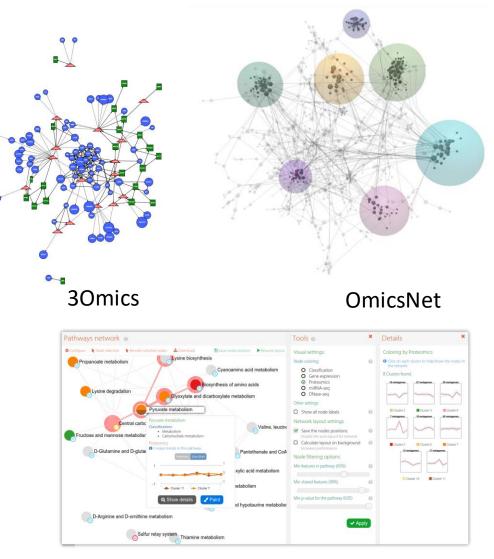# OmicsAnalyst

- a comprehensive platform for visual analytics

of multi-omics data

Existing web-based tools

- **3Omics**: Correlation and co-expression analysis coupled with functional enrichment and pathway analysis

- **Paintomics**: Mapping to KEGG pathways coupled with visualization and functional enrichment

- **IMPaLA**: Joint pathway over-representation and enrichment analysis with transcriptomics/proteomics and metabolomics data.

- **OmicsNet**: Mapping to molecular interactions for 3D network visual analytics coupled with functional enrichment analysis

- **GeneTrail2**: Multiple-omics integration coupled with enrichment analysis and identification of dysregulated subnetwork
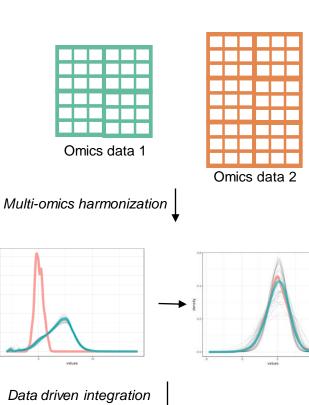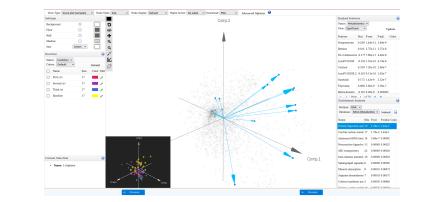
3Omics

OmicsNet

PaintOmics

Overview

- Gap
  - Most bioinformatics tool dedicated for data-driven multi-omics integration are standalone and require programming knowledge. Existing web-based tools mainly focus on knowledge-driven multi-omics integration through pathway and enrichment analysis.
- Goal
- To provide an intuitive platform for clinicians and bench scientists to perform multi-omics integration in a data-driven and unbiased manner.
  - Omics abundance tables and corresponding metadata
  - Supports transcriptomics, proteomics, metabolomics and miRNA data.
- Approaches
  - Multivariate statistics, univariate correlation coupled with clustering analysis and visual analytics

Workflow

- Upload normalized data matrices and metadata file

- Perform multi-omics harmonization to make the data more comparable

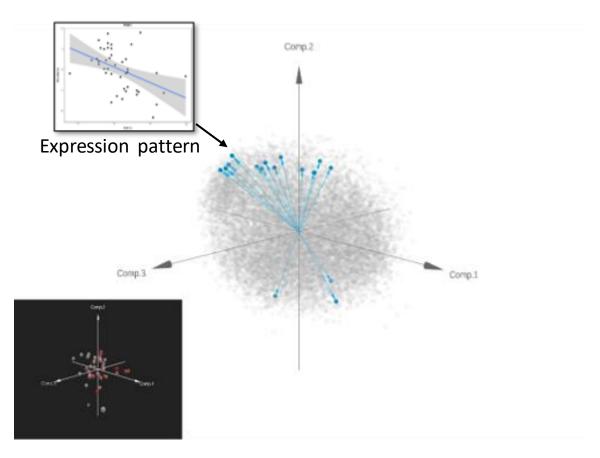- Data-driven integration to study relationships, clusters and identify biomarkers.

Processed tables

Omics data 1

Omics data 2

Multi-omics harmonization

Data driven integration

Requirements

- Modern browser supporting WebGL.

- Ensure that WebGL is enabled in your browser!
  - Go to this page https://get.webgl.org/ to verify your browser supports WebGL.
  - Refer to the FAQs for instructions on how to enable WebGL.

- For the best performance and visualization, use the latest version of Google Chrome.
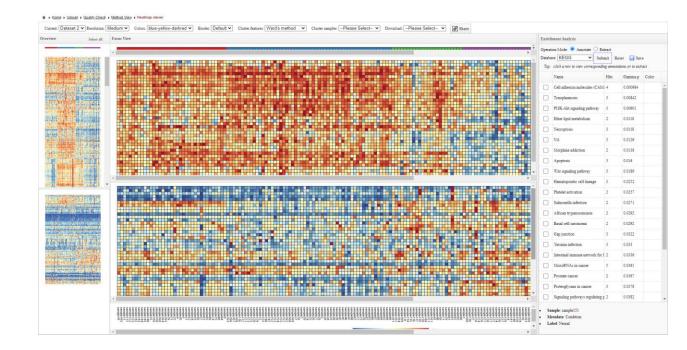
Multivariate Statistics

- Supports several well-established algorithms for integrating multiple-omics data
  - Dimensionality reduction to visualize hidden patterns and clusters
  - Identify sets of features that maximize correlation between omics datasets
  - Identify enriched functional groups in signature features
- Both supervised and unsupervised methods
  - **Supervised**: DIABLO
  - **Unsupervised**: MOFA, MCIA
  - Visualize overall sample and loading space using our interactive scatter plot viewer.
  - Visualize correlated features using our interactive network viewer.

Expression pattern

Joint visualization of loading and sample space with a set of features from an enriched pathway highlighted in blue.
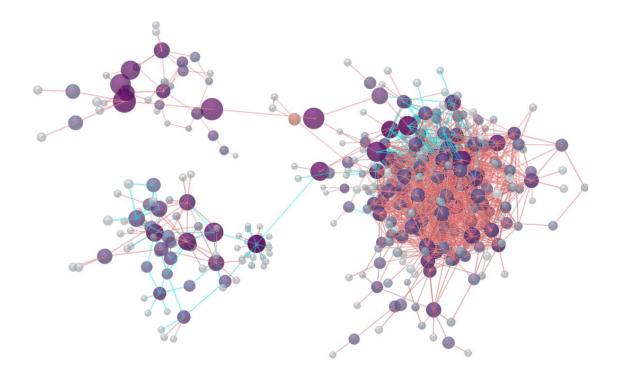
Unsupervised Clustering

- OmicsAnalyst aims at identifying and visualizing discrete clusters and patterns within user's omics data that would be difficult to identify manually.

- Visualize the inherent clusters using heatmap and integrative scatter plot viewer.
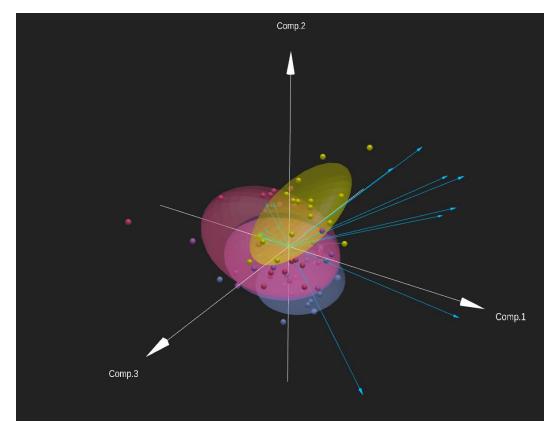
Correlation analysis

- OmicsAnalyst uses well-established univariate correlation methods to identify pairs of highly correlated features across omics layers.
  - Univariate correlation and partial correlation
  - **Parametric**: Pearson
  - **Non-parametric**: Spearman, Kendall

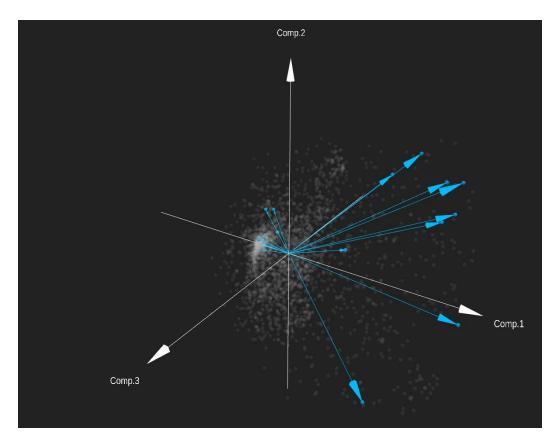- Visualize the results in the form of correlation network using our network viewer

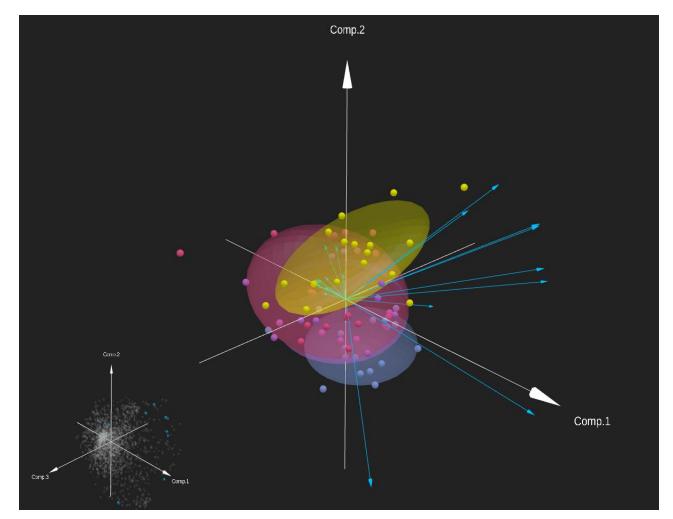Multi-omics correlation network in 3D

Interactive scatter plot viewer

Biplot projecting loading contributions of features from an enriched pathway on sample space
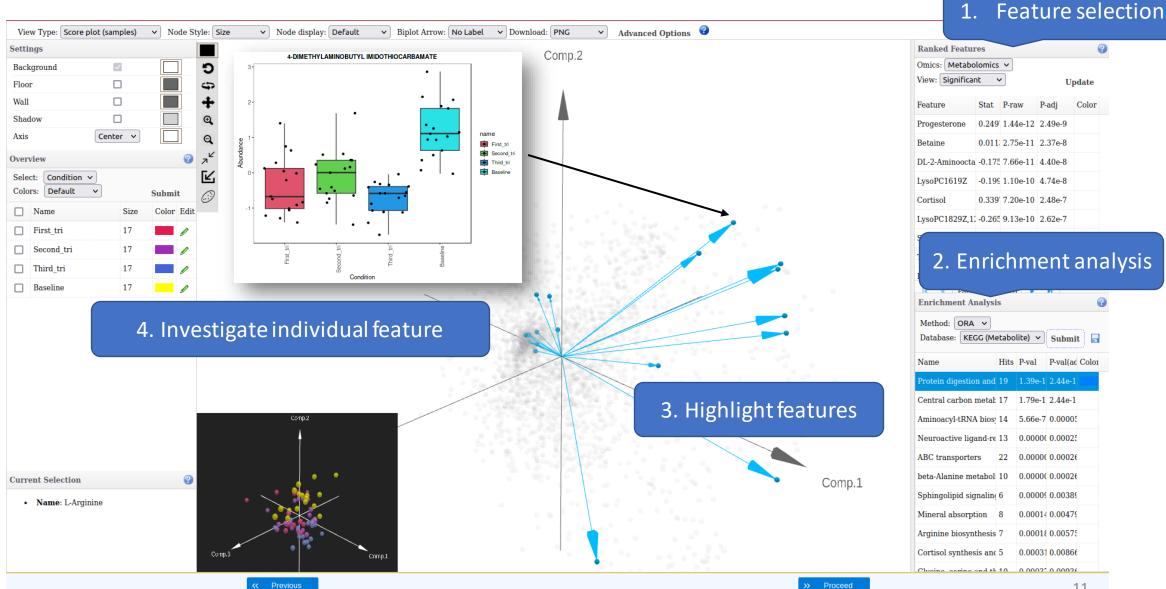

Loading plot highlighting the same features

Integrative view

View both sample and loading space simultaneously

From overview to detailed analysis

The End

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