

Web resources

NCBI (<http://www.ncbi.nlm.nih.gov/>)

Public repositories of published data.

GEO – Gene Expression Omnibus

Both microarray and next-gen sequencing from experiments related to gene expression

<http://www.ncbi.nlm.nih.gov/geo/>

SRA – Short Read Archive

Next-gen sequencing data from any sort of experiment; including gene expression.

<http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?>

UCSC Genome Browser (<http://genome.ucsc.edu/>)

For browsing reference genomes and associated data.

Currently has ~ 50 species genomes, all eukaryotic, of various stages of assembly.

Custom tracks for privately viewing your own data.

Sessions for storing and sharing data with others.

ENCODE, other publically available data.

Comparative genomics (phyloP and phastCons scores, elements, pair-wise nets-chains)

UCSC Table Browser (<http://genome.ucsc.edu/cgi-bin/hgTables?command=start>)

Downloading data stored on browser.

Joining tables by linked entries.

Intersecting tables (e.g. get only SNPs in coding regions of a gene annotation database).

Sending to Galaxy website for analysis

UCSC Cancer Genomics (<https://genome-cancer.soe.ucsc.edu/>)

Lots of cancer-related data already loaded.

Much more analysis functionality than regular browser site.

GO/COGs

AmiGO and links to lots of other GO programs

(<http://www.geneontology.org>)

GeneCodis (<http://genecodis.dacya.ucm.es/>) easy to use, and powerful, GO program.

Clusters of Orthologous Groups of proteins

(<http://www.ncbi.nlm.nih.gov/COG/>) Primarily for bacterial genes but also supports eukaryotes.

Galaxy (<http://main.g2.bx.psu.edu/>)

Online analysis of genomic data.

Easy interface with UCSC Genome Browser.

Operate on genomic intervals – merge overlapping regions, get flanking regions, etc.

Online analysis – statistics, regression.

New Next Gen Sequencing (NGS) Toolbox – QC, mapping, peak calling, etc.

Tutorials

OpenHelix (<http://www.openhelix.com/>)

Online bioinformatics tutorials, some free but many for a fee.