USC Libraries

BIOINFORMATICS SERVICES

COMPUTING RESOURCES

To support computation-intensive data analysis, the USC LIBRARIES has purchased several high-performance computer workstations and also teamed up with USC HIGH PERFORMANCE COMPUTING to provide users access to a wide range of bioinformatics computing resources. To further facilitate user data analysis, a variety of bioinformatics software have been installed on these computers.

"We are grateful for the exceptional support the USC Libraries Bioinformatics Core has been providing our lab and the school of Gerontology over the last few years. The expertise, professionalism, and courtesy of their team is unmatched."
—Pinchas Cohen, MD
   Dean, USC Leonard Davis School of Gerontology

"The Bioinformatics program provides extremely good training for our researchers and is always available to help solve problems."
—Yang Chai, DDS, PhD
   George and MaryLou Boone Professor of Craniofacial Biology,
   and Associate Dean, Ostrow School of Dentistry of USC

"The USC Libraries Bioinformatics Service educates and empowers our students and research fellows in the application of powerful analytical tools to examine a range of biomedical data. This resource has facilitated several exciting discoveries in our laboratory."
—Andrew McMahon, PhD, FRS
   W. M. Keck Provost Professor of Stem Cell Biology and Regenerative Medicine,
   and Biological Sciences, Keck School of Medicine of USC

BIOINFORMATICS SERVICES
libraries.usc.edu/bioinformatics

CONTACT
nmlbio@usc.edu

MAILING LIST
libraries.usc.edu/bioinformatics/mailing-list

OFFICE LOCATIONS
UPC: Electron Microscopy and Microanalysis Center | CEM 202
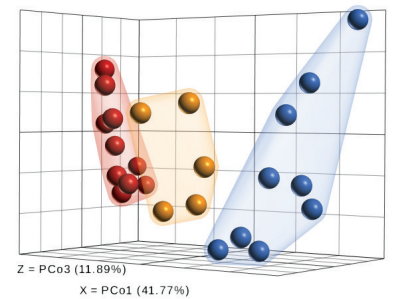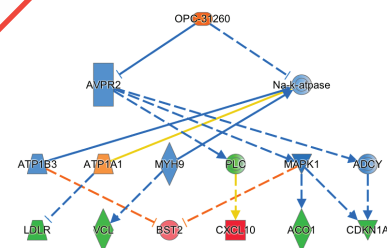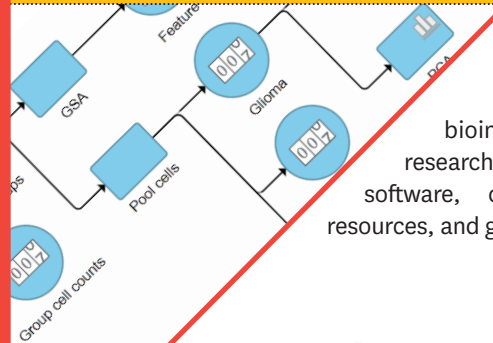HSC: Norris Medical Library | NML 203
usc.edu/maps

USC Libraries

ABOUT THE PROGRAM

The USC Libraries offers a university-wide bioinformatics support service that provides research consultation and training, bioinformatics software, collaborative data analysis, computing resources, and grant applications support.

SERVICES

CONSULTATION is available to individuals, departmental units, and lab groups to address bioinformatics-related research questions and needs. The bioinformatics team offers in-person meetings, emails, or phone calls, special lectures, support letters for grant applications, or collaborative data analysis for complex high-throughput projects.

WORKSHOPS AND TRAINING SESSIONS on software usage, as well as specialized bioinformatics topics, are scheduled regularly or by request. Subscribe to our mailing list to receive the latest announcements.

PREMIUM BIOINFORMATICS SOFTWARE TOOLS are available to USC researchers. Check the bioinformatics web page to learn more about their features, functions, and access instructions.

BIOINFORMATICS COMPUTING RESOURCES, including virtual servers and workstation computers, are available to support the analysis of high-throughput genomic data.

SOFTWARE TOOLS

NGS DATA ANALYSIS TOOLS

Next-generation sequencing generates massive amounts of data that require further bioinformatics processing and analysis. We have subscriptions to multiple commercial and open-source software packages that are able to perform a wide repertoire of analysis tasks. These intuitive software packages are available to all USC researchers.

Typical Analysis Tasks

Sequencing quality control and alignment

Single-cell population classification

Genome and transcriptome assembly

Differential expression analysis

Alternative splicing and novel gene discovery

Variant detection, annotation, and filtering

Peak calling and annotations

Microbial community analysis

Publication-ready graphics generation

Main Supported Data Types

RNA SEQUENCING (whole transcriptome, targeted RNA, small RNA)

DNA SEQUENCING (whole genome, whole exome, ChIP-seq, targeted resequencing)

SINGLE-CELL SEQUENCING

BISULFITE SEQUENCING

MICROARRAY

Available Software

Partek Flow | Partek Genomics Suite | CLC Genomics Workbench with Microbial Module | Galaxy (local server)

FUNCTIONAL ANALYSIS TOOLS

Functional analysis is an important procedure to investigate the biological underpinnings of your experiments. Several top-of-the-line and well-cited functional analysis software packages are available for use.

Typical Analysis Tasks

Find out which pathways, molecular functions, diseases, or networks are potentially impacted

For a list of (perturbed) genes, infer upstream regulators that lead to the observed gene expression changes

Annotate variants and apply sophisticated filtering to uncover the most relevant or novel variants

Gene set enrichment analysis

Compare your results with thousands of public studies to gain insights and form novel hypotheses

Available Software

Ingenuity Pathway Analysis (IPA) | Ingenuity Variant Analysis (IVA) | BaseSpace Correlation Engine | TRANSFAC/PROTEOME

LITERATURE AND PUBLIC GENOMIC DATA MINING TOOLS

The USC Libraries subscribes to specialized human-curated or computational natural language processed knowledge bases that will greatly enhance your search efficiency. The Libraries also maintains software subscriptions that have preanalyzed public data, which can be mined and compared against your own, reducing weeks of search effort into a day.

Typical Analysis Tasks

Quickly find if there are any published relationships among diseases, genes, drugs, and other areas of your interest

Reanalyze public genomic datasets to support or refine your hypothesis

Available Software

Qinsight | Oncomine Premium | Genevestigator | BaseSpace Correlation Engine | Ingenuity Pathway Analysis