

NetworkAnalyst: Tutorial 1

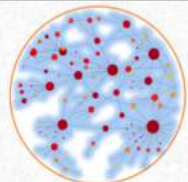
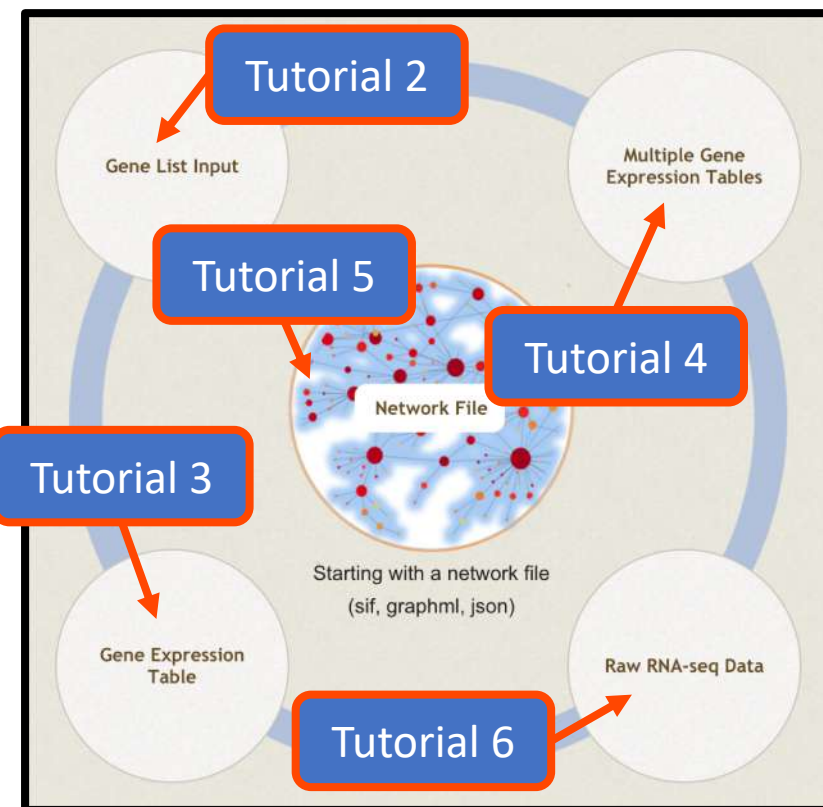
Overview

-- Gene expression, meta-analysis, functional profiling and network visualization, leading to system-level insights

Intro to NetworkAnalyst

- Web application that enables complex meta-analysis and visualization
- Designed to be accessible to biologists rather than specialized bioinformaticians
- Integrates advanced statistical methods and innovative data visualization to support:
 - Efficient data comparisons
 - Biological interpretation
 - Hypothesis generation

Tutorial 1: Overview

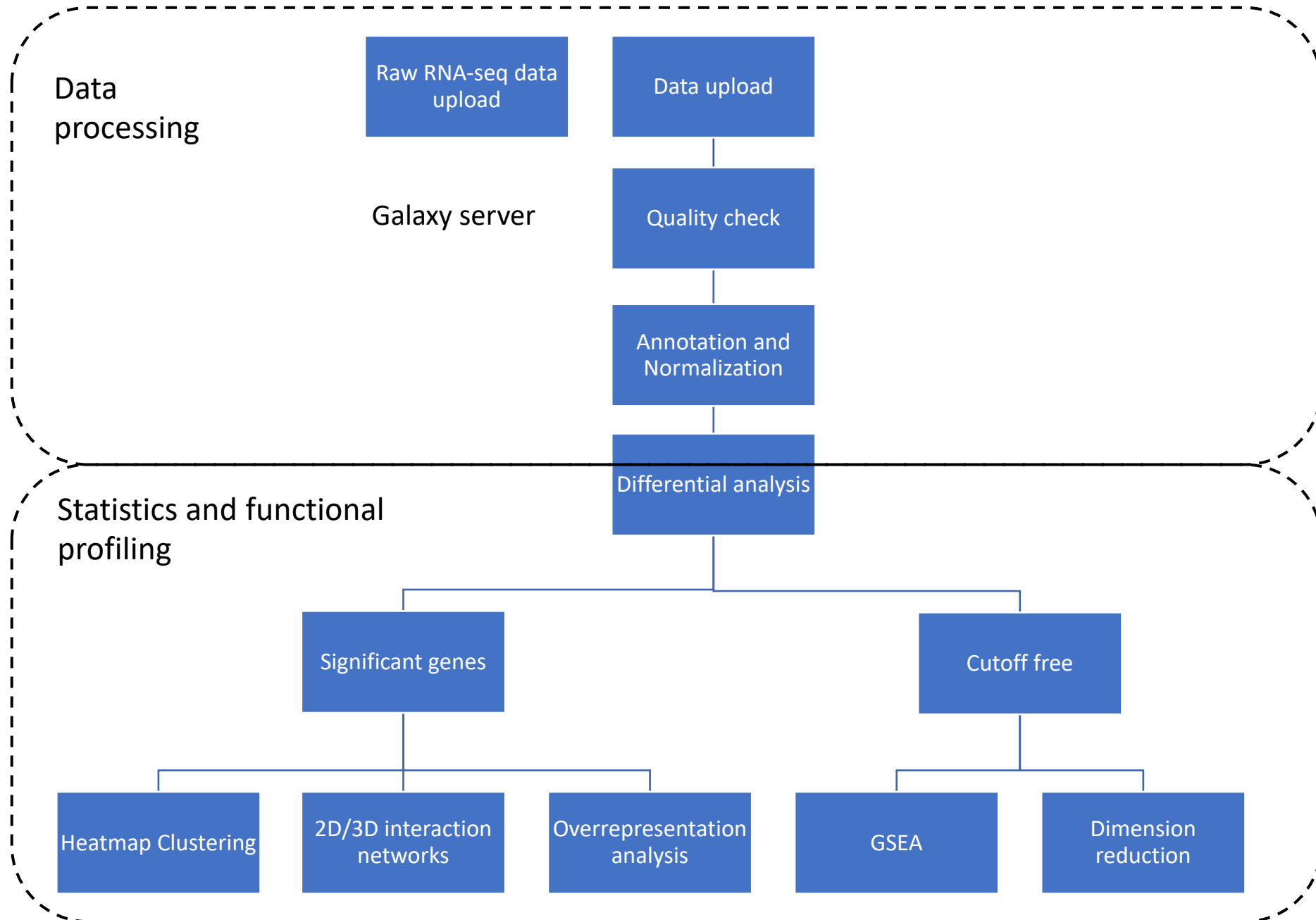


NetworkAnalyst -- a web-based platform for gene expression profiling & biological network analysis

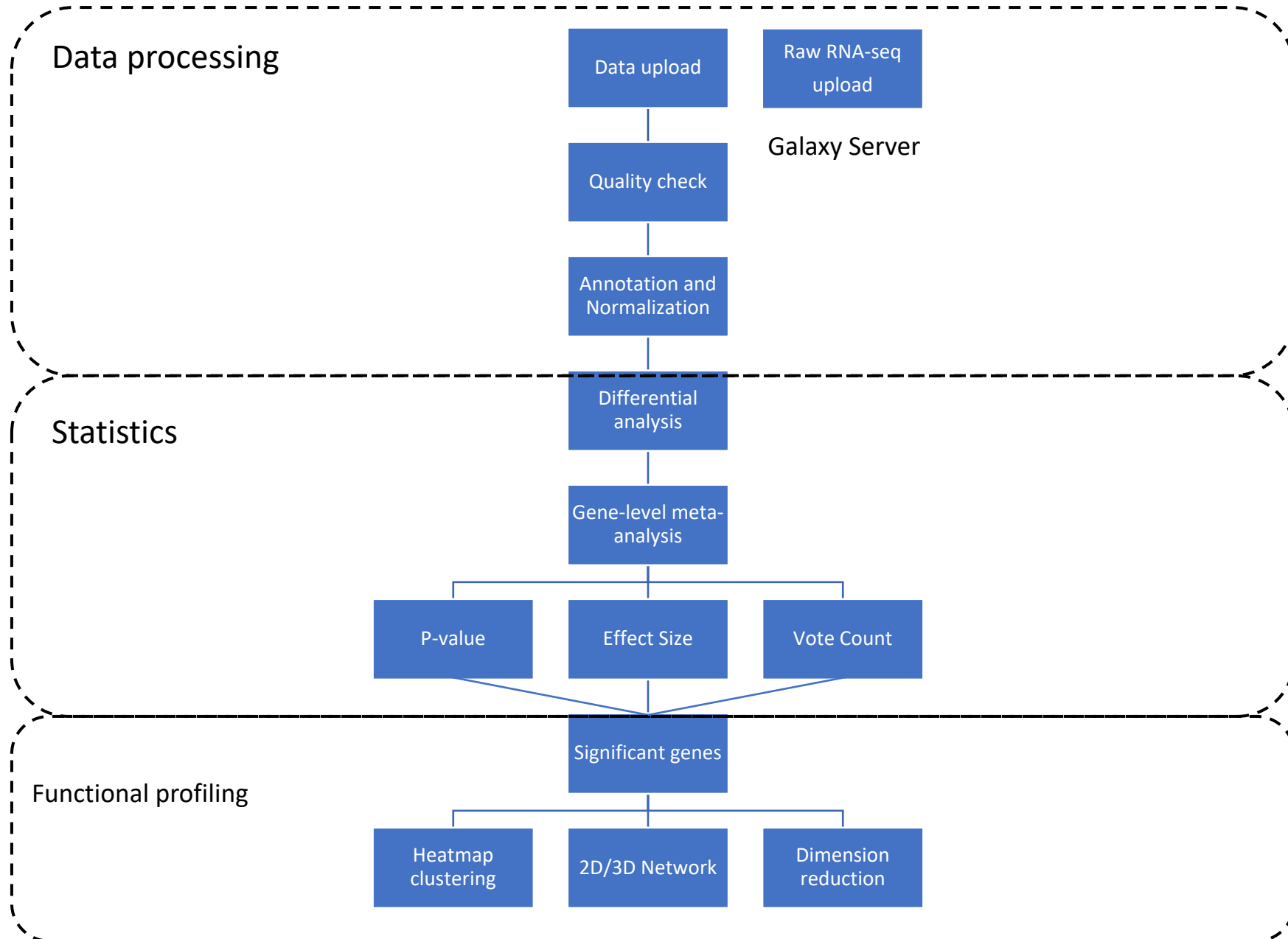
Overview

- Goal: To provide an integrative web-based framework for data processing, functional analysis and visualization of various forms of gene expression data.
 - Gene list(s)
 - Gene expression data (raw and processed)
 - Multiple gene expression data sets
 - Network files
- Overall approaches:
 - Advanced statistical methods coupled with interactive data visualization system.
- 50MB limit for data upload
 - ~300 samples for gene expression data with 20 000 genes

Single gene expression analysis



Gene expression meta-analysis



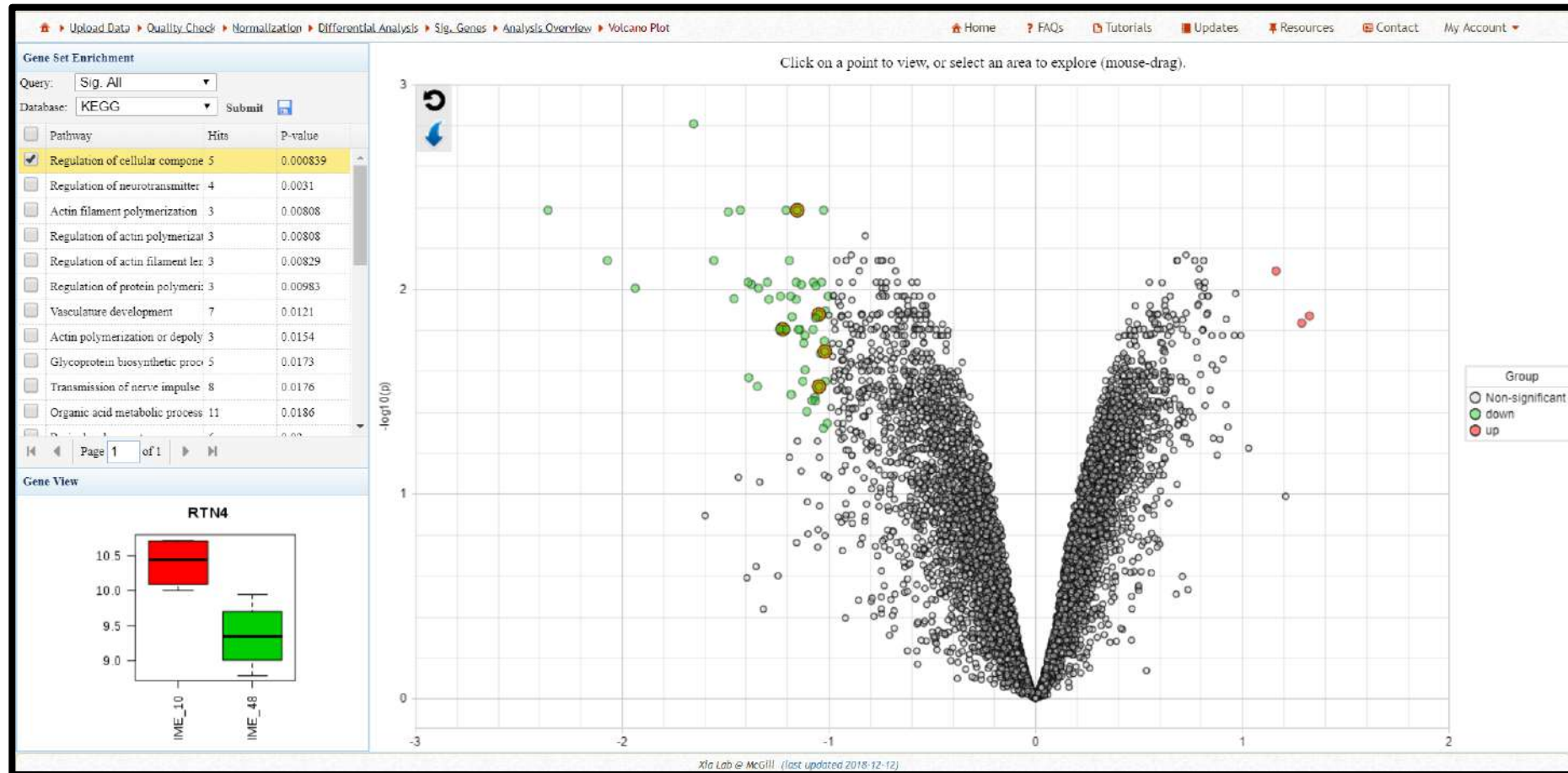
New features

- Process raw RNA-seq data through our Galaxy server
- Enable users to save work state
- Additional functional profiling methods (GSEA)
- Enrichment networks for visualization of functional profiling results
- Larger collection of interaction networks (beyond PPI)
- Support for 3D visualization and VR

Functional profiling

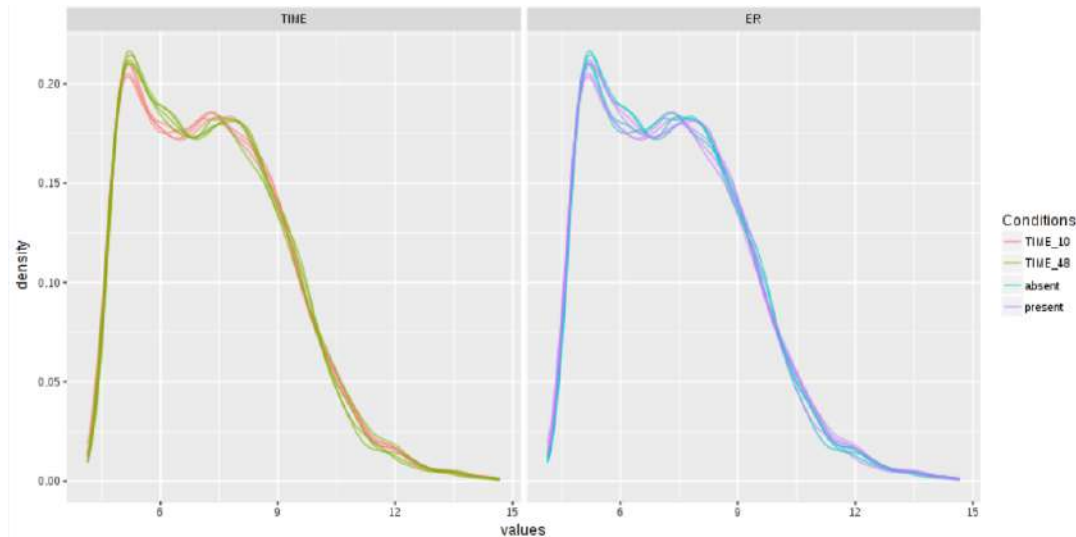
- Overrepresentation analysis (ORA)
- Cut-off free functional enrichment analysis methods
 - Gene Set Enrichment Analysis (GSEA)
- Interactive volcano plot
- Advanced diagnostic plots for quality check purposes
- Dimension reduction: 3D PCA, t-sne

Interactive volcano plot

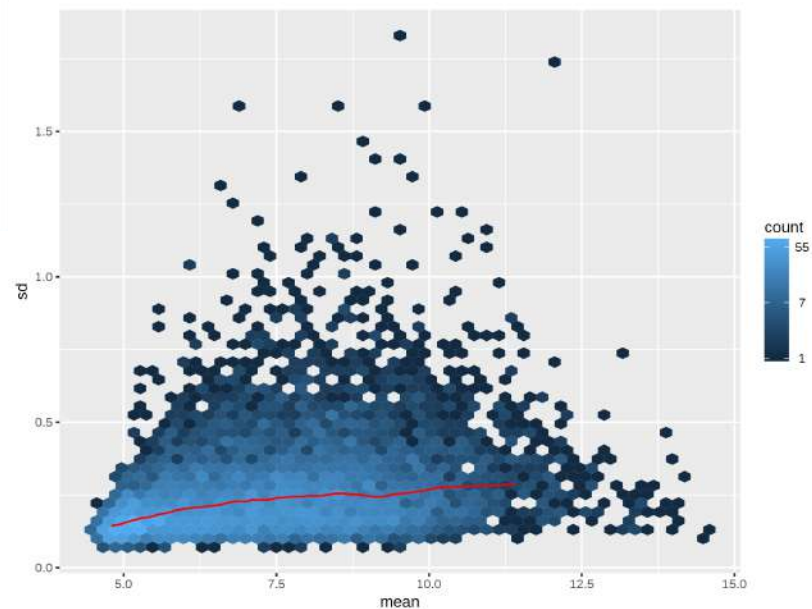


Diagnostic plots

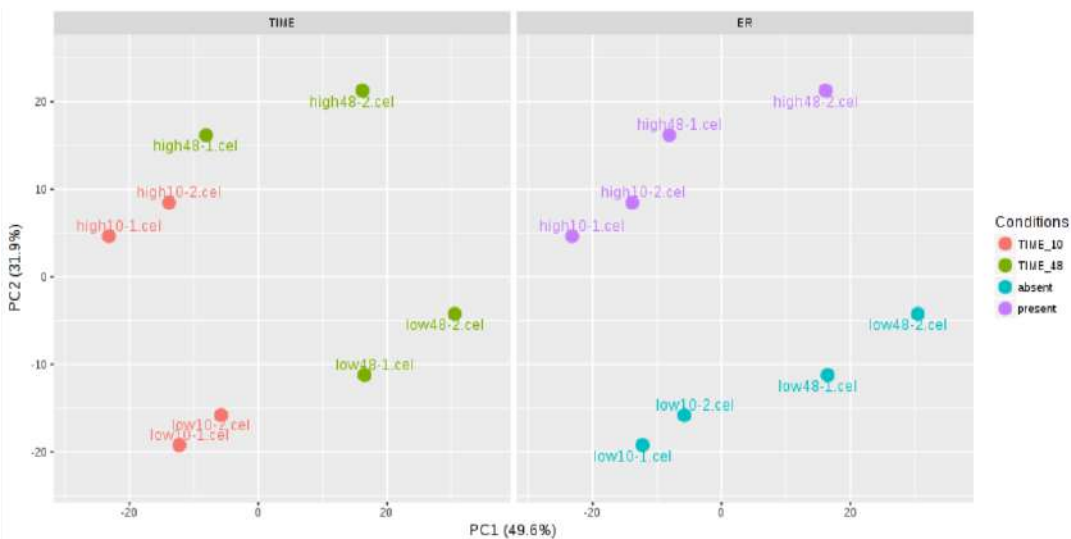
Density plot



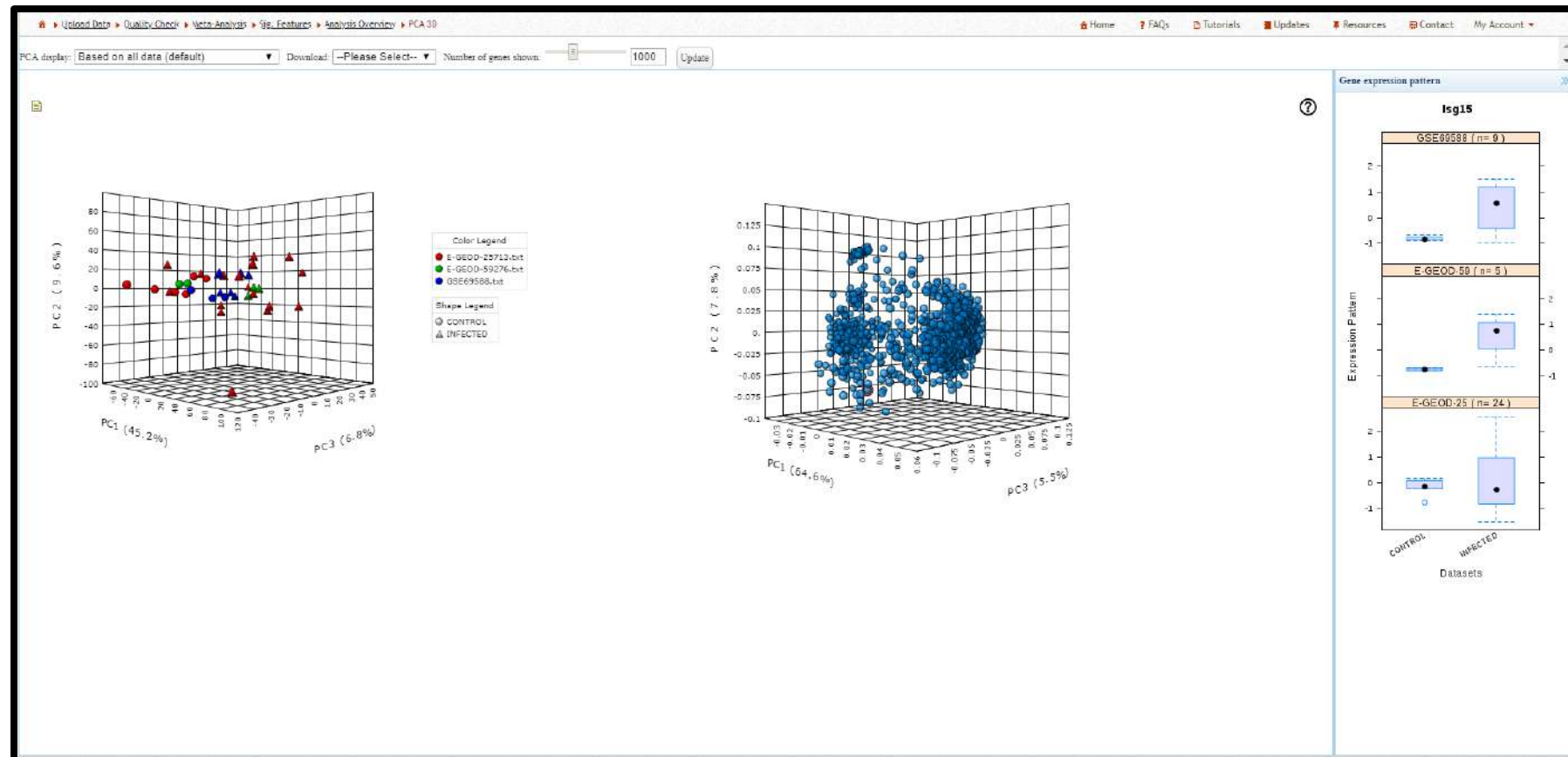
Mean Standard Deviation (MSD) plot



PCA plot

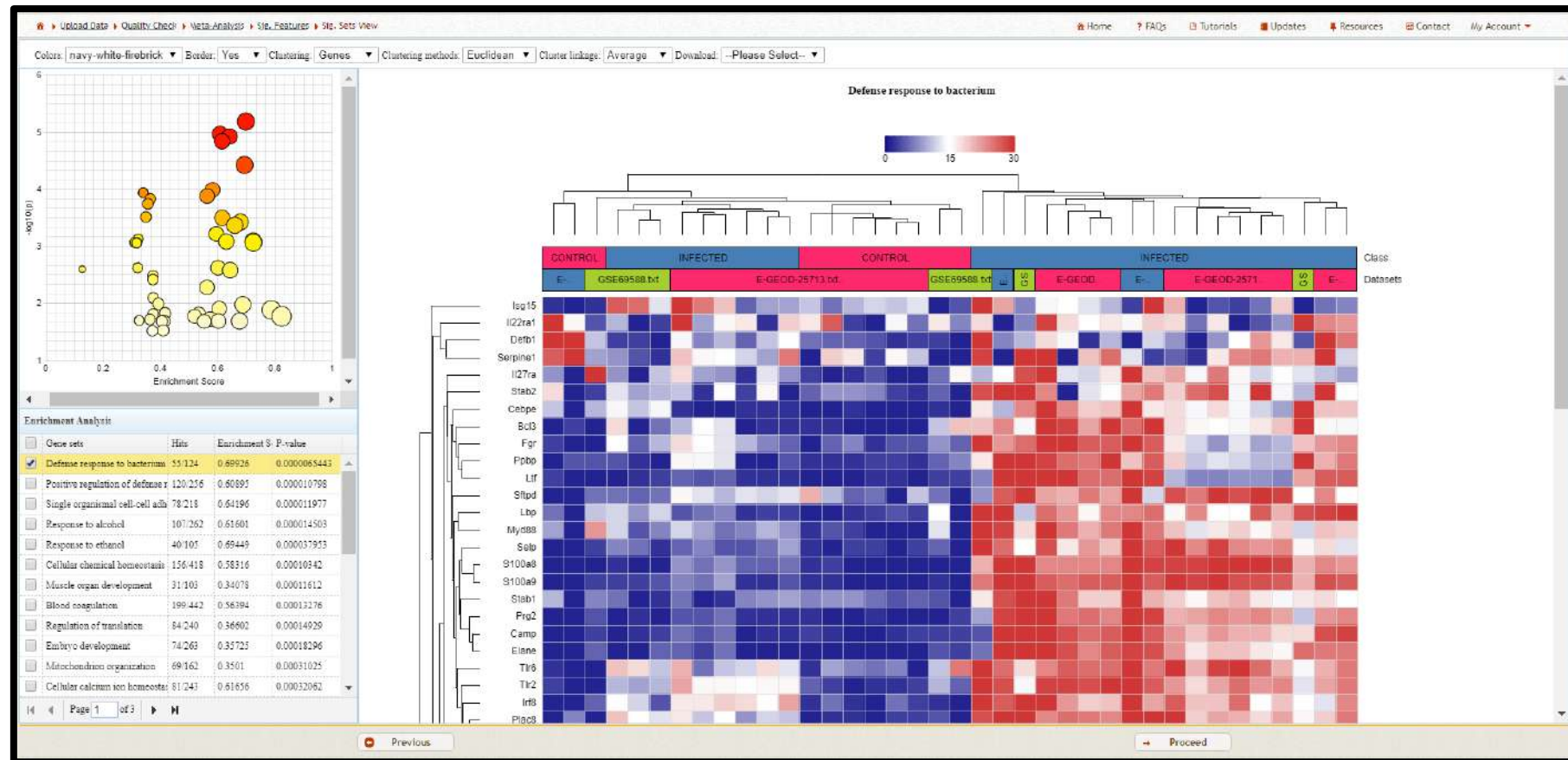


Dimension reduction: PCA



Synchronized view of score and loading plot

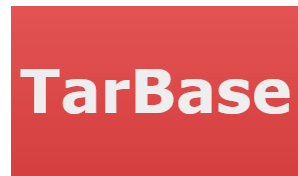
GSEA Heatmap Clustering



Network Analysis

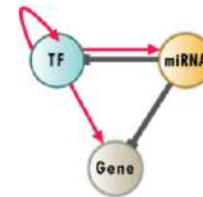
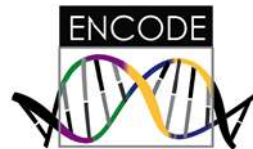
- Knowledgebase expansion including additional types of interaction:
 - Tissue specific PPI
 - Tissue and cell specific co-expression
 - TF and miRNA regulation
 - Gene-chemical, gene-drug, gene-disease networks
- Prize Collecting Steiner Forest (PCSF) algorithm to identify high confidence subnetwork relevant to the context.
- Additional customization features for 2D network visualization
- Added support for 3D and VR

Interaction databases



Immuno
Navigator

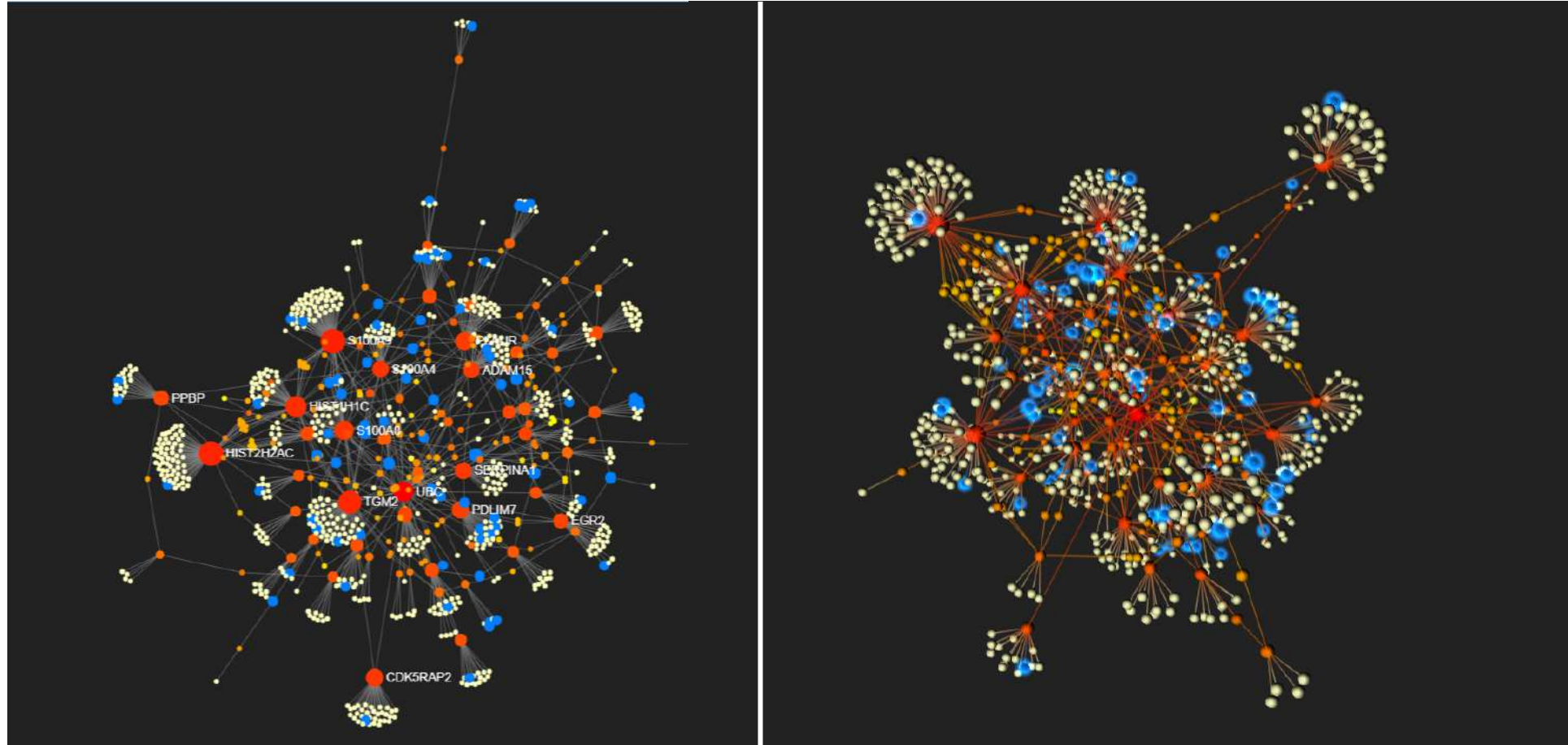
TCSBN : a database of tissue and cancer
specific biological networks



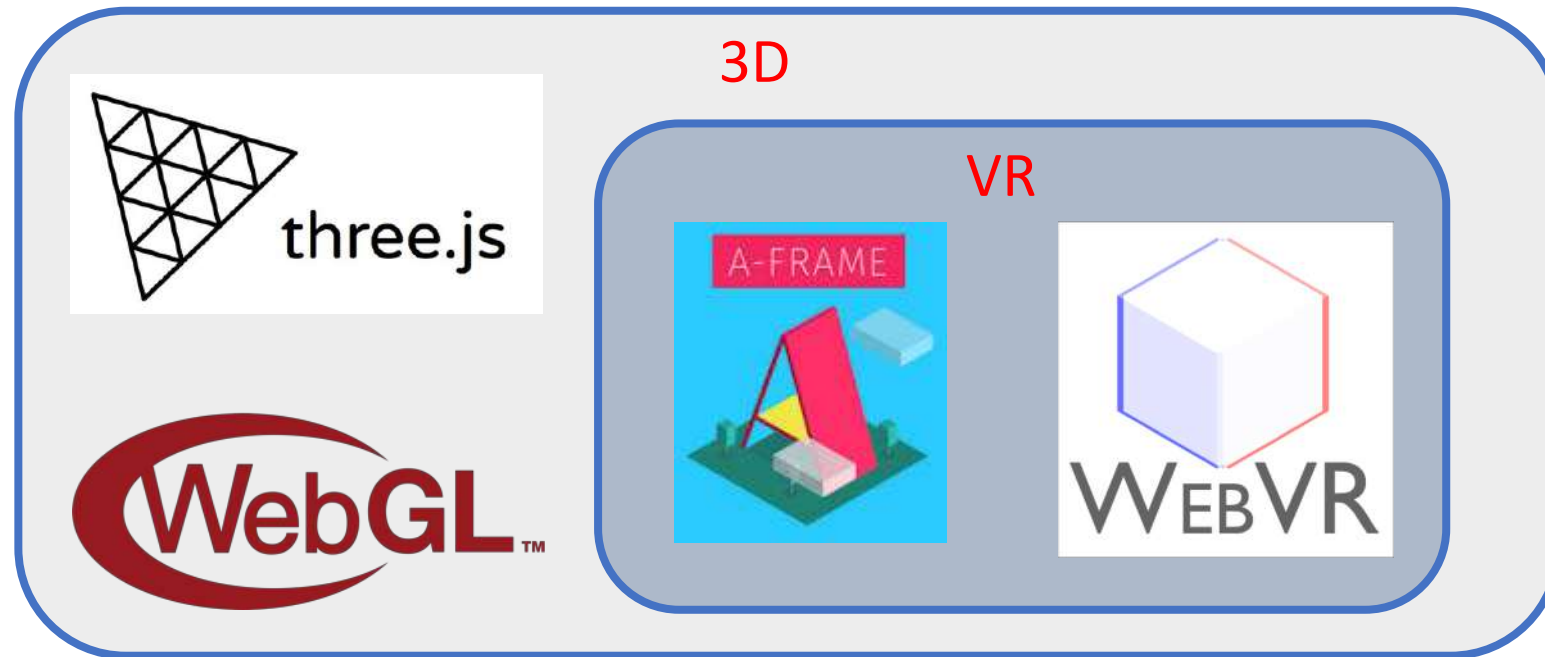
miRTarBase

RegNetwork

2D vs 3D



Implementation of 3D and VR



Galaxy server for processing raw RNA-seq data

- Galaxy is a web-based platform for integrating various computational tools and resources into a cohesive workspace for comparative genomics.
- NetworkAnalyst Galaxy server
 - You can easily upload your own data
 - 34 workflows (i.e. customized pipelines for RNA-seq raw data processing) are provided for 17 species and 2 different RNA-seq alignment programs
 - Results and step-by-step analysis can be recorded (Data Libraries and Histories)

Galaxy.networkanalyst.ca main page


Galaxy / NetworkAnalyst

Welcome to NetworkAnalyst Galaxy Server

This NetworkAnalyst Galaxy server is designed for mapping and quantification of raw RNA-seq data and it is integrated with [NetworkAnalyst](#) for statistical analysis and visualization.

How does it work?

If this is your first time to visit a Galaxy server and would like to gain more familiarity, please visit [Galaxy 101](#) for an introduction of several fundamental concepts.

- 1) **Account registration:** you need to first [register](#) in order to upload files to our server.
- 2) **Data upload:** to upload your RNA-seq **fastq.gz** files using FTP ([details](#)).
- 3) **Building collection:** this is a very practical step when you have tens or more of RNA-seq samples to process ([details](#)).
- 4) **Import workflow:** you need to first specify alignment program ([details](#)), sequencing type and organism. Click "View workflow". Then, just click on  icon at the top right corner to import the workflow.

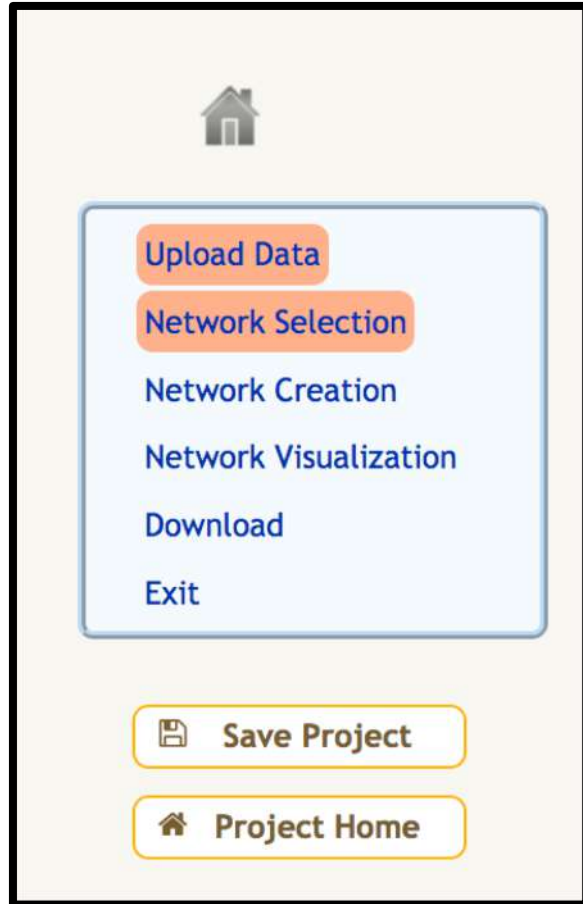
Alignment program: Sequencing type: Organism:

- 5) **Run workflow:** after importing workflow, you can visit the list of all imported workflows. From the drop down menu attached to the workflow name, click on "Run workflow".
- 6) Download your gene count table.

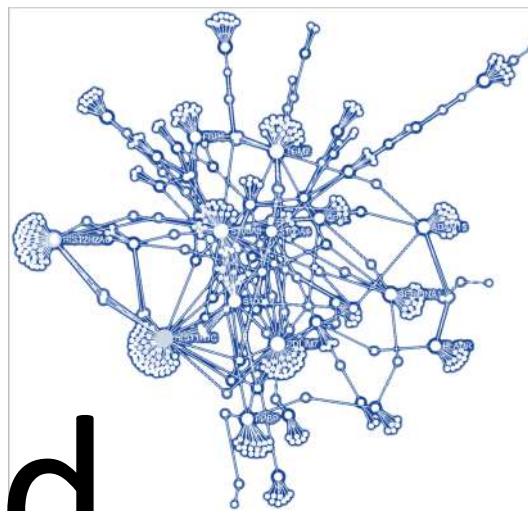
Choose alignment program, sequencing type and organism

Click on "View workflow"

New user registration system



- Allows recurrent users to register and save their work state.
 - The projects are saved for one year upon creation
- Total number of 10 projects are allowed.



The End

*For more information, visit the **FAQs, Tutorials, Resources,**
and **Contact** pages on www.networkanalyst.ca*