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

Blair Hamilton, Department of Mathematics
Emma Tyrnauer, Department of Biology
Katie Wright, Department of Chemistry and Biochemistry
Zach Van Ysseldyke, Department of AIMS

December 12, 2017
BIOL/CMSI 367-01: Biological Databases, Loyola Marymount University

Outline

- Coding new GRNsight functionality and performing yeast data analysis can lead to new insights in gene regulatory research

- Individual milestones contribute 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

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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
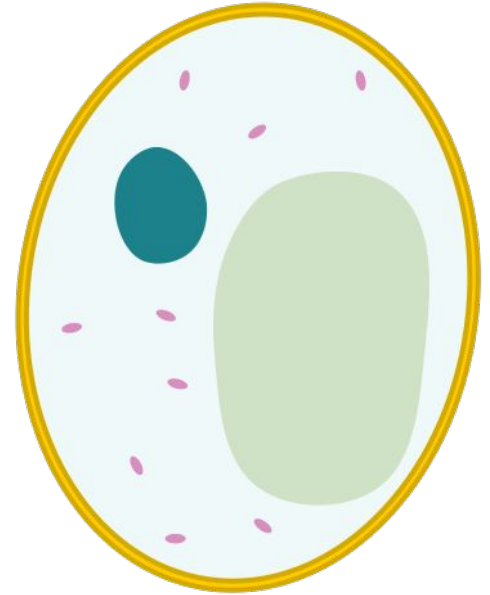
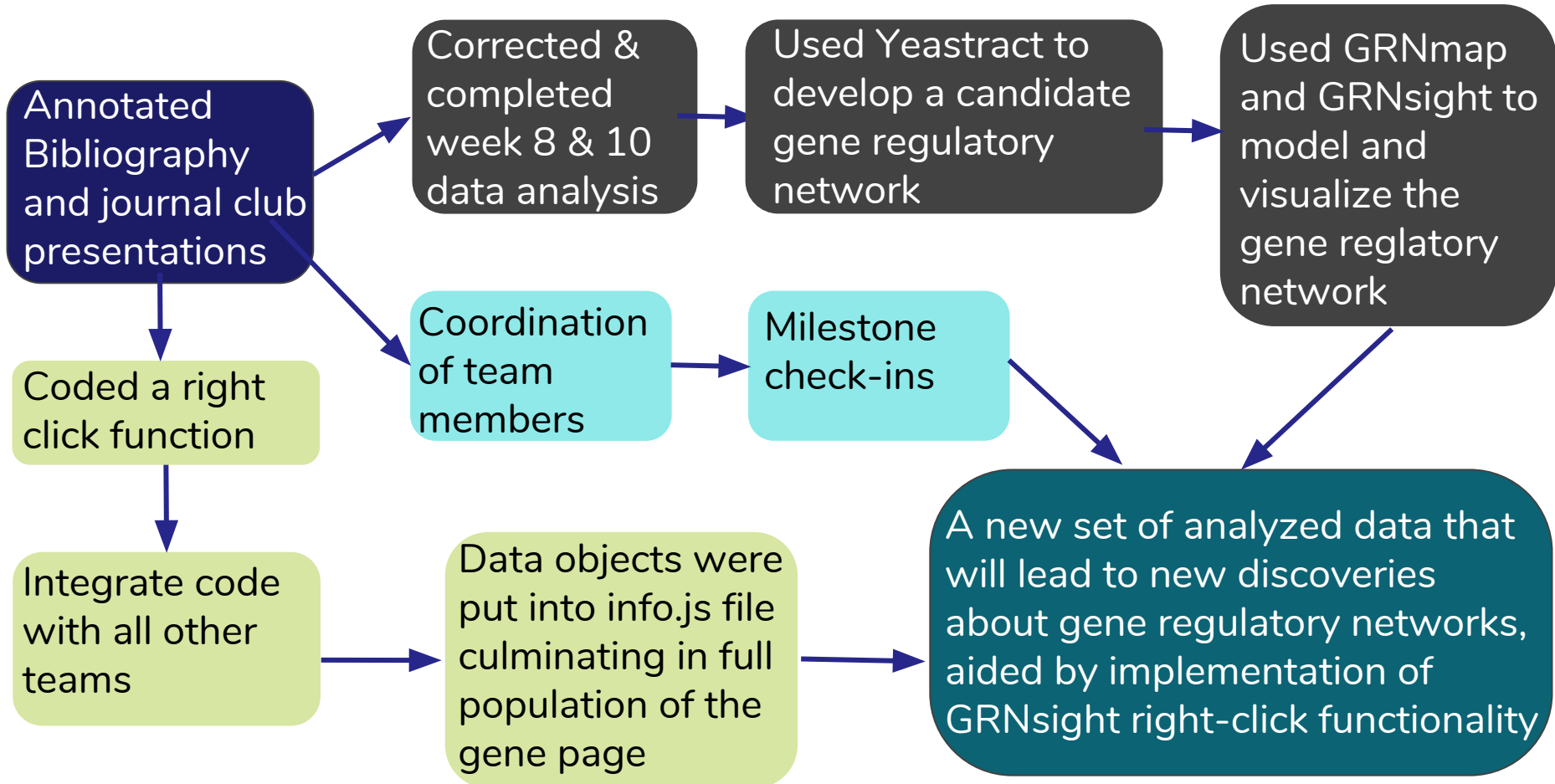# The right click functionality will be very useful for gene research

- Adding right click functionality

  - Readily available gene information

  - No need for extensive database searching

- Teamwork can be both rewarding and frustrating

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Individual milestones contribute to group effort

Annotated Bibliography and journal club presentations

Corrected & completed week 8 & 10 data analysis

Used Yeastract to develop a candidate gene regulatory network

Used GRNmap and GRNsight to model and visualize the gene reglatory network

Coded a right click function

Coordination of team members

Milestone check-ins

Integrate code with all other teams

Data objects were put into info.js file culminating in full population of the gene page

A new set of analyzed data that will lead to new discoveries about gene regulatory networks, aided by implementation of GRNsight right-click functionality

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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)
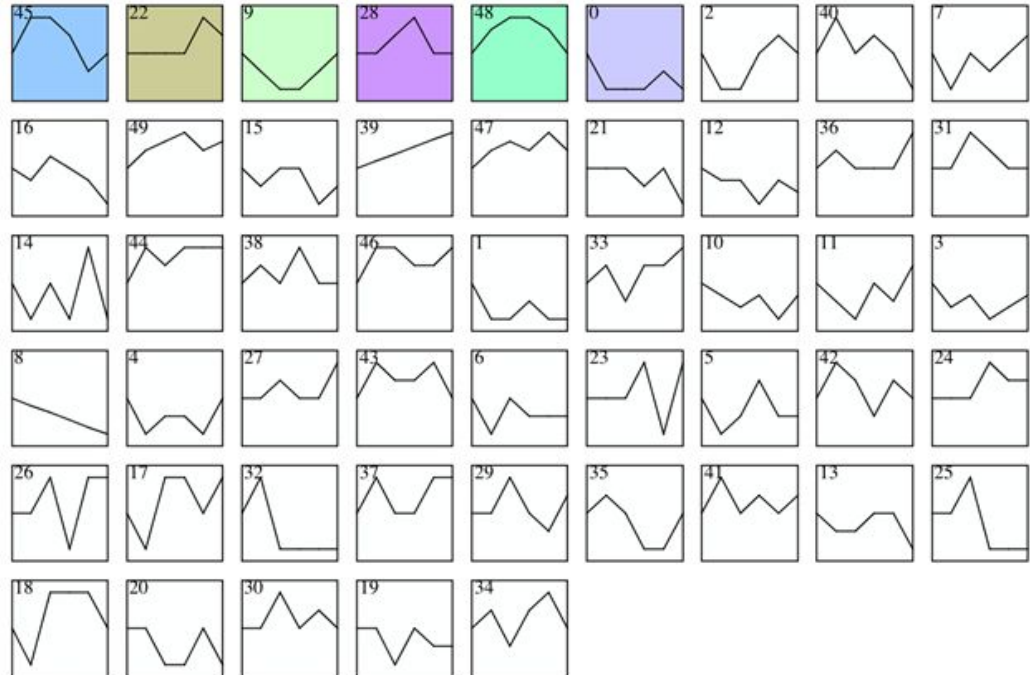
Profile 45 demonstrates clear upregulation after cold shock

Profile #45: (0, 2, 2, 1, −1, 0)

549.0 Genes Assigned; 47.1 Genes Expected; p–value = 0.00 (significant)
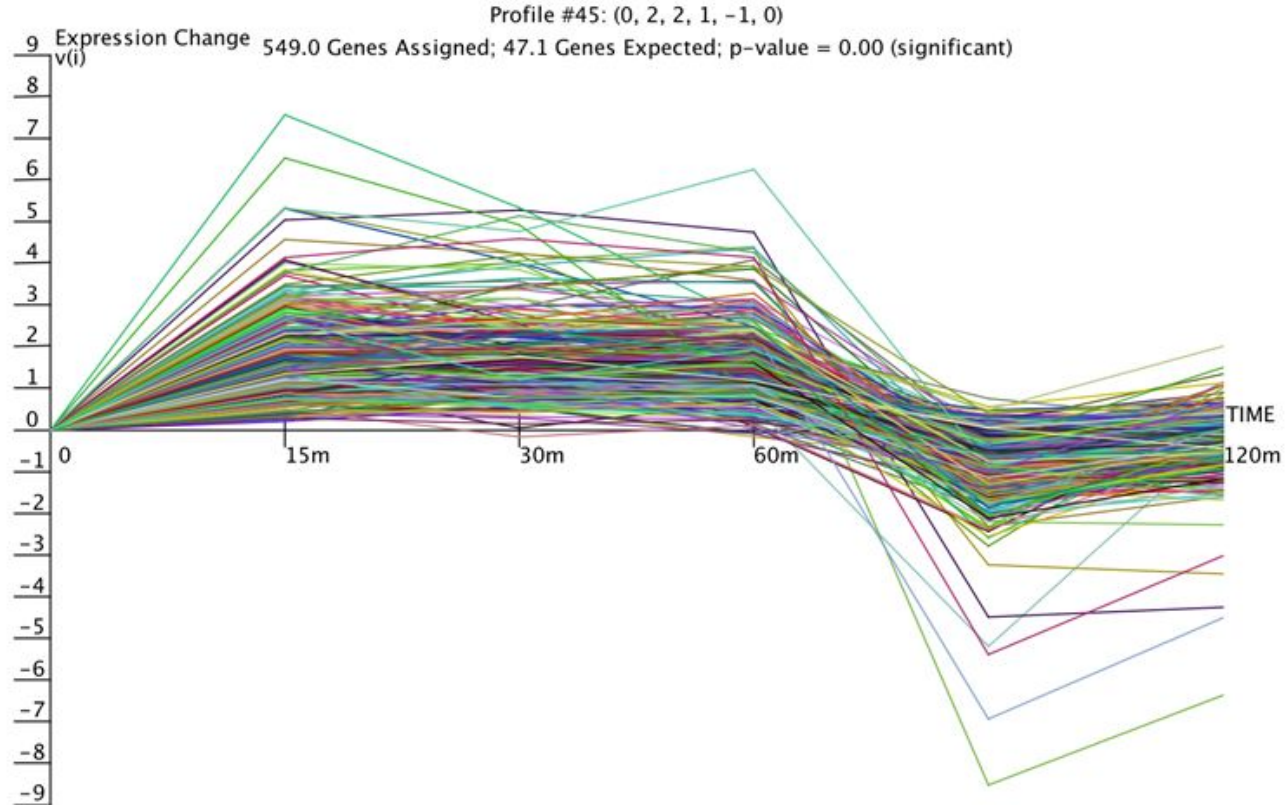
A table of GO terms sheds light on the function of the regulatory genes

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
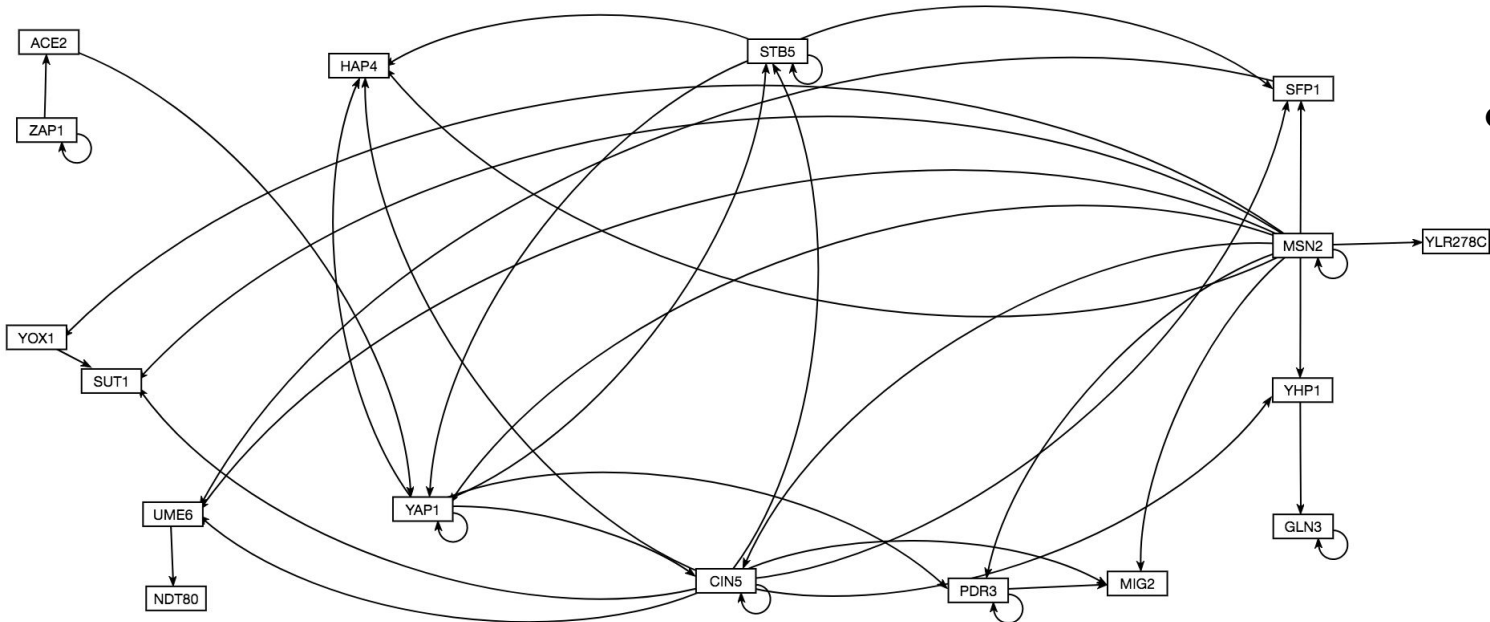
- **Arrows indicate induction**
- **Bars indicate repression**

A weighted network details the nature of the interaction
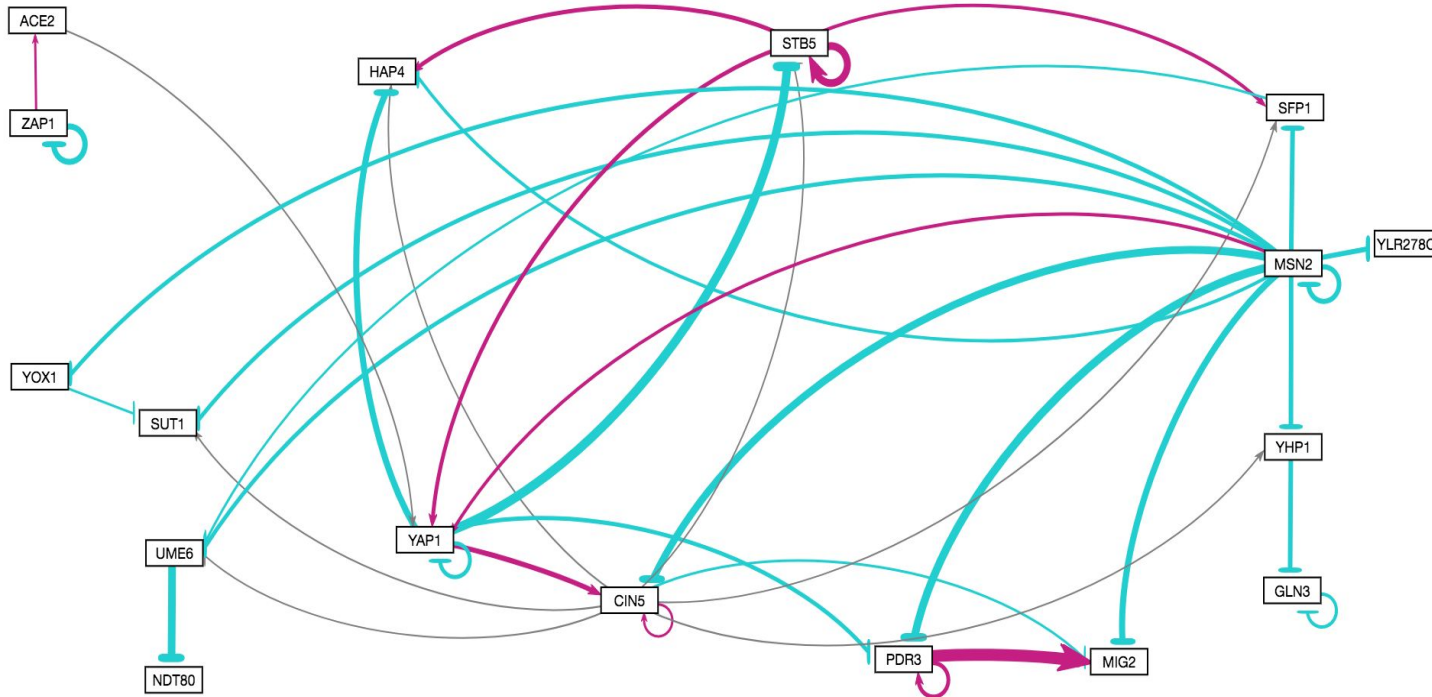
- **Pink** lines indicate induction
- **Blue** lines indicate repression
- Thickness of lines indicate magnitude of interaction

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Right click functionality allows for easy access to additional gene information

```javascript
.on("dblclick", nodeTextDblclick)
.on("contextmenu", function (gene) {
    var tempLink = $("<a></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

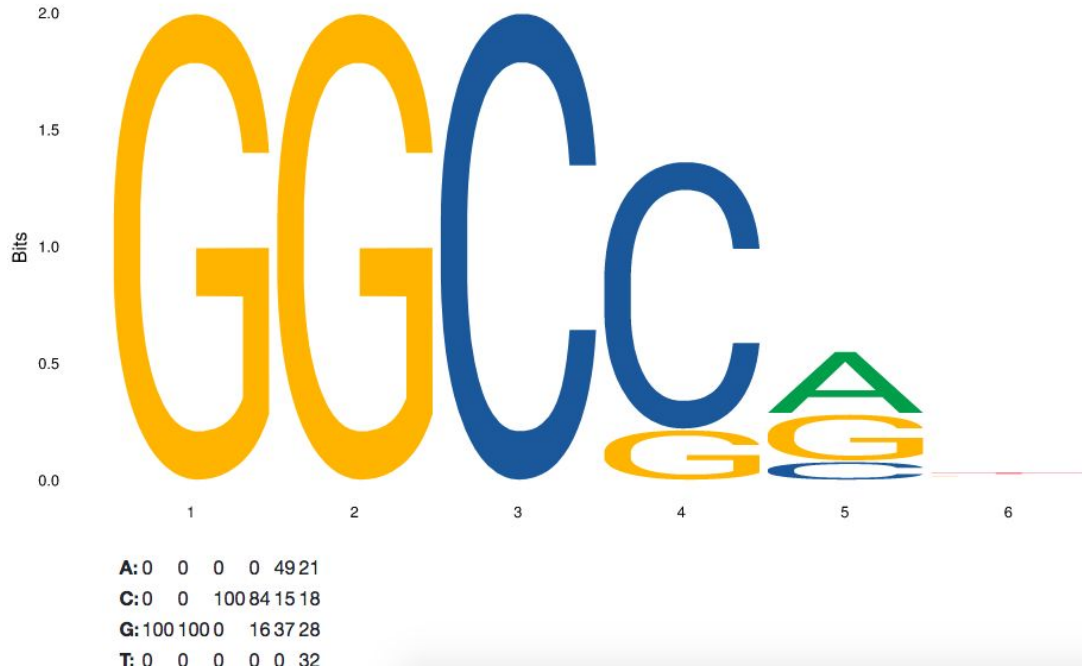Frequency Matrix and Sequence Logo

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

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

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

Conclusions

- 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.

Future Directions

- 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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Acknowledgements

Loyola Marymount University, Seaver College of Science and Engineering

The Departments of Biology, Mathematics, Computer Science, Chemistry and Biochemistry, and AIMS

Professor Dionisio and Professor Dahlquist

The Eddies

Students of BIOL/CMSI 367-01: Biological Databases

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