

Network Visualization

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1 Introduction

Network visualizations are notoriously difficult to parse and extract relevant biological information from multi-omics datasets. By creating a multilayer network will allow researchers to sort not only by annotation, but by clustered trends as well. Currently, this type of search is done with two excel sheets and manually search through clusters of interest and then switching sheets to that cluster and filtering through by annotation of interest. This visualization will provide ease of access to search the entire transcriptome for annotation as well as creating easier access per cluster.

2 One-sentence description

We aim to build a tool for multilayer network visualization for RNA-Seq transcriptomic data.

3 Project Type

Visualization / Application

4 Audience

Who is the audience for this project? How does it meet their needs? What happens if their needs remain unmet?

Scientists looking at multi-omic datasets is the audience - specifically, this tool can be implemented for anyone looking at transcriptomic data. It can be used to elucidate meaning from individual RNA-seq datasets as well as for comparison across organisms for comparative genomics.

5 Approach

5.1 Details

What is your approach?

We plan to use d3 to implement the multilayer network. The first layer will be the trends for each node/cluster with the connection strength, and the second layer to be the count, FC, and annotation information for each gene in the cluster.

5.2 Evidence for Success

Why do you think it will work?

We have all the data for this to work, as long as we can implement our ideas into d3, it should work. The papers below show similar visualization with less interactivity, and with our technical experience in making interactive charts, we are confident we will be able to accomplish this task.

6 Best-case Impact Statement

In the best-case scenario, what would be the impact statement (conclusion statement) for this project?

We set out to build an interactive multilayer network tool for multi-omics analysis.

7 Major Milestones

1. Format data
2. Build skeleton multilayer network
3. Add interactivity
4. Add search tools