GEO

Gene Expression Omnibus

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Microarray Databases I

- GeneNetwork system: Open access standard arrays, exons arrays, and RNA-seq data for genetic analysis (eQTL studies) with analysis.
- UNC modENCODE Microarray database: Nimblegen customer 2.1 million array 6.
- UPSC-BASE: data generated by microarray analysis within Umeå Plant Science Centre (UPSC).
- UPenn RAD database: MIAME compliant public and private studies, associated with ArrayExpress.
- UNC Microarray database: provides the service for microarray data storage, retrieval, analysis, and visualization.

Microarray Databases II

- MUSC database: The database is a repository for DNA microarray data generated by MUSC investigators as well as researchers in the global research community.
- caArray at NCI: Cancer data, prepared for analysis on caBIG.
- ArrayTrack: ArrayTrack hosts both public and private data, including MAQC benchmark data, with integrated analysis tools.
- NCI mAdb: Hosts NCI data with integrated analysis and statistics tools.
- ImmGen database: Open access across all immune system cells; expression data, differential expression, coregulated clusters, regulation.

Microarray Databases III

- Genevestigator database: Gene expression search engine based on manually curated microarray data.
- **Gene Expression Omnibus (GEO)**: NCBI any curated MIAME compliant molecular abundance study.
- **ArrayExpress**: at EBI Any curated MIAME or MINSEQE compliant transcriptomics data.
- Stanford Microarray database: private and published microarray and molecule abundance database.

Source: http://en.wikipedia.org/wiki/Microarray_databases

GEO

Gene Expression Omnibus: a public functional genomics data repository supporting MIAME-compliant data submissions. Array and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.

MIAME: Minimum Information About a Microarray Experiment)

Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. Brazma et. al (2001) Nat Genet. 2001 Dec;29(4):365-71. PMID: 11726920 [PubMed - indexed for MEDLINE]

MIAME

- The raw data for each hybridization (e.g., CEL or GPR files)
- The final normalized data for the set of hybridizations in the study (e.g. gene expression data matrix)
- The essential sample annotation (e.g., compound and dose in a dose response experiment, class)
- The experimental design including sample data relationships (e.g. technical and biological replicates)
- Sufficient annotation of the array (e.g. gene identifiers, genomic coordinates, probe oligonucleotide sequences)
- The essential laboratory and data processing protocols (e.g., what normalization method)

Data Organization in GEO I

Original data (submitted by researchers)

- **Platform** record: summary description of the array template.
  GEO accession number: **GPL**xxx
- **Sample** record: individual sample data (genomic, phenotypic, experimental . . .)
  GEO accession number: **GSM**xxx
- **Series** record: a group of related samples, usually from one experiment or study.
  GEO accession number **GSE**xxx.

Data Organization in GEO II

Curated data (organized by GEO)

- **DataSet** records: a curated collection of *biologically and statistically comparable* samples reassembled by GEO staff form one or several series
  GEO accession number **GDS**xxx.
  For them GEO has data display and analysis tools.
- **Gene Profiles**: measurements for an individual gene across all Samples in a DataSet.

GEO Web Query

Query

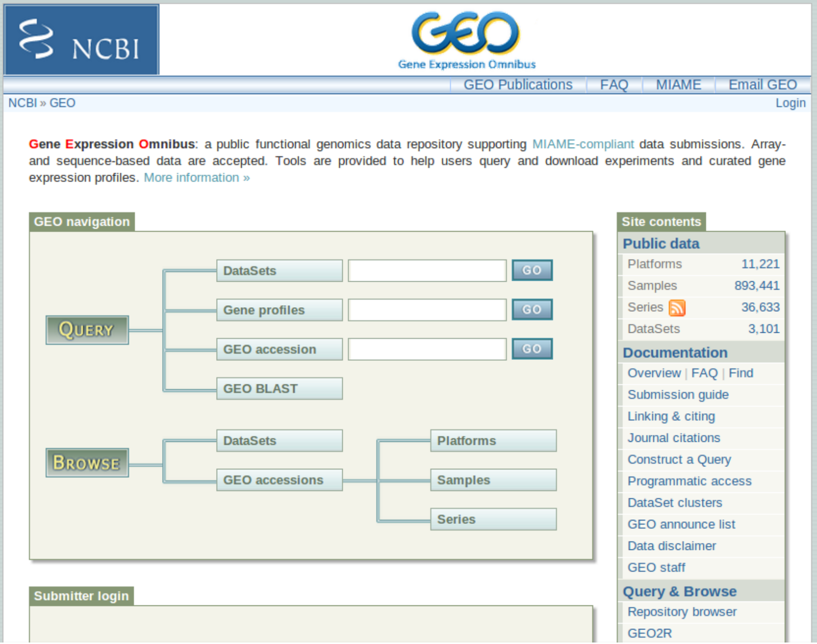
- DataSets: Stores curated gene expression DataSets.
  Search example: *melanoma*
- Gene profiles: Stores individual gene expression profiles from curated DataSets.
  Search example: *melanoma*
- **GEO accession**: Searches GEO Accessions.
  Search example: *GSE37761*

Browser: *nicer interface; exports searches*

- DataSets
  Search example: *melanoma*
- GEO accession: Platforms; Samples; Series
  Search example: *melanoma*

`http://www.ncbi.nlm.nih.gov/geo/`

GEO Web



Gene Expression Omnibus: a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles. More information »

Site contents

Public data

Platforms	11,221
Samples	893,441
Series	36,633
DataSets	3,101

Documentation

Overview | FAQ | Find

Submission guide

Linking & citing

Journal citations

Construct a Query

Programmatic access

DataSet clusters

GEO announce list

Data disclaimer

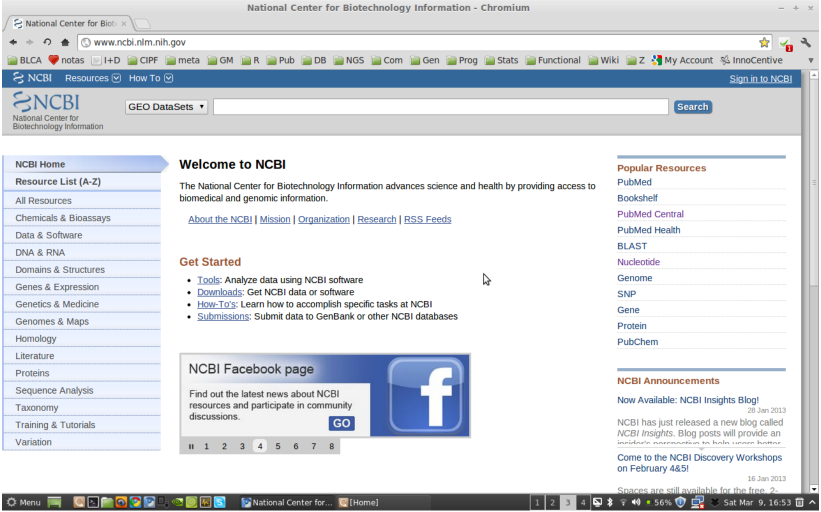
GEO staff

Query & Browse

Repository browser

GEO2R

GEO at NCBI



Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

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NCBI Announcements

Now Available: NCBI Insights Blog!

28 Jan 2013

NCBI has just released a new blog called *NCBI Insights*. Blog posts will provide an insider's perspective to help users better

Come to the NCBI Discovery Workshops on February 4&5!

16 Jan 2013

Spaces are still available for the free, 2-

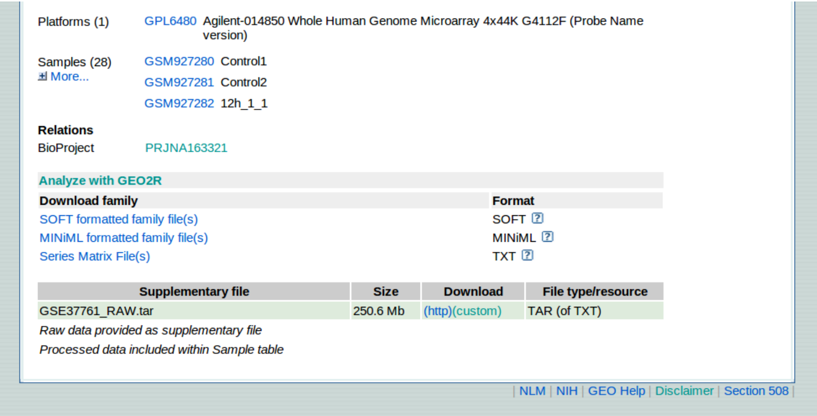
Usual searches

- Search for a GEO accession . . . form a publication.
- Search for example data for a particular platform
- Keyword
- Date . . .

Download GEO data

- Links on Series records are provided at the foot of each GEO Series record web page. Ex. GSE37761 web.
- FTP download: `ftp://ftp.ncbi.nlm.nih.gov/geo/`. Ex. `ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE37nnn/GSE37761/`
- Programmatic access to GEO: server-side programs to retrieve data; can be used with a fixed URL syntax.

Series Data Formats I



Platforms (1)	GPL6480	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
Samples (28) ⊞ More...	GSM927280	Control1
	GSM927281	Control2
	GSM927282	12h_1_1

Relations

BioProject	PRJNA163321

Analyze with GEO2R

Download family	Format
SOFT formatted family file(s)	SOFT ?
MINiML formatted family file(s)	MINiML ?
Series Matrix File(s)	TXT ?

Supplementary file	Size	Download	File type/resource
GSE37761_RAW.tar	250.6 Mb	(http)(custom)	TAR (of TXT)

Raw data provided as supplementary file

Processed data included within Sample table

Series Data Formats II

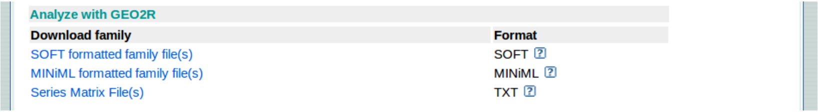
- SOFT formatted family file(s): complete data and metadata (gene information) in a single file.
- MINiML formatted family file(s): complete data and metadata in separated files.
- Series Matrix File(s): complete data in a tab delimited matrix; no metadata information.

- Supplementary files: usually raw data.

We generally use the *Series Matrix* format and may be the *platform* file within the *MINiML* folder.

GEO internal tools

GEO2R: simple analysis for GEO Series or DataSets



Analyze with GEO2R

Download family	Format
SOFT formatted family file(s)	SOFT ?
MINiML formatted family file(s)	MINiML ?
Series Matrix File(s)	TXT ?

- explore *Value distribution*: box-plot and summary statistics.
- explore single gene expression *Profile graph*
- perform a differential expression analysis to compare two or more groups of Samples.
- clustering (just for DataSets)

Bioconductor Packages

http://www.bioconductor.org/packages/release/

- GEOmetadb: A compilation of metadata from NCBI GEO.
- GEOsubmission: Prepares microarray data for GEO submission.
- GEOquery: **Get data** from NCBI Gene Expression Omnibus.

References

- http://www.ncbi.nlm.nih.gov/geo/info/
- http://en.wikipedia.org/wiki/Microarray_databases
- http://en.wikipedia.org/wiki/MIAME