

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

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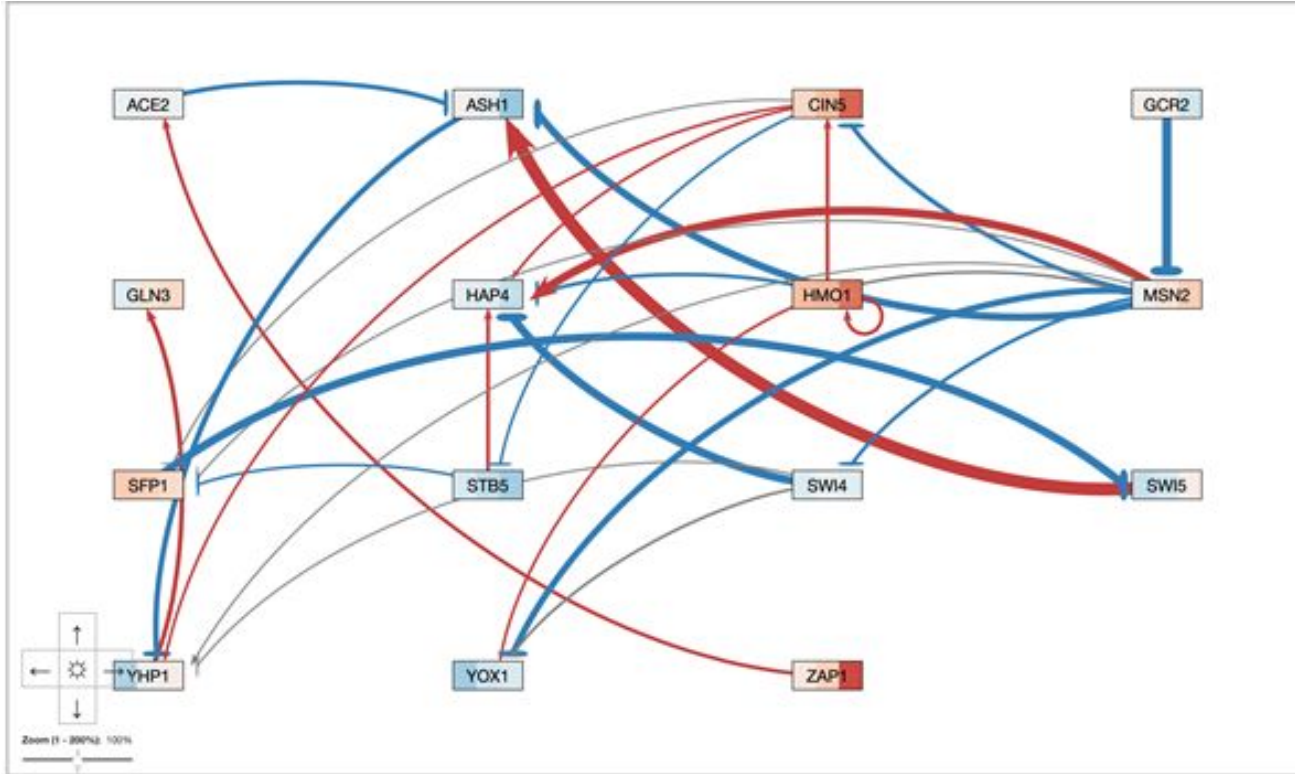
Some Helpful Terms!

- A **gene regulatory network (GRN)** shows how different genes are connected, how they affect each other
- **Network data** is the baseline data required to visualize a GRN
 - Shows which genes are connected
- **Expression data** shows how much a gene is expressed or repressed over time

GRNsight Overview

- GRNsight is an open source web application that allows users to better visualize the connections in gene regulatory networks
- Uses spreadsheets of data to show these connections

GRNsight Overview (Cont.)



Node coloring is based on the change in expression over time for each gene

Arrow coloring is based on the regulatory relationship, activation or repression.

Expression Database Project

- To visualize a colored network graph, users upload an Excel Workbook with multiple worksheets
- Network data shows the 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

- The goal is to create a backend database populated with public expression data
- Users can use this data to color their GRNs
 - Allows node coloring even if user does not have their own expression data
- Produces uniform example for how expression data should be formatted

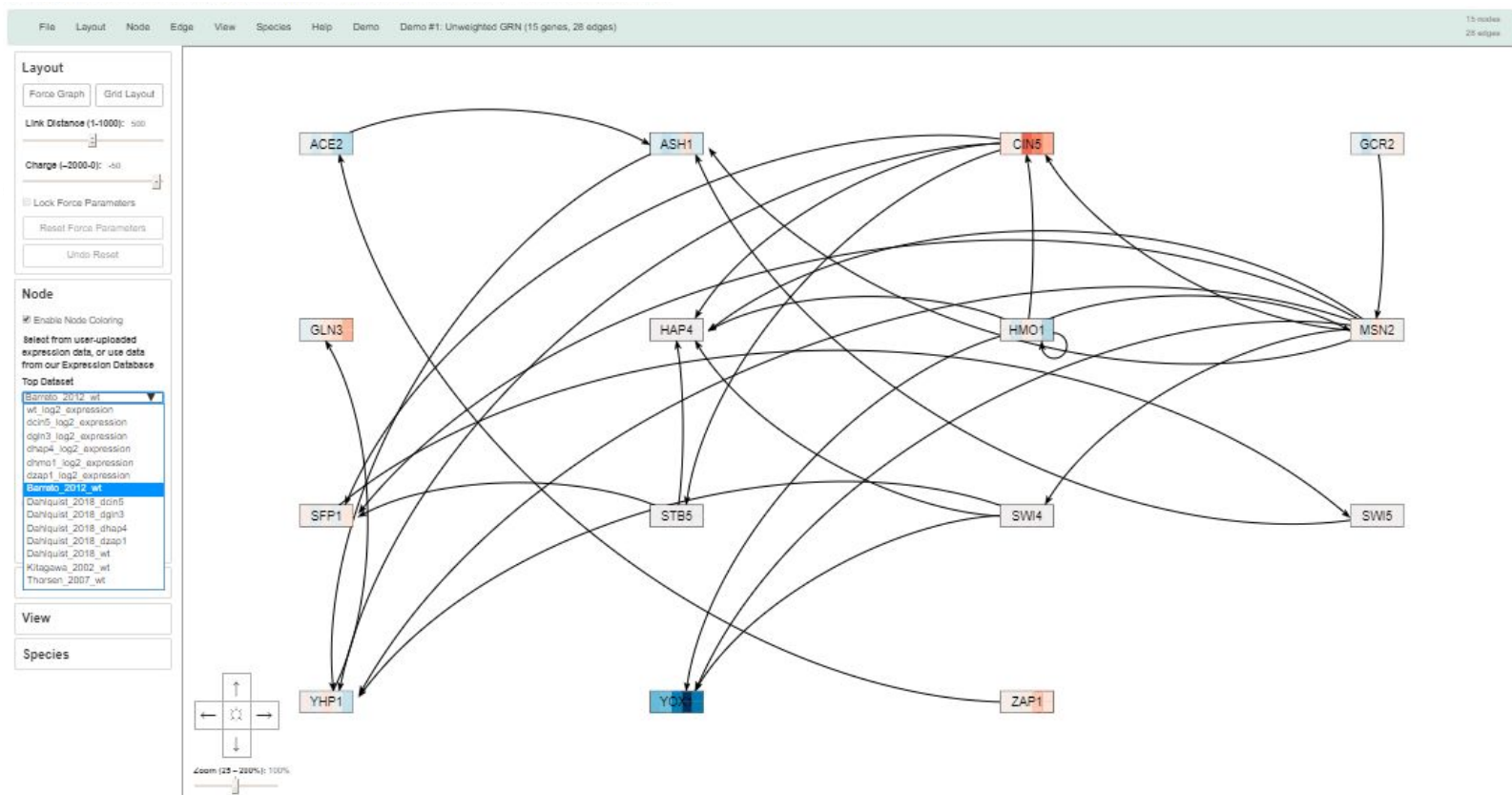
Goals

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

Project Justification

- Worked on 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 Database Project Demo!

Challenges

- General learning curve of working with a new set of tools (AWS, REST API writing)
- Challenging to work on a project that has existed for a long time

Future Directions

- Add more data to the database, including network data
- Give users a meaningful way to access the other data already stored (production rates, degradation rates, publication data, etc.)

Gene Page

- Right-clicking on a node opens a web page which displays information retrieved from various databases
- Currently hardcoded for yeast (*Saccharomyces cerevisiae*) only.

GLN3

Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

| General Information | Protein Information | Regulation | Gene Ontology | Sources |
|----------------------------|--|------------|---------------|---------|
| <u>General Information</u> | | | | |
| SGD ID: | S000000842 ^[1] | | | |
| NCBI Gene ID: | 856763 ^[4] | | | |
| Ensembl ID: | Not found ^[3] | | | |
| Uniprot ID: | GLN3_YEAST ^[2] | | | |
| JASPAR ID: | MA0307.1 ^[5] | | | |
| Description: | Transcriptional activator of genes regulated by nitrogen catabolite repression; localization and activity regulated by quality of nitrogen source and Ure2p ^[1] | | | |
| Species: | Saccharomyces cerevisiae (strain ATCC 204508 / S288c) ^[2] | | | |
| Locus Tag: | YER040W ^[4] | | | |
| JASPAR Family: | GATA-type zinc fingers ^[5] | | | |
| JASPAR Class: | Other C4 zinc finger-type factors ^[5] | | | |
| Chromosome Sequence: | NC_001137.3 ^[4] | | | |
| <u>Protein Information</u> | | | | |
| <u>Regulation</u> | | | | |
| <u>Gene Ontology</u> | | | | |
| <u>Sources</u> | | | | |

Gene Page Species Expansion

- Add functionality to the gene page by expanding the species that GRNsight supports (additional 5)
- Provide the user with multiple avenues to update the species they are working in
- Update biological database API calls to reflect the selected species

Goals

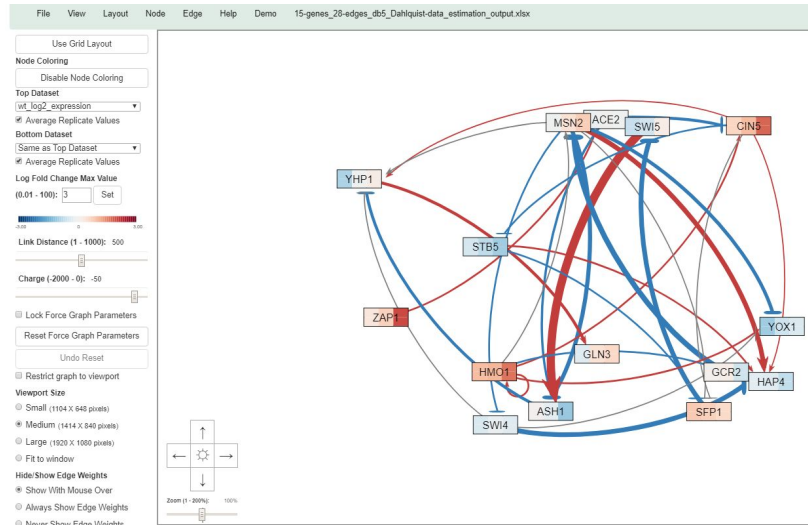
- Create and seamlessly integrate new UI elements and error messages to already existing code
- Write code that checks user data and updates the species to reflect what is uploaded
- Menus that allow the user to update the species without having to update their data
- Change how APIs are called and how data is displayed to handle different species

Project Justification

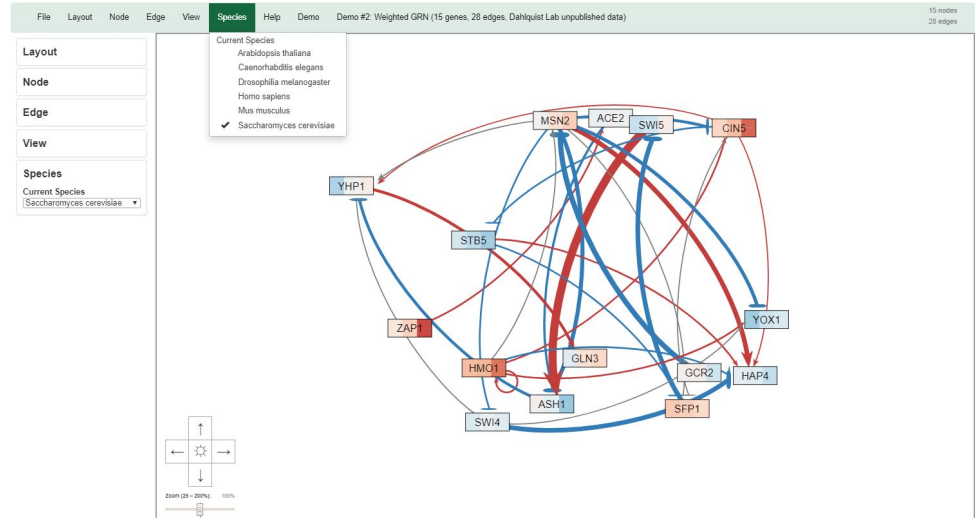
- Work in a environment similar to the real world as a member of a larger project team with weekly meetings and goals
- Full stack development working on both front and backend components
- Research project which Dr. Dahlquist uses each year in her biological databases class, meaning my work has an immediate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

User Interface- Drop Down Menu

Live



Beta



Users can select from among six species in a panel or menu

User Interface - Gene Page

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 ^[1] |
| NCBI Gene ID: | 853390 ^[4] |
| Ensembl ID: | YJL056C ^[3] |
| Uniprot ID: | ZAP1_YEAST ^[2] |
| JASPAR ID: | MA0440.1 ^[5] |
| 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 ^[1] |
| Species: | <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) ^[2] |
| Locus Tag: | YJL056C ^[4] |
| JASPAR Family: | Factors with multiple dispersed zinc fingers ^[5] |
| JASPAR Class: | C2H2 zinc finger factors ^[5] |
| Chromosome Sequence: | NC_001142.9 ^[4] |

Protein Information

Regulation

Gene Ontology

Sources

Sources

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

Gene Page Species Expansion Project Demo!

Challenges

- 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
- Working with a lot of different biological databases
- API errors and different databases for different species

Future Directions

- Writing API calls to specific interMine databases for each species
- Adding extra species to GRNsight
- Updating how data is displayed

Acknowledgements

Thank you to Dr. Dahlquist of LMU Biology and Dr. Dionisio of LMU Computer Science for advising us on these projects.

Visit GRNsight at <http://dondi.github.io/GRNsight>

Visit our repository at <https://github.com/dondi/GRNsight>



Thank you!
Questions?