

New data analysis and development of new GRNsight functionality will aid researchers in discovering more about gene regulatory networks

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Outline

- Coding new GRNsight functionality and performing yeast data analysis can lead to new insights in gene regulatory research.
- Achieving Individual milestones contributes to group effort.
- Cold shock regulation differs between gene clusters.
- Right click function links to a new gene page which helps biologists find information quickly.
- This team's work will aid future research
- There are many avenues available for further research.



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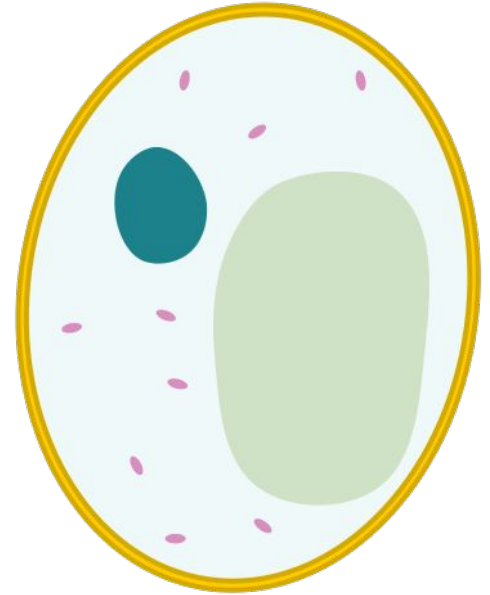
Organisms have mechanisms that allow them to withstand environmental stresses

- Organism -- Shivering
- Organ Systems -- Endocrine, Circulatory
- Organ -- Digestion
- Tissue -- Muscle movement
- Cellular -- Cold shock proteins



Yeast is an ideal model organism for learning about Eukaryotic cells

- Significant growth in a matter of days
- Easy to manipulate in lab
- Can resist and respond to many different environmental stressors
- Controls cell division in a way similar to ours





The right click functionality will be very useful for gene research

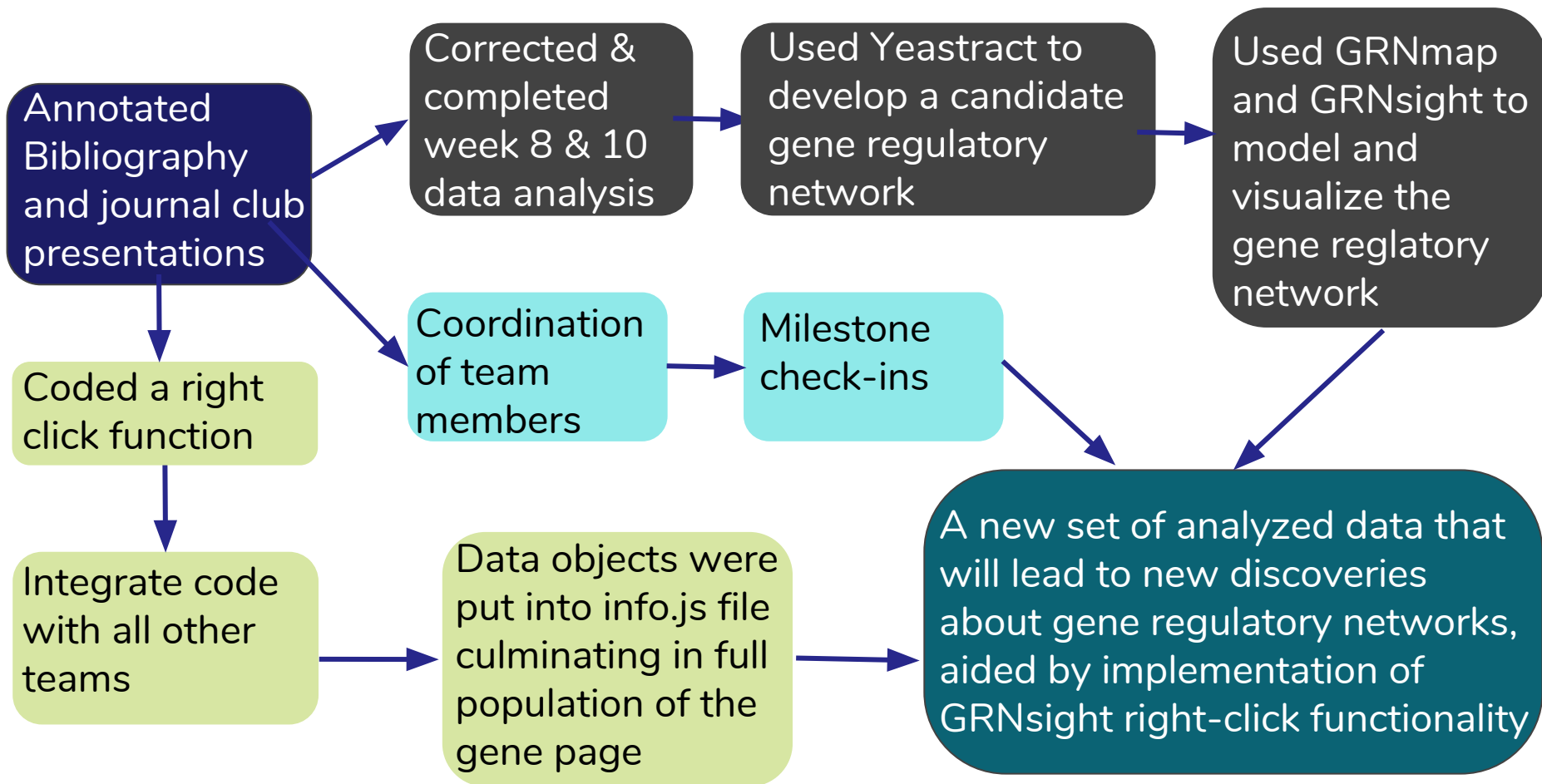
- **Current Functionality: Visualize gene regulatory networks**
- **Goal: ability to easily open gene information page**
- **Solution: Adding right click functionality**
 - **Readily available gene information**
 - **No need for extensive database searching**



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Individual milestones contribute to group effort





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Percentage of genes demonstrating a cold shock response decreased with stricter p-values

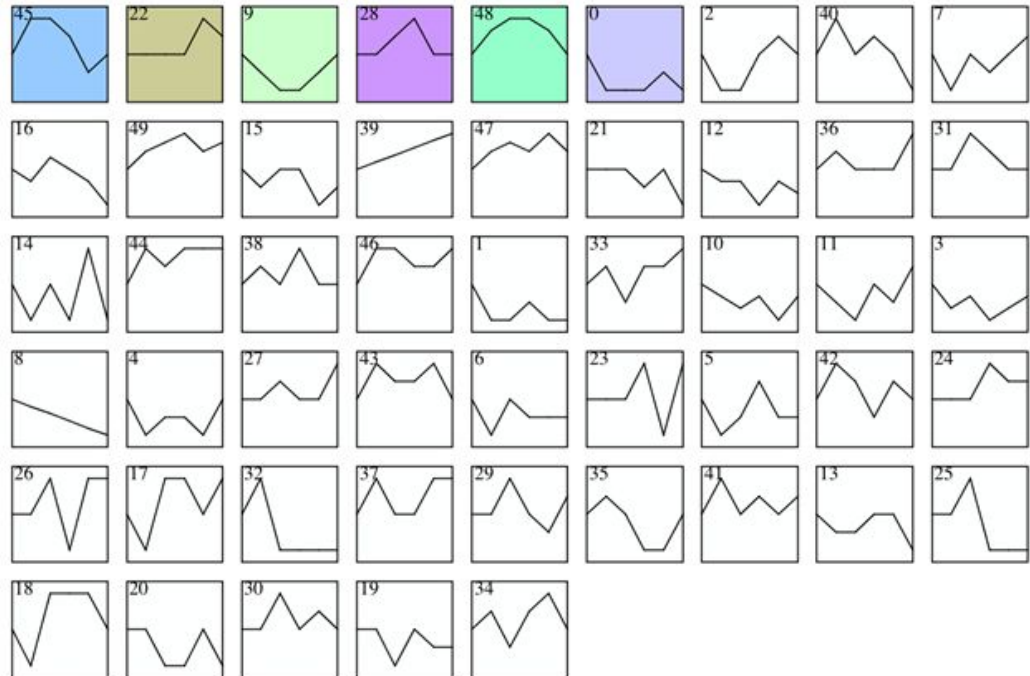
- Standard $p < 0.05$ revealed ~41% of genes demonstrating significant response to cold shock
- B & H corrected $p < 0.05$ revealed second largest percentage
- Bonferroni-corrected $p < 0.05$ was the most strict

ANOVA	WT
$p < 0.05$	2528 (40.85%)
$p < 0.01$	1652 (26.70%)
$p < 0.001$	919 (14.85%)
$p < 0.0001$	496 (8.01%)
Benjamini & Hochberg-corrected $p < 0.05$	1822 (29.44%)
Bonferroni-corrected $p < 0.05$	248 (4.01%)

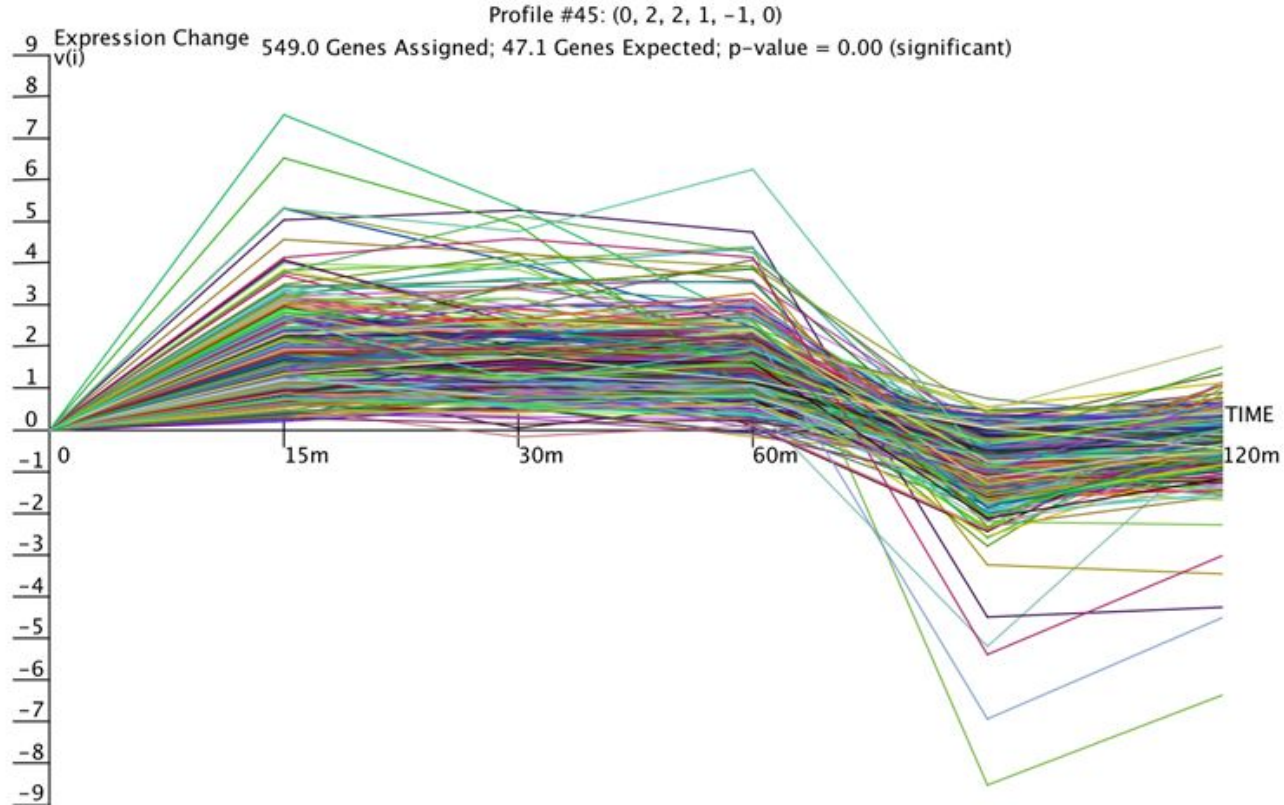
Genes were clustered into groups with similar regulation mechanisms

- Clusters ordered by significance
- Cluster 45 and 48 genes demonstrate upregulation
- Cluster 9 and 0 demonstrate downregulation

Clusters ordered based on number of genes and profiles ordered by significance (default)



Profile 45 demonstrates clear upregulation after cold shock





A table of GO terms sheds light on the function of the regulatory genes

Category Name	#Genes Category	#Genes Assigned	#Genes Expected	#Genes Enriched	p-value	Corrected p-value	Fold
cellular component organization (GO:0016043)	540	161	162.7	-1.7	0.6	1	1
nuclear lumen (GO:0031981)	327	183	98.5	84.5	2.40E-27	<0.001	1.9
RNA binding (GO:0003723)	215	116	64.8	51.2	6.30E-15	<0.001	1.8

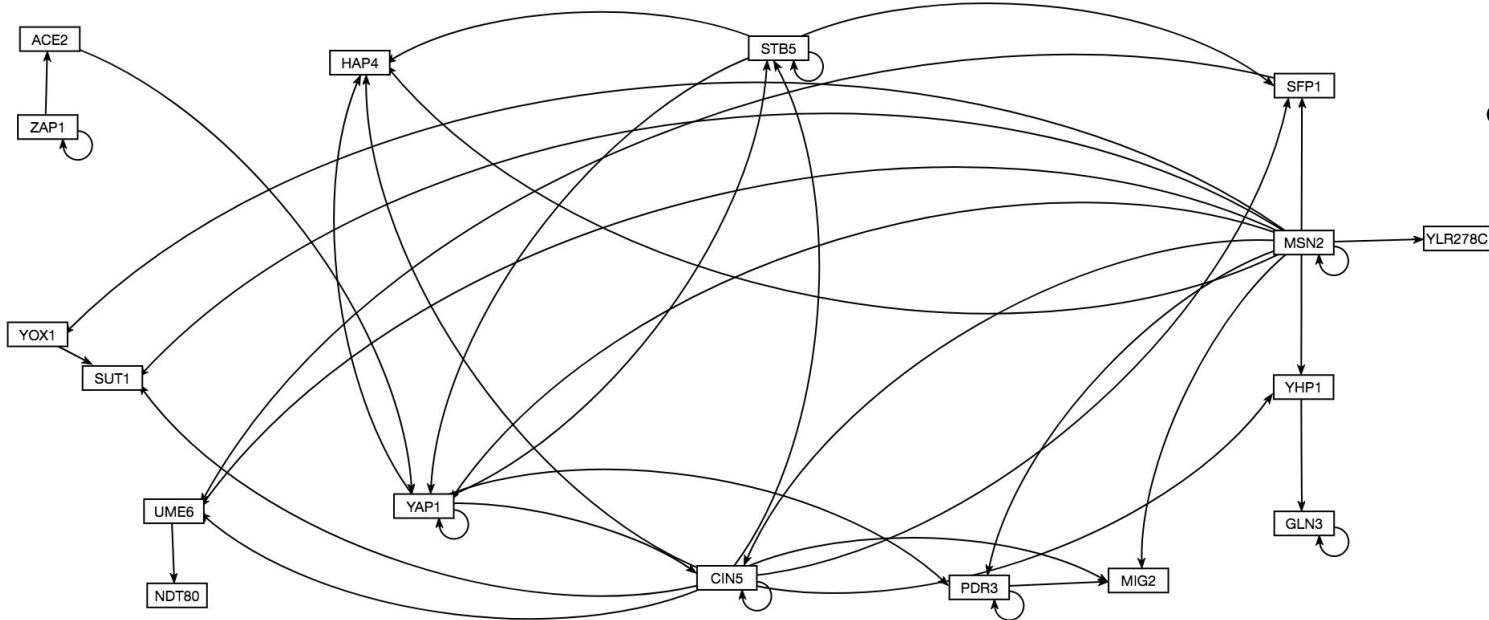


Transcription factors for the network were selected based on significance

TF	NDT80	YAP1	PDR3	UME6	MIG2	ZAP1	HAP4	CIN5
P-value	9.74E-10	1.31E-09	2.82E-09	6.12E-09	1.96E-08	2.99E-03	3.02E-02	0.806

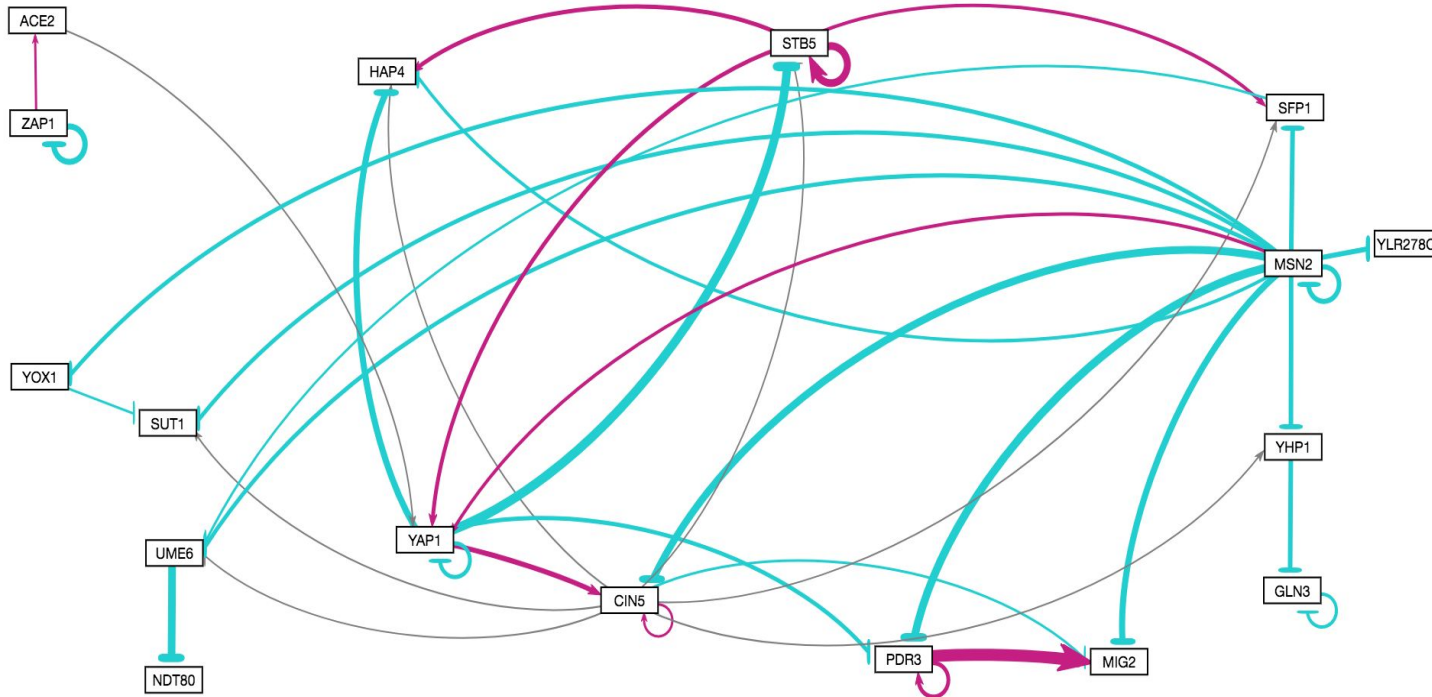
TF	YOX1	SFP1	YHP1	SUT1	STB5	ACE1	MSN2	GLN3
P-value	0	0	0	7E-15	7E-15	1.9E-14	2.72E-13	9.15E-11

Some genes are interconnected more than others



- Arrows indicate induction
- Bars indicate repression

A weighted network details the nature of the interaction



- **Pink** lines indicate induction
- **Blue** lines indicate repression
- **Thickness** of lines indicate magnitude of interaction



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Right click functionality allows for easy access to additional gene information

```
.on("dblclick", nodeTextDbclick)
.on("contextmenu", function (gene) {
    var tempLink = $("</a>")
        .attr({
            href: "/gene/info.html?" + $.param({symbol: gene.name}),
            target: "_blank"
        });
    $("body").append(tempLink);
    tempLink.get(0).click();
    tempLink.remove();
    d3.event.preventDefault();
});
```

Inter team collaboration aided in development of new functionality

GRNSight



Web app and service for visualizing models of gene regulatory networks

[S000005111](#) etc. [YNL167C](#) [<name xmlns="http://uniprot.org/uniprot">SKO1_YEAST</name>](#) [MA0382.1](#)

SKO1 Genus Species

[General Information](#)

[DNA Sequence](#)

[Protein Information](#)

[Gene Map](#)

[Regulation](#)

[Interaction](#)

[Gene Ontology](#)

[Frequency Matrix and Sequence Logo](#)



Inter team collaboration aided in development of new functionality

```
var sgdHrefTemplate = "https://www.yeastgenome.org/locus/";  
var sgdId = gene.sgd.sgdID;  
$(".sgd-link").text(sgdId).attr({ href: sgdHrefTemplate + sgdId });
```

```
// DNA Sequence Tab  
var ensemblDNA = gene.ensembl.dnaSequence;  
$(".dnaSequence").text(ensemblDNA).attr({ href: ensemblHrefTemplate + ensemblDNA });
```

Frequency Matrix and Sequence Logo help visualize data from JASPAR





Code for Frequency Matrix and Sequence Logo

```
var frequencyMatrix = gene.jaspar.frequencyMatrix;
var a = "";
for (var i = 0; i < frequencyMatrix.A.length; i++) {
    a += "<td>" + frequencyMatrix.A[i] + "</td>";
}
```

```
var sequenceLogo = gene.jaspar.sequenceLogo;
$(".sequenceLogo").attr({ src : sequenceLogo });
```



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This team is confident that our contributions will aid future research

- Studying wild type yeast can show importance of certain genes in cold shock response when compared to mutated cells.
- Dynamic integration enhances user interface by providing the user with in depth information on the desired gene.
- Newly analyzed data and newly coded functionality will both lead to new discoveries about gene regulatory networks.



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There are many avenues available for further research

- **Microarray data of cold shock response in other eukaryotes**
- **Microarray data of other stress responses in yeast**
- **Prediction of related genes once right click function has been executed**
- **A function on the new gene page to alert the user that the page is loading or that data is being pulled**



Summary

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The Eddies

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