


# GRNsight Expression Database *and* Expansion of Species for Gene Page Projects

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4/6/2020



# GRNsight Overview

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- GRNsight is an open source web application that allows users to better visualize the connections in gene regulatory networks
- Uses spreadsheets of data that show these connections
- Node/connection coloring shows how strongly and in what way genes affect each other
  - Coloring is based on expression data

# Expression Database Project Description

- Network data shows basic regulatory network connections
- Expression data shows the level of expression of genes, which we display with node coloring

## Network Data

	A	B	C	D	E	F	G	H
1	cols regulators	ACE2	ASH1	CIN5	GCR2	GLN3	HAP4	HMO1
2	ACE2	0	0	0	0	0	0	0
3	ASH1	1	0	0	0	0	0	0
4	CIN5	0	0	0	0	0	0	1
5	GCR2	0	0	0	0	0	0	0
6	GLN3	0	0	0	0	0	0	0
7	HAP4	0	0	1	0	0	0	1
8	HMO1	0	0	0	0	0	0	1

## Expression Data

	A	B	C	D	E	F
1	id	15	15	30	60	60
2	ACE2	0.6139	-1.0689	0.3377	0.817	0.5566
3	ASH1	0.97	0.3043	-0.7236	-1.3477	-1.0468
4	ZAP1	0.6594	0.6135	-0.394	2.9606	3.5569

# Expression Database Project Description (cont.)

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- Want to create a database with existing expression data
- Users can use this data to color their GRNs
  - Allows node coloring even if user does not have expression data
- Produces uniform example for how expression data should be formatted

# Goals

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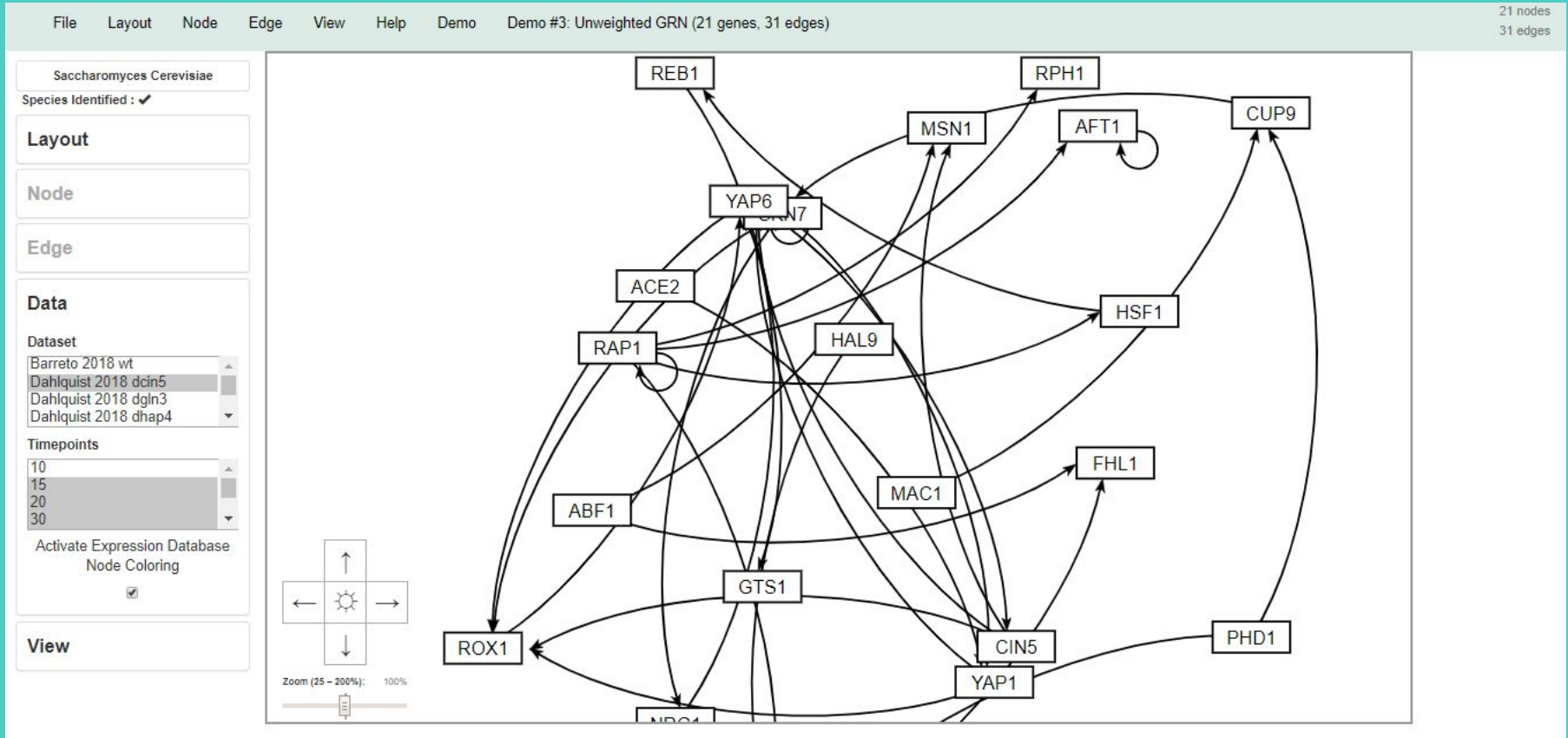
- Create and utilize RDS and EC2 instances
- Normalize data and populate RDS with existing lab data
- Create UI that makes it easy for users to interact with expression database
- Write APIs that connect the front end functionality to the back end database

# Project Justification

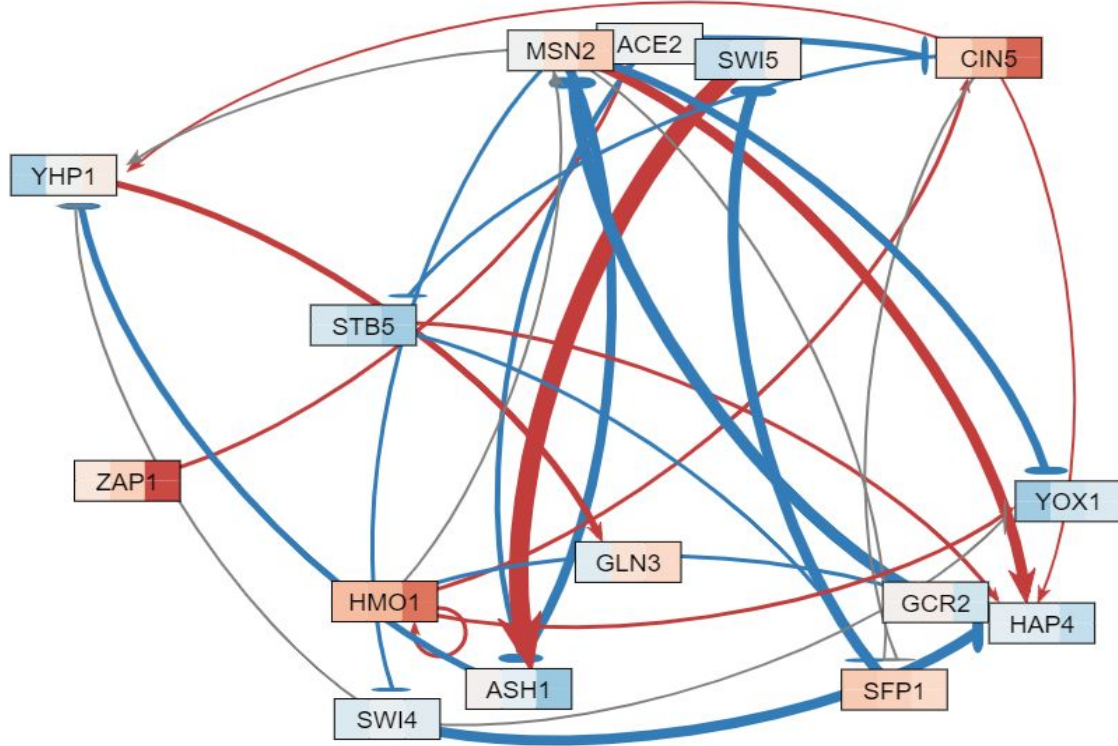
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- Worked on the GRNsight project for a year, specifically with expression data
- Learning many new skills and concepts
  - Networks
  - AWS
  - REST API writing
- Working on a project that existed for a long time (similar to how it might be to work in industry)

# User Interface



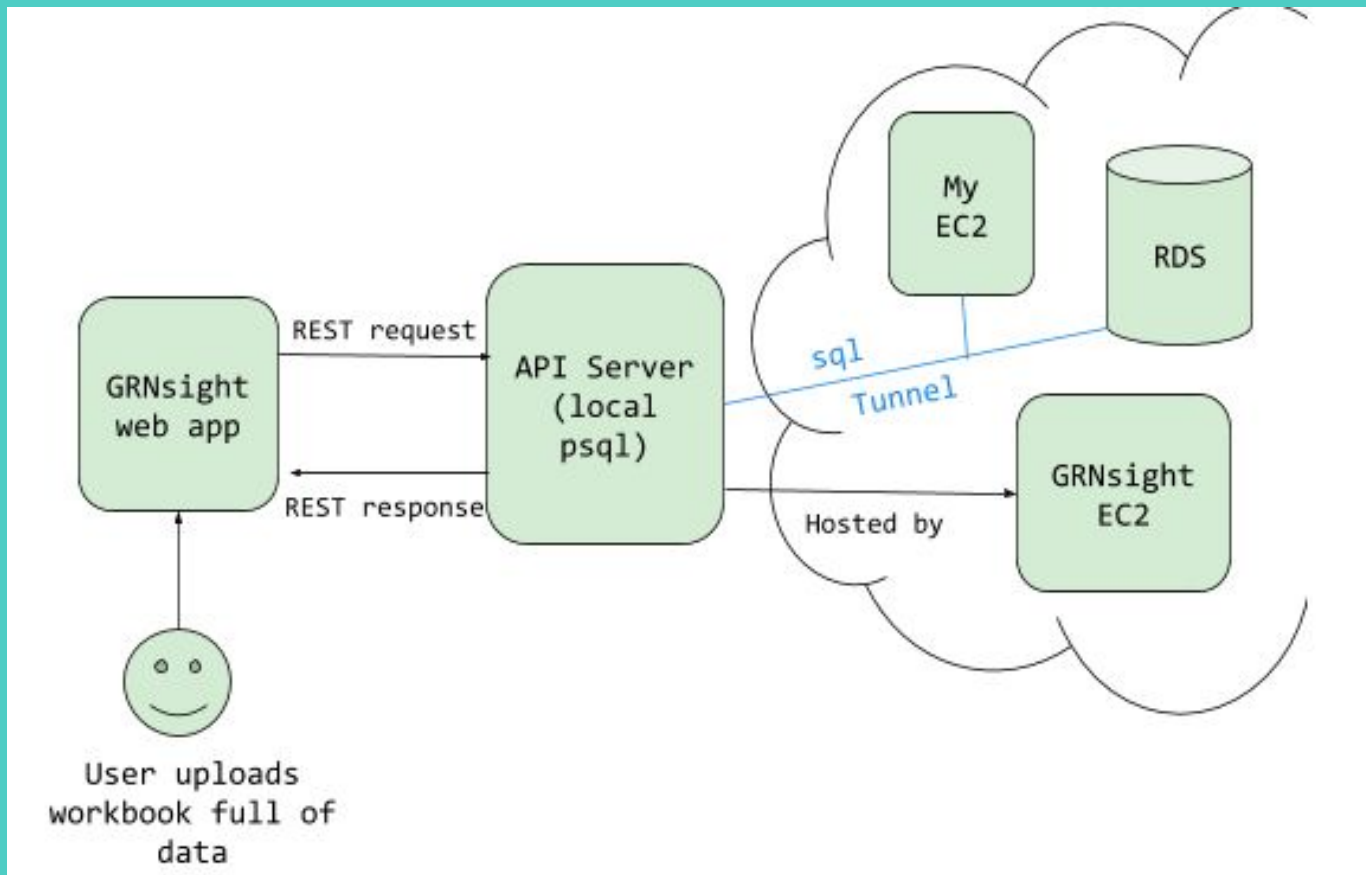
# Expression data allows for node coloring





# Expression Database Project Demo!

# A Quick Diagram



# Challenges

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- AWS is tricky!
- General learning curve of working with a new set of tools
- Challenging to work on a project that has existed for a long time (but good practice for industry!)

# Status Update

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## Top Priority

- Write API to be dynamic and adjust queries based on user selection
- Format API output into JSON object that can be read usefully to color nodes
- Reformat data as necessary

## Other to-do's

- Add Data panel options to navigation bar dropdown
- Add options for users to utilize data besides just expression data (degradation rates, metadata, etc.)
- Testing

# Gene Page Feature Expansion

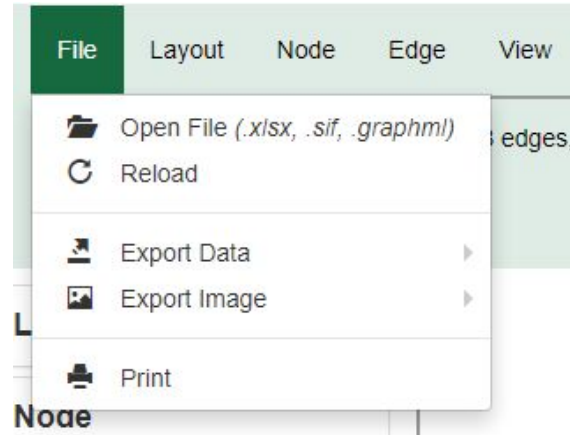
- Add functionality for the gene page by expanding the species that GRNsight supports
- Allow users to upload file with species data or choose which species they are working with through a dropdown menu

The screenshot shows the GRNsight web application interface. At the top, there is a dark green header with the text "GRNsight" in white, followed by "Web app and service for visualizing models of gene regulatory networks." in smaller white text. To the right of the header is the LMU|LA logo, which includes the text "A Joint Project of the LMU Bioinformatics and Biomathematics Groups" and "Loyola Marymount University". Below the header, the gene name "ZAP1" is displayed on the left, and the species "Saccharomyces cerevisiae (strain ATCC 204508 / S288c)" is displayed on the right. Below this, there is a horizontal navigation bar with five colored buttons: "General Information" (green), "Protein Information" (purple), "Regulation" (brown), "Gene Ontology" (teal), and "Sources" (maroon). Below the navigation bar, there are five horizontal tabs, each corresponding to one of the navigation buttons. The "General Information" tab is currently selected and highlighted in light green. The other tabs are "Protein Information", "Regulation", "Gene Ontology", and "Sources".

Currently hardcoded for yeast (*Saccharomyces cerevisiae*) only.

# Goals

- Ability to read in species data from a user uploaded file
- Dropdown menu that displays the current species and lets the user update the species at any time
- Expand API queries beyond the currently hardcoded yeast



# Project Justification

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- Work in a environment similar to the real world as a member of a larger project team with weekly meetings
- Full stack development working on both front and backend components
- Research project which Dr. Dahlquist uses each year in her biological databases class, meaning my work has an immediate impact

# User Interface - Beta(Current)

## GRNsight

Web app and service for visualizing models of gene regulatory networks.

Beta v4.0.12

**Disclaimer:** This is the beta version of GRNsight

File Layout Node Edge

Saccharomyces Cerevisiae

Saccharomyces Cerevisiae

Homo Sapien

Drosophila Melanogaster

Caenorhabditis Elegans

Mus Musculus

Arabidopsis Thaliana

## GRNsight

Web app and service for visualizing models of gene regulatory networks.

Beta v4.0.12

**Disclaimer:** This is the beta version of GRNsight for live testing of new functionality. For the most stable version, please go to the [GRNsight home page](#).

File Layout Node Edge View Help Demo Demo #2: Weighted GRN (15 genes, 28 edges, Dahlquist Lab unpublished data)

Saccharomyces Cerevisiae

Species Identified : ✓

Layout

Node

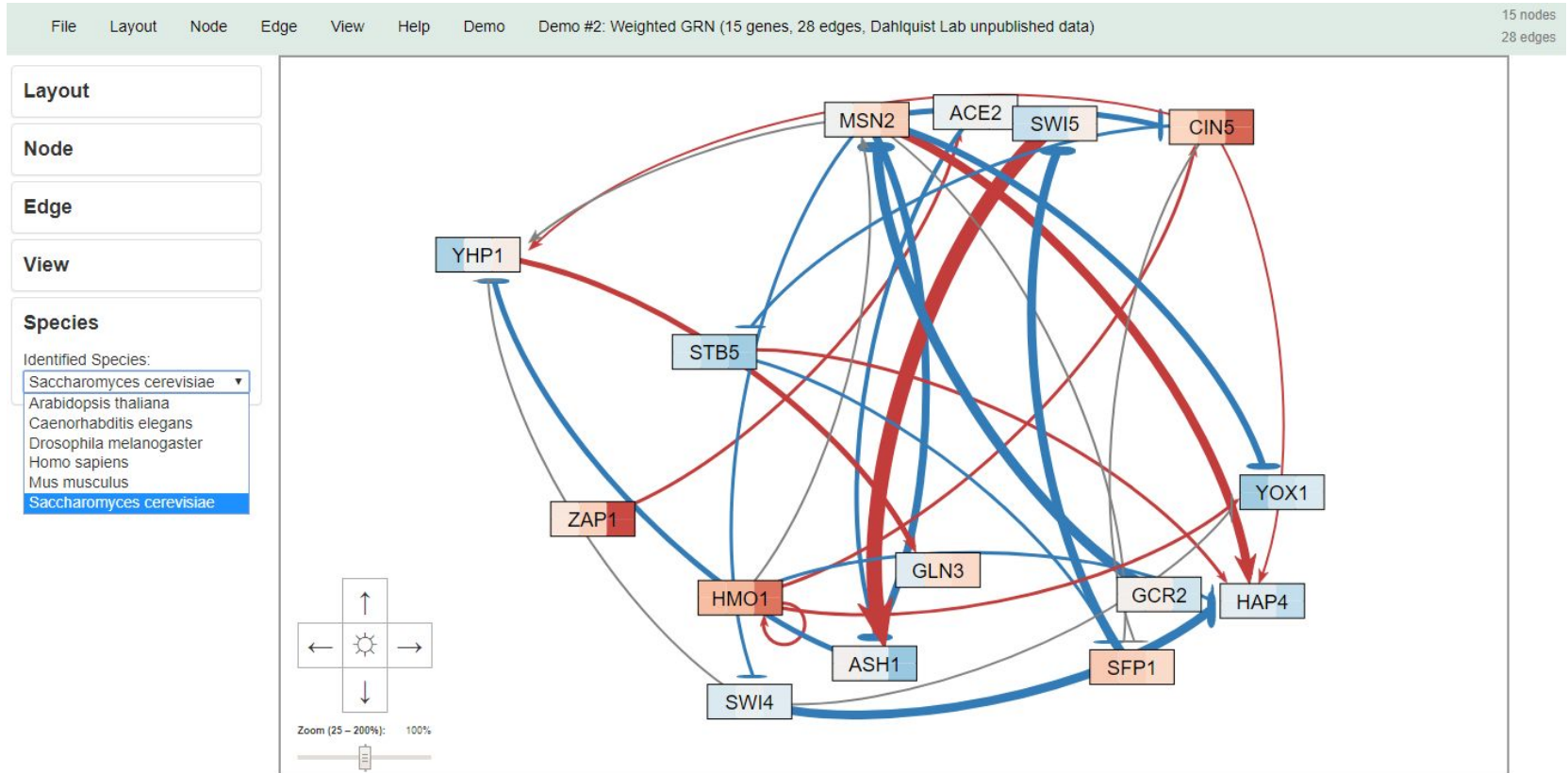
Edge

View





# User Interface - Beta(Revision)



# User Interface - Gene Pages

## GRNsight

Web app and service for visualizing models of gene regulatory networks.

A Joint Project of the  
LMU Bioinformatics and  
Biomathematics Groups

LMU|LA  
Loyola Marymount  
University

ZAP1

*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)

General Information

Protein Information

Regulation

Gene Ontology

Sources

### General Information

SGD ID:	S000003592 <sup>[1]</sup>
NCBI Gene ID:	853390 <sup>[4]</sup>
Ensembl ID:	YJL056C <sup>[3]</sup>
Uniprot ID:	ZAP1_YEAST <sup>[2]</sup>
JASPAR ID:	MA0440.1 <sup>[5]</sup>
Description:	Zinc-regulated transcription factor; binds to zinc-responsive promoters to induce transcription of certain genes in presence of zinc, represses other genes in low zinc; regulates its own transcription; contains seven zinc-finger domains <sup>[1]</sup>
Species:	<i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) <sup>[2]</sup>
Locus Tag:	YJL056C <sup>[4]</sup>
JASPAR Family:	Factors with multiple dispersed zinc fingers <sup>[5]</sup>
JASPAR Class:	C2H2 zinc finger factors <sup>[5]</sup>
Chromosome Sequence:	NC_001142.9 <sup>[4]</sup>

### Protein Information

### Regulation

### Gene Ontology

### Sources

#### Sources

1. Saccharomyces Genome Database
2. UniProt
3. Ensembl
4. NCBI Gene Database
5. JASPAR Database

# Demo!

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- Dropdown menu and uploading data functions
- Gene pages feature

# Challenges

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- Learning and working on preexisting code that has been written by multiple different students over the years
- Rewriting code to fit a clients expectations, and all the bugs that come with a rewrite
- Multidisciplinary project, so I needed a biology refresh to understand the function of my code
- Working with a lot of different biological databases

# Status Update

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- I just finished changing the front end to meet new layout requests by Dr. Dahlquist
- I am currently working on the gene page, making sure that data setup on one page is successfully transferred to another
- Next:
  - API calls, and adding new APIs to support added species
  - Testing

**Thank you!**  
**Questions?**