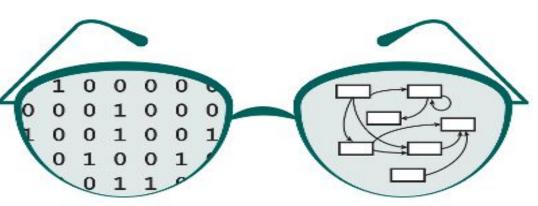
More Robust Testing of Data and UI for GRNsight: a Web Application for Visualizing Models of GRNs

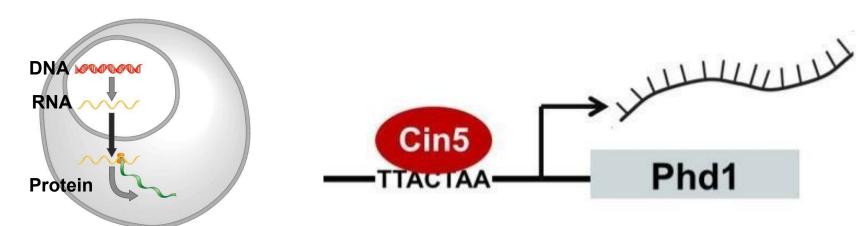


Onariaginosa O. Igbinedion*, Ian M. Green*, Ahmad R. Mersaghian**, John David N. Dionisio*, Kam D. Dahlquist**
*Department of Computer Science, **Department of Biology Loyola Marymount University, 1 LMU Drive, Los Angeles, CA 90045 http://dondi.github.io/GRNsight/

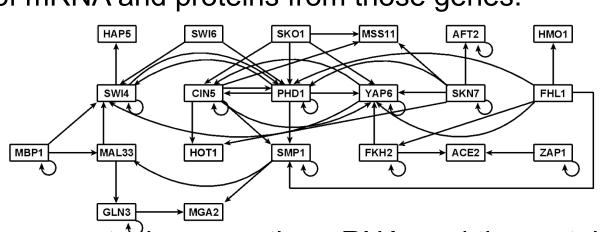


Gene Regulatory Networks Can Be Illustrated by Directed Graphs

- The central dogma of molecular biology describes the flow of information in a cell during gene expression from DNA to RNA to protein.
- Transcription factors control gene expression by binding to regulatory DNA sequences.
- Activators increase gene expression.
- Repressors decrease gene expression.
- Transcription factors are themselves proteins encoded by genes.



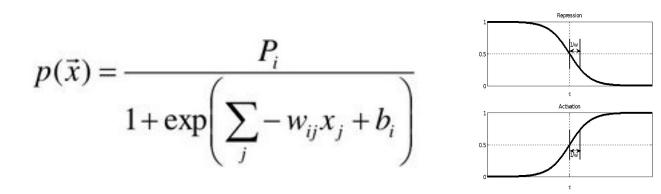
• A gene regulatory network (GRN) consists of genes, transcription factors, and the regulatory connections between them, which govern the level of expression of mRNA and proteins from those genes.



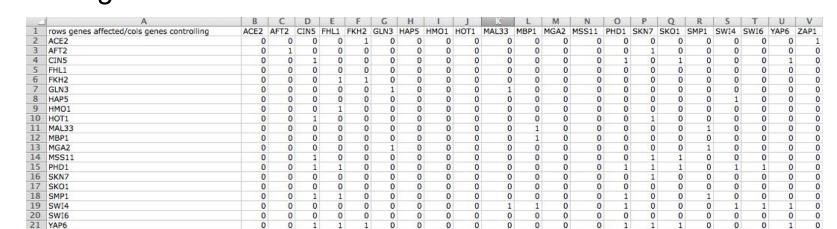
- Each node represents the gene, the mRNA, and the protein expressed from the gene.
- Each edge represents a regulatory relationship.
- All the nodes are transcription factors themselves.

GRNmap: Gene Regulatory Network Modeling and Parameter Estimation

The MATLAB model is available at http://kdahlquist.github.io/GRNmap/



- GRNmap is a differential equations model of the changes in gene expression over time for a gene regulatory network (Dahlquist et al. 2015)
- Each gene (node) in the network has an equation.
- The parameters in the model are estimated from laboratory data.
- The weight parameter, w, gives the direction (activation or repression) and magnitude of the regulatory relationship.
- GRNmap produces an Excel spreadsheet with an adjacency matrix representing the network.



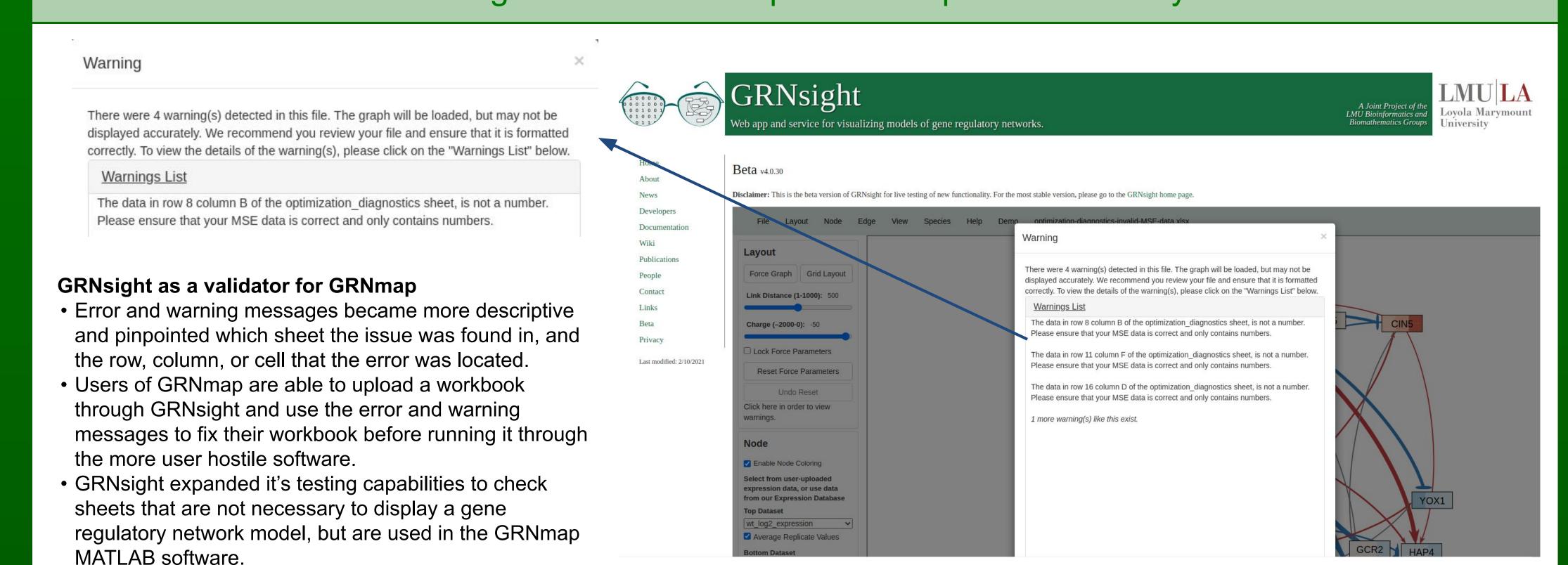
- 0 represents no relationship.
- Initially, 1 represents a regulatory relationship where the gene specified by the column controls the gene specified by the rows.
- After the parameters have been estimated, a positive weight value indicates activation and a negative weight value indicates repression.
- The magnitude of the weight defines the strength of the relationship. However, GRNmap does not generate a visual representation of GRNs.

GRNsight Accepts Microsoft Excel Files (.xlsx)

in the Proper Format • Excel workbooks need a "network" sheet (for unweighted graphs) or a

- "network_optimized_weights" sheet (for weighted graphs).
- The adjacency matrix can be symmetrical or asymmetrical. GRNmap input and output workbooks are accepted without adjustment.
- Adjacency matrices generated from other databases, such as
- YEASTRACT (Miguel et al., 2014), can be used with some modification.

Testing Suite can test Import and Export functionality



The Client Side Testing Documents Streamlines Testing of Frontend

"title": "Format Menu",

"text": "The edge weight should",

Export Data To Unweighted SIF To Weighted SIF Export Image Print To Unweighted GraphMI To Weighted GraphML Lock Force Parameters ZAP1 To Unweighted Excel Reset Force Parameters To Weighted Excel

• Client Side tests are generated for a subset of features by permuting all possible combinations

• These features are listed in JSON files, separated by their location in the user interface. These

• The generator script can include features based on an activation state in the features JSON, by

• The client side testing document was updated so that the features include their ID and the wiki

set the sidebar menu 'Enable Edge Coloring'

Client side features' descriptions were updated to better reflect the features intentions.

JSON files are read by the script and the requested features are used to generate the tests

• Each feature is given a unique static ID that is used to reference it easily.

command line arguments, or by a separate JSON file created by the tester.

Update Client Side Test Generator Script

GRNsight Client Side Testing Overview

> Enable Edge Coloring

Testing

was updated.

of feature states, creating steps for the user to follow.

Refactored Existing GRNsight import test, and expanded export

- Refactored existing GRNsight code to consolidate error and warning messages, as well as added new tests for additional sheets in a GRNsight workbook.
- Updated test to reflect additional features that GRNsight recently developed.
- Expanded export tests to increase user visibility on possible errors that occurred during the import process.
- Fixed bugs within the existing GRNsight export functionality and created a system to automatically fix minor issues within a workbook, alert the user of issues within a file that they must fix, or send an error message that something went wrong with the export process.

· Dropdown Menu: View -> Restrict Graph to Viewport - Check

The viewport should always be contained within the viewport

"Select \"Show With Mouse Over\"": "display when user mouses over an edge.",

"availability": {"NoGraphLoaded": true, "WeightedGraphLoaded": true, "UnWeightedGraphLoaded": true }

"Select \"Always Show Edge Weights\"": "always be visible." "Select \"Never Show Edge Weights\"": "not be displayed."

"included": true, // Includes this interaction group when generating tests.

Node coloring should become disabled, and Node Coloring Toggle Button text in sidebar menu should toggle off, if

LIbrary Updates

Updated Dependencies

- Dependencies had grown out of date and were updated
- Issues arose with outdated dependencies and Firefox versions above 80 as a result of increased privacy controls and protections
- Security vulnerabilities were identified within the dependencies as a result of outdated versions

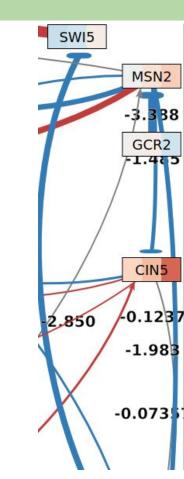
Began Migration of Deprecated Dependencies

- · Some dependencies, notably Jade, have been deprecated, threatening future iterations of GRNsight
- Migration of these libraries to their contemporary versions has begun to address this problem.

User Interface Improvements

Feature Addition

- Improved edge detection for nodes, eliminating issues with nodes going out of the viewport
- Gray Edge Threshold was fixed to properly gray out all edges at 100% threshold
- Toggle buttons were fixed so that all buttons properly represent the state of the program
- Viewport resizing was modified to account for window resizing

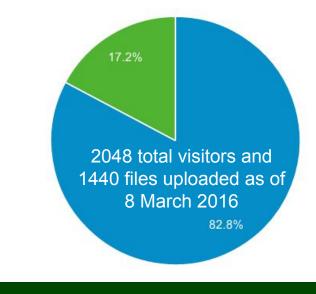


Future Directions

- Allow the Gene Page feature to support species beyond Saccharomyces cerevisiae by identifying the species name from a given datasheet.
- Implement tests for the Gene Page through the SinonJS testing framework.
- Add detailed tests for Excel export feature to ensure success with all data input formats.

Availability

- GRNsight is free and open to all users and there is no login requirement.
- Web site content is available under the Creative Commons Attribution Non-Commercial Share Alike license.
- GRNsight code is available under the open source BSD license.
- Usage is being tracked through Google





Acknowledgments

• This work is partially supported by NSF award 0921038 (K.D.D., B.G.F.), a Kadner-Pitts Research Grant (K.D.D.), the Loyola Marymount University Rains Research Assistant Program (N.A.A.), and the Loyola Marymount University Summer Undergraduate Research Program (A.V.).

References

- Bootstrap: https://getbootstrap.com/
- Dahlquist, K.D., Fitzpatrick, B.G., Camacho, E.T., Entzminger, S.D., and Wanner, N.C. (2015) Parameter Estimation for Gene Regulatory Networks from Microarray Data: Cold Shock Response in Saccharomyces cerevisiae. Bulletin of Mathematical Biology, 77(8), 1457-1492, DOI: 10.1007/s11538-015-0092-6
- Ensembl: https://uswest.ensembl.org/index.html
- Freeman, S. (2002) Biological Science. Upper Saddle River, New Jersey: Prentice Hall.
- GRNmap: http://kdahlquist.github.io/GRNmap
- JASPAR: jaspar.genereg.net
- National Center for Biotechnology InformationI: https://www.ncbi.nlm.nih.gov/
- Saccharomyces Genome Database: https://www.yeastgenome.org/
- SinonJS: https://sinonjs.org/