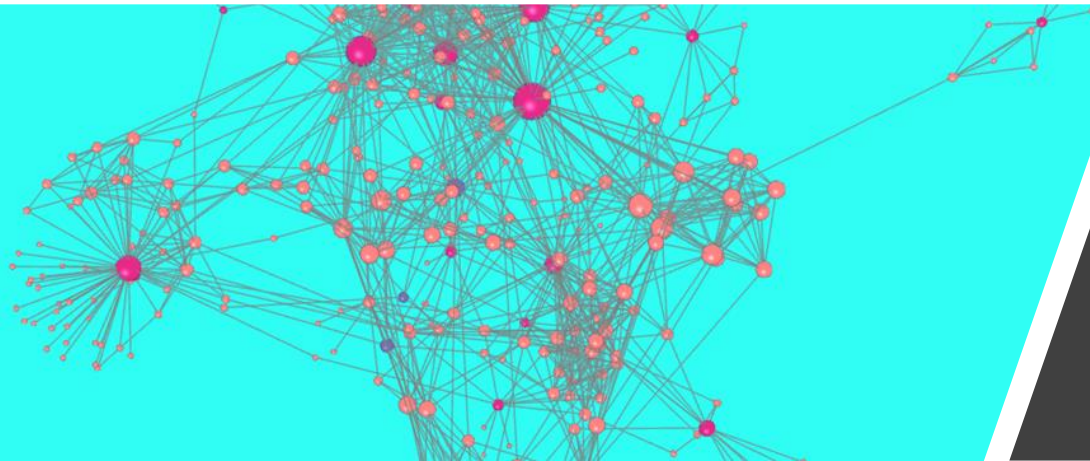


OmicNet

---a web-based 3D visual analytics tool
for biological networks

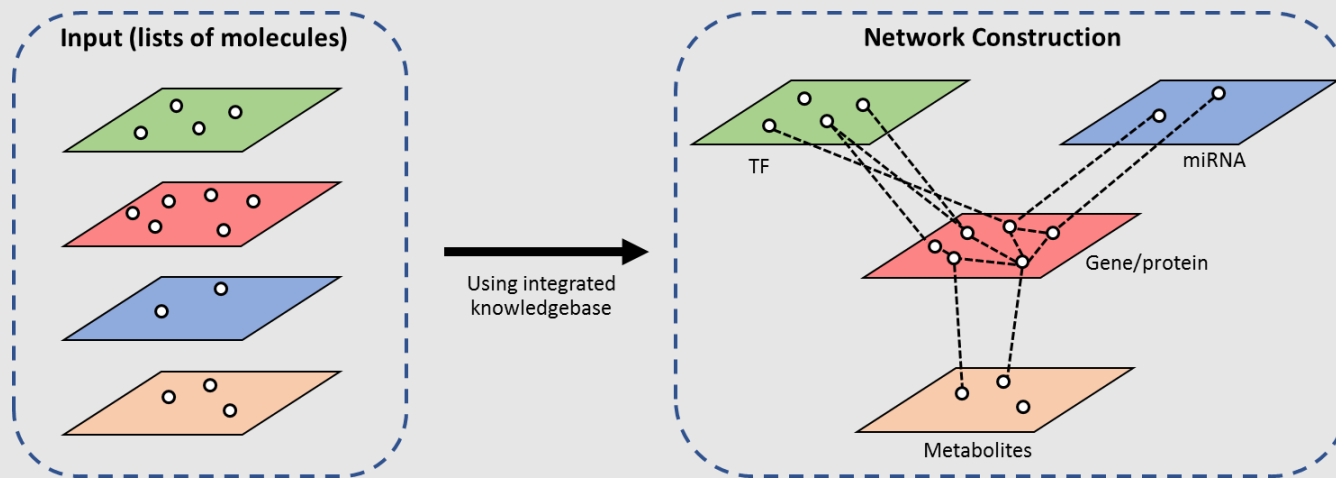


Requirement

- Modern browser supporting **WebGL**
 - Chrome 50+, Firefox 47+, Safari 10.1+ and Edge 12+
- Please make sure WebGL is enabled in your browser
 - Please consult this web page to verify: <https://get.webgl.org/>
 - If not enabled, please consult our **FAQ** page for instructions
- For best performance and visualization, use:
 - Latest version of **Google Chrome**
- A modern computer with at least 4GB of physical RAM
 - A 15-inch screen or bigger (larger is better)
- Retina Display is supported

Overview

- Goal: provide a web-based application supporting 3D network visualization and integration of multiple types of molecular interaction.
- Conventional molecular interaction networks
 - Protein-protein interaction
 - TF-gene regulation
 - miRNA-gene regulation
 - Enzyme-metabolite interaction
- Composite network encompassing more than one interaction type



Workflow

Data Upload

Genes/proteins

TFs

miRNAs

Metabolites

Graph files

Network Construction

PPI

miRNA-gene

TF-gene

Metabolite-protein

Composite networks

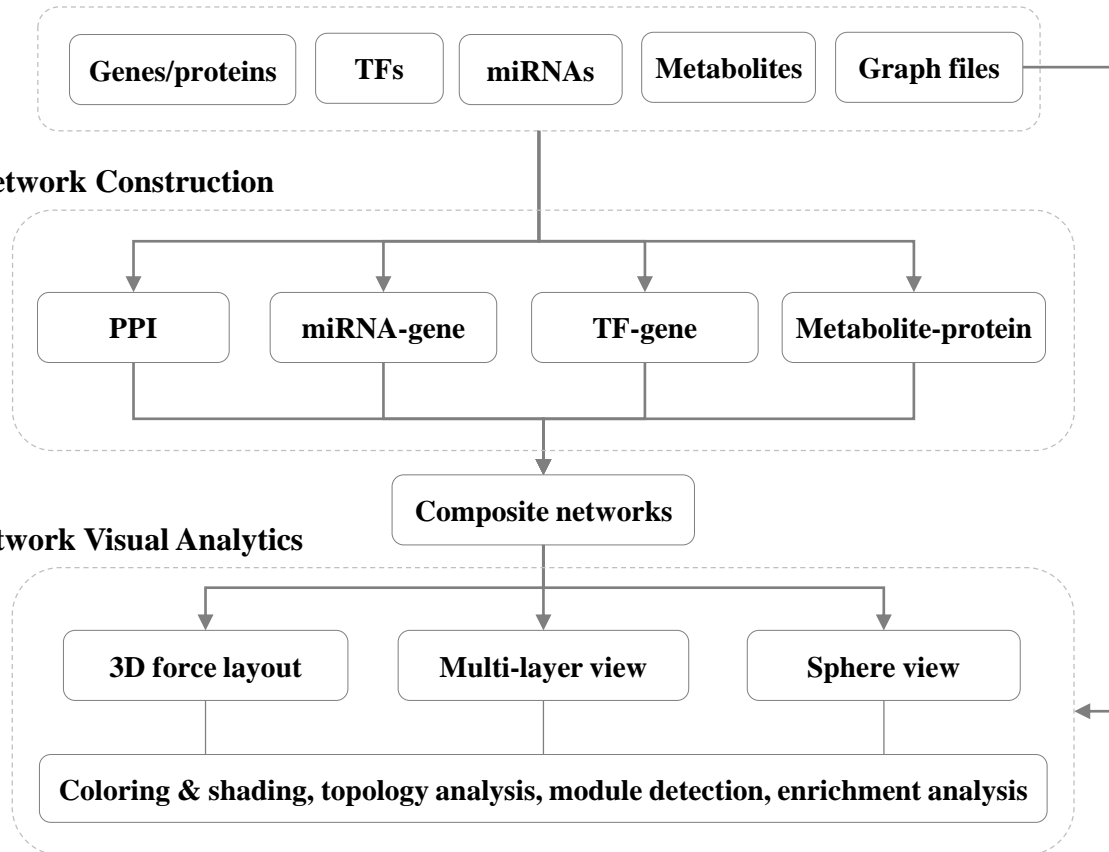
Network Visual Analytics

3D force layout

Multi-layer view

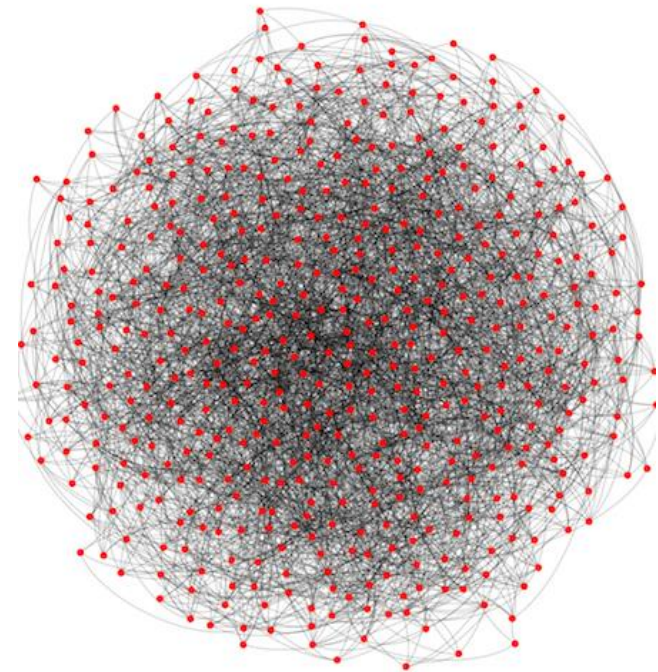
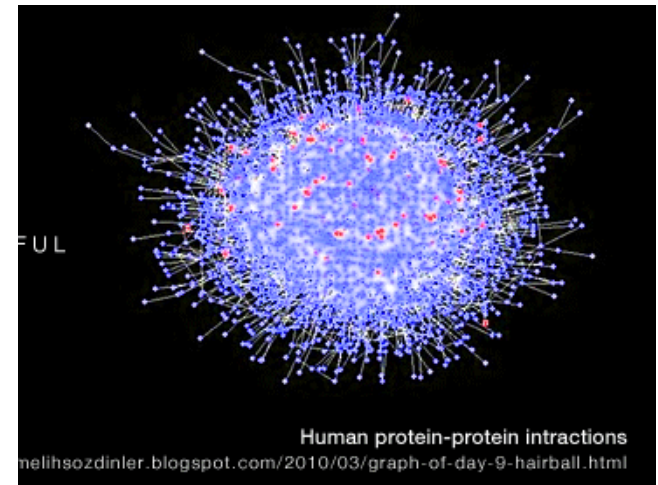
Sphere view

Coloring & shading, topology analysis, module detection, enrichment analysis

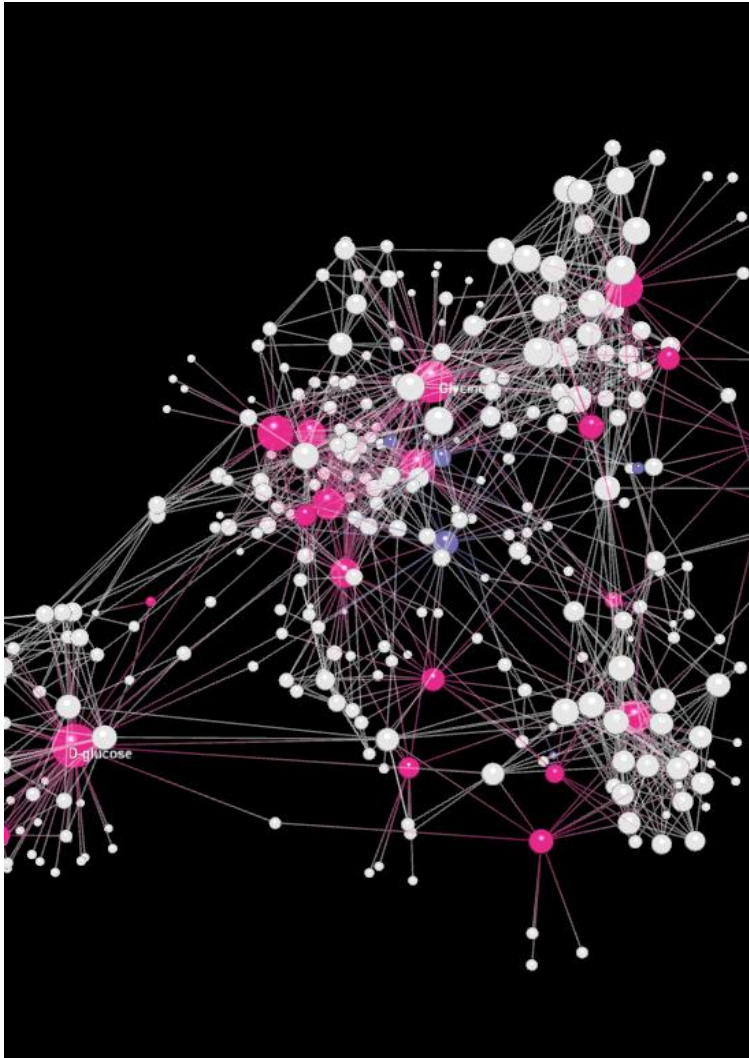


Current limitations in network visualization

- Lack of web-based tools for network visualization and analysis.
- Network visualization often hindered by “hairball effect” due to large number of nodes and edges.
- Support for composite networks containing multiple interaction types are lacking.

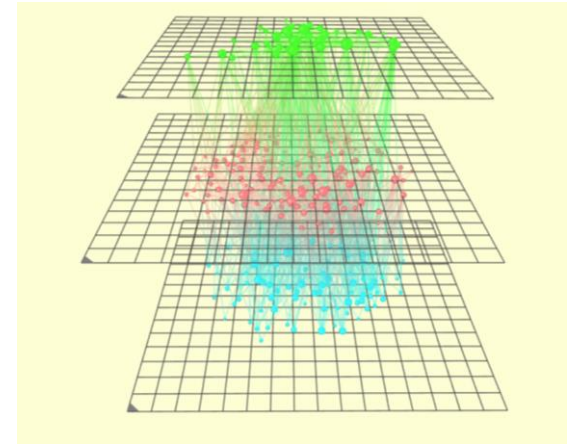
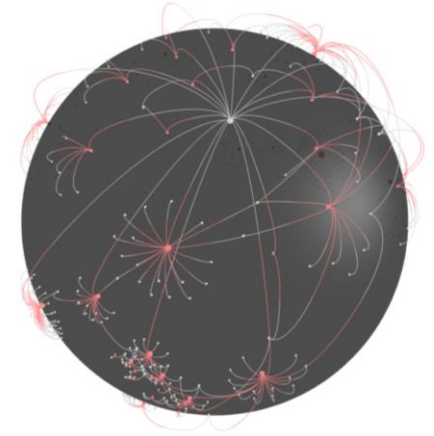
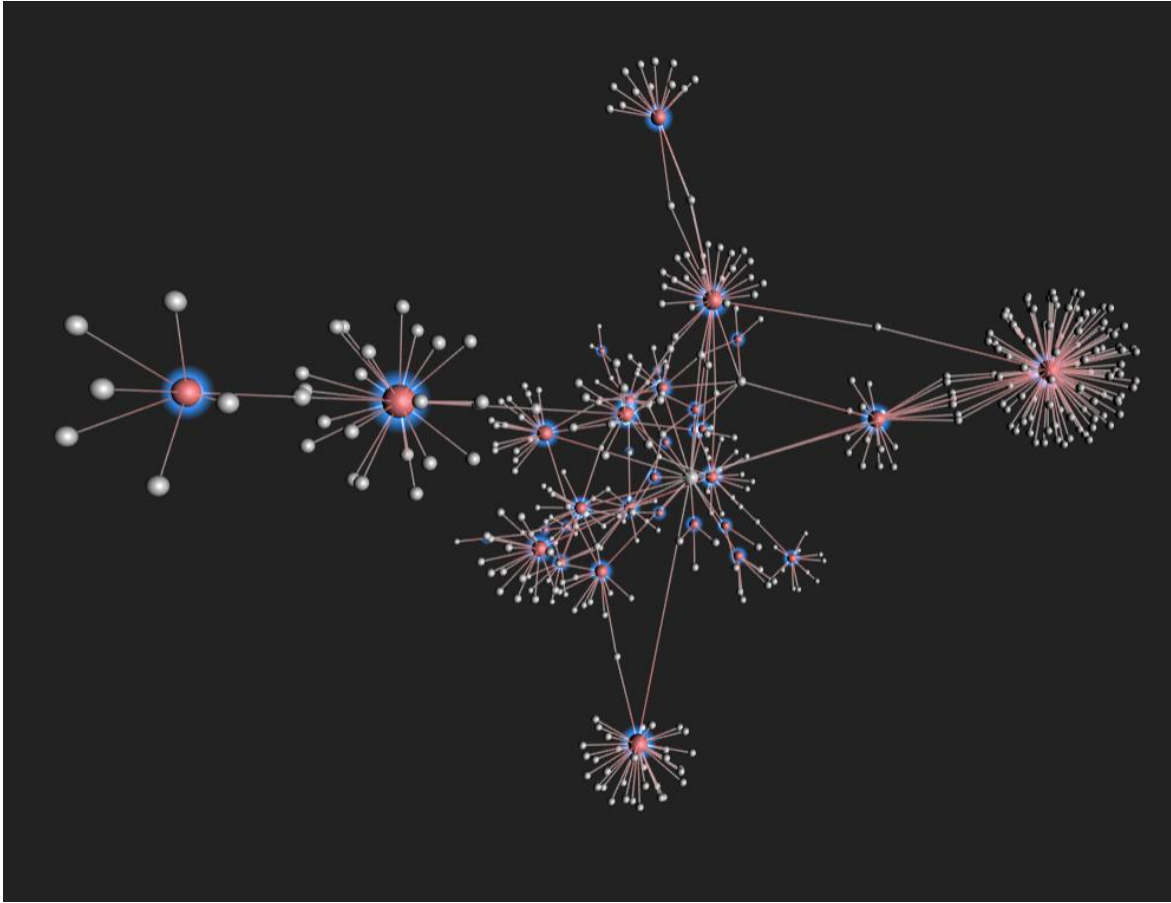


3D visualization can improve visual experience

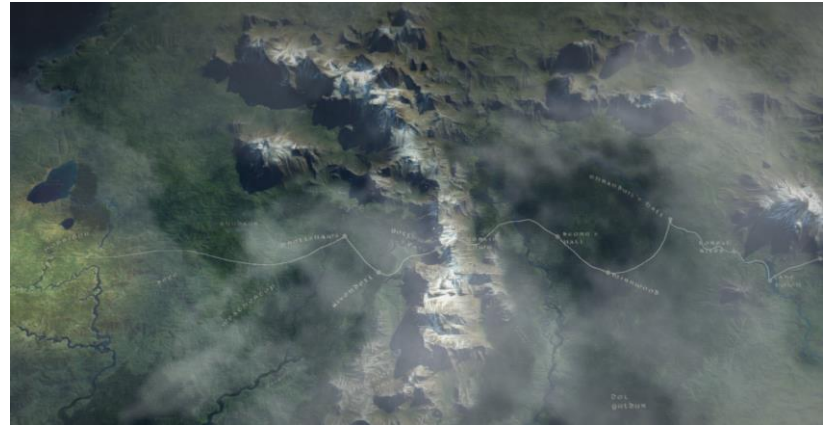


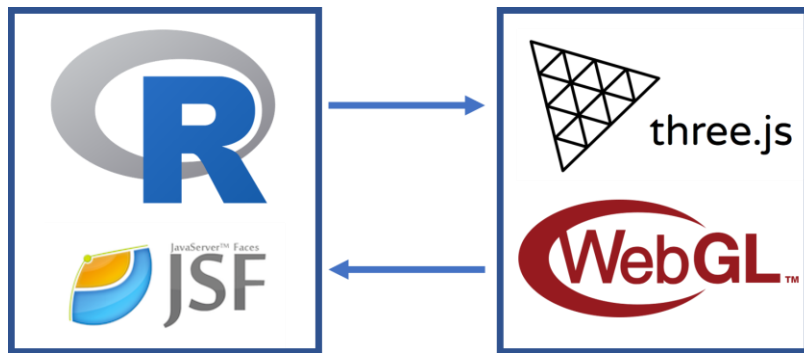
- Flexible graph exploration and navigation with more viewing perspectives
- Additional dimension gives more space for graph layout, facilitating the visualization of larger data
 - Multilayer layout improves the visualization of network containing multiple interaction types
- Human visual system prefers network represented in 3D.
 - Irani, P. and C. Ware (2003). "Diagramming information structures using 3D perceptual primitives." ACM Transactions on Computer-Human Interaction (TOCHI) **10**(1): 1-19.

3D network visualization



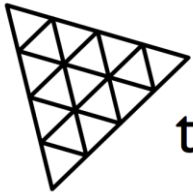
WebGL supports high quality 3D graphics





Implementation

- Client-server framework that uses Java and R server for network construction and some analysis functions.
- Browser-based application using WebGL interfaced by Three.js to visualize 3D network interactively.



three.js

Core Technologies



- HTML5 and JavaScript
- WebGL
 - JavaScript API allowing the rendering of 3D graphics in web browser without plug-ins
 - High performance, GPU accelerated
 - Steep learning curve: requires developers to have extensive math knowledge about 3D, lighting and shading.
- Three.js
 - Framework interfacing with WebGL to display 3D graphics
 - Abstract away the difficulties of WebGL.

Key Features

- Interactive 3D network visualization in web browser using WebGL technology
- Enable integration of multiple types of molecular interaction
- Built-in knowledgebase for network building
 - Protein-protein interaction
 - Transcription factor-gene regulation
 - miRNA-gene regulation
 - Metabolite-protein interaction

Databases

PPI

innateDB

STRING

IntAct

TF-gene

TRRUST



miRNA-gene

mirNet

Enzyme-metabolite

Recon 2



The End
