- Qinsight
- Ingenuity Pathway Analysis
- BaseSpace Correlation Engine
- BIOBASE

Public Genomic Data Mining

Explore and mine huge collections of pre-analyzed public genomic data to help hypothesis formulation, experimental design and results interpretation.

- BaseSpace Correlation Engine
- Oncomine
- Genevestigator Advanced

Making Sense of Gene Lists—Downstream functional analysis

Find the most relevant molecular functions, canonical pathways, diseases, and interactive networks for gene lists.

- Ingenuity Pathway Analysis
- BaseSpace Correlation Engine
- Ingenuity Variants Analysis

Making Sense of Gene Lists—Upstream regulation analysis

Find the transcription regulators (transcription factors, microRNA etc.) affecting the observed gene expression patterns in a list of genes.

- Ingenuity Pathway Analysis
- TRANSFAC (BIOBASE)

NGS Data Analysis

Analyze raw and aligned NGS data (RNA-seq, ChIP-seq, DNA-seq, etc.) with open source and proprietary bioinformatics and biostatistics methods.

- Partek Flow
- CLC Genomic Workbench
- Galaxy
- Partek Genomics Suite

Microarray Data Analysis

Analyze all types of microarray data (gene/exon expression, SNP/CNV, methylation, microRNA, etc.) with these user-friendly tools.

- Partek Genomics Suite

USC University of Southern California

USC Libraries | Bioinformatics

Next Generation Sequencing Data Analysis Support

Free software/hardware integrated biocomputing resources

Norris Medical Library and Wilson Dental Library

Hardware: Four Dell Precision T3600/T7910 workstations (6-core Intel Xeon processors, 48-128GB RAM); 120 TB total storage
Software: Partek Flow, Partek Genomics Suite; CLC Gx with Microbial Genomics and Genome Finishing Modules; Galaxy, R & Bioconductor

Bioinformatics Servers

Hardware: Two Dell PowerEdge R630 servers, dual 12-core Intel Xeon processors, 512GB RAM, 30TB RAID storage
Software: Partek Flow, Partek Genomics Suite; CLC Gx with Microbial Genomics and Genome Finishing Module; Galaxy, R & Bioconductor

Dedicated Computing Cluster in USC High-Performance Computing

Hardware: One head node and 9 worker nodes. Each with dual processors (AMD Opteron 6176 or Intel E5-2650, 48/64 GB RAM)
Software: Partek Flow

Consultation on Experimental Design and Data Analysis Service

We provide **free consultation** on NGS experimental design and data analysis. We also provide collaborative data analysis service whenever possible. Use the contact information below to tell us your needs!

On-demand Service

For your specific research questions, we offer:

- Individual and group consultation on bioinformatics resources and applications
- Instruction and training on using our licensed bioinformatics software
- Collaborations on bioinformatics analysis of 'omics data
- Bioinformatics support of grant application

Stay Informed

Join our mailing list to stay informed about the latest training and offerings.
https://tinyurl.com/nmlbio-l

Website: nml.usc.edu/bioinformatics

Locations: Norris Medical Library, 203A (HSC)
Wilson Dental Library, DEN21 (UPC)

Contact: Yibu Chen, Meng Li, Eddie Loh
nmlbio@usc.edu

High-throughput Data Analysis Tools

Partek Genomics Suite

Advanced statistical analysis and visualization tool for microarray and NGS data

- Complete data analysis workflows for all major types of microarray and NGS data, such as:
  - Gene expression and exon arrays
  - SNP and copy number arrays
  - Methylation arrays and ChIP-chip
  - RNA-seq, DNA-seq, ChIP-seq, microRNA-seq
- Direct data import from all major platforms
- Versatile visualizations (PCA plot, histogram, heatmap, dot plot, etc.)
- Genomic data integration

Partek Flow

Web-based application for NGS data alignment, QA/QC, gene expression, variant detection and more

- Complete RNA-seq analysis workflow with proprietary differential expression methods
- Workflows for DNA-seq, ChIP-seq, and single-cell sequencing data analysis
- Speedy implementation of popular open-source aligners, including TopHat2, BWA, Bowtie2, TMAP, Isaac2, STAR, GSNAP, SHRiMP2
- PCA, hierarchical clustering, k-means clustering
- Integrated genome browser

CLC Gx with Microbial Genomics Module

Cutting-edge tools for molecular biology and genomic research, particularly NGS data

- RNA-seq/small RNA-seq analysis pipeline
- Local realignment, variant detection and annotation
- ChIP-seq peak calling and annotation
- Bisulfite sequencing analysis
- De novo assembly
- Primer design, protein analysis, cloning and cutting
- Microbial Module for Metagenomics analysis

Galaxy

Web-based platform with many cutting-edge tools for genomic research, particularly NGS data

- Popular open-source tools for analyzing NGS data
- ChIP-seq
- DNA-seq
- RNA-seq
- File manipulation and data visualization (BedTools, samtools, Deeptools, NGSplot, Picard)

Vector NTI Advance

Comprehensive software package for DNA/ protein sequence analysis and manipulation

- Recombinant cloning strategies and protocols preparation
- PCR primer design and analysis
- Multiple DNA/protein sequence alignment
- DNA sequence assembly
- DNA/protein annotation and visualization

Vector NTI Advance®

See next page for functional genomics tools

- Pathway/network analysis
- Transcription regulation analysis
- Public genomic data mining
- Advanced literature study

Functional Genomics Software Tools

Ingenuity Pathway Analysis

Ingenuity Variants Analysis

- Excellent literature-based pathway, network, and functional analysis tool for gene lists
- Infer upstream regulator and causal network for a list of differentially expressed genes
- Rich annotation of your variants call result (VCF)
- Find disease-causing variants faster
- Narrow down variants with powerful genetic and statistical tools
- Gateway to extensive cohorts of diverse human genome samples.

INGENUITY SYSTEMS

BIOBASE

Comprehensive biomolecule knowledgebase for proteins, transcription factors, and mutations

- Comprehensive protein knowledgebase (PROTEOME)
- Largest eukaryotic gene transcriptional regulation knowledgebase (TRANSFAC)
- Transcription factor binding site prediction (MATCH)
- Infer function for novel proteins (KnowledgeTransfer)

BIOBASE BIOLOGICAL DATABASES

BaseSpace Correlation Engine

Advanced search and analysis of curated and pre-analyzed public genomic data and PubMed

- Search over 21,000 pre-analyzed public genomic studies (expression, mutation, copy number changes, methylation, etc.) for targeted genes, diseases, or chemicals
- Power search and easy visualization of PubMed abstracts and clinical trials. Quick grasp of key concepts with ad-hoc keyword extraction and tag cloud display

BaseSpace CORRELATION ENGINE

Qinsight

Powerful relationship search of PubMed abstract and full-text literature

- State-of-art AI-driven text mining of 24 million PubMed abstracts, 4.5 million full text journal articles, and US Patent and grant proposals
- Quickly retrieve relationships among diseases, genes, drugs, and other concepts.
- Versatile and easy search with Power Term® and natural language expression query

Qinsight™

Oncomine Research Premium

World's largest cancer transcriptome profiles database and data-mining platform

- Determine expression profiles of selected gene(s) across 41 cancer types, tissues, perturbations, treatments, or other clinical parameters
- Analyze your own sets of genes or signatures against all Oncomine concepts (gene sets)
- Use Outlier-analysis for biomarkers discovery
- Use Meta-analysis to look for consistency across independent experiments

ONCOMINE research premium edition

Genevestigator Advanced

Multi-organism pre-analyzed microarray database and gene expression meta-analysis tool

- Explore gene expression patterns using Meta-Profile analysis tool
- Identify genes specifically expressed in given experimental conditions for biomarker discovery
- Identify co-expressed genes under various experimental conditions with bi-clustering analysis
- Find the most stably-expressed genes as qPCR reference genes

GENEVESTIGATOR shaping biological discovery