

GRNsight: a web application and service for visualizing models of small- to medium-scale gene regulatory networks

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Figure 1: This is a teaser image.

ABSTRACT

GRNsight is a web application and service for visualizing small- to medium-scale gene regulatory networks (GRNs). A GRN consists of genes, transcription factors, and the regulatory connections between them which govern the level of expression of mRNA and protein from genes. GRNsight produces weighted or unweighted network graphs based on an Excel spreadsheet containing an adjacency matrix where regulators are named in the columns and target genes in the rows, a Simple Interaction Format (SIF) text file, or a GraphML XML file. GRNsight represents genes as nodes and regulatory connections as edges with colors, end markers, and thicknesses corresponding to the sign and magnitude of activation or repression. GRNsight visualizations can be modified through manually dragging nodes or adjusting sliders that change the force graph parameters. GRNsight's diagrams are based on force graph layout algorithms of the D3.js data visualization library, which was then extensively customized to support the specific needs of GRNsight. GRNsight is best-suited for visualizing networks of fewer than 35 nodes and 70 edges, although it accepts networks of up to 75 nodes or 150 edges. GRNsight has general applicability for displaying any small, unweighted or weighted network with directed edges for systems biology or other application domains. The GRNsight application (<http://dondi.github.io/GRNsight/>) and code (<https://github.com/dondi/GRNsight>) are available under the open source BSD license.

CCS CONCEPTS

• Human-centered computing → Scientific visualization; Visualization toolkits;

KEYWORDS

ACM proceedings, \LaTeX , text tagging

ACM Reference format:

Anonymous Author(s). 2017. GRNsight: a web application and service for visualizing models of small- to medium-scale gene regulatory networks. In *Proceedings of SIGGRAPH 2017 Posters, Los Angeles, CA, USA, August 2017*, 2 pages. https://doi.org/10.475/123_4

1 INTRODUCTION AND MOTIVATION

GRNsight is a web application and service for visualizing models of small- to medium-scale gene regulatory networks (GRNs). 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 protein from genes. A review by Pavlopoulos et al. [Pavlopoulos et al. 2015], describes the types, trends, and usage of visualization tools available for genomics and systems biology. Their list of 47 tools for network analysis is representative of what was available to us at our project inception in January 2014 (given the caveat that the list itself is a moving target with some tools dropping out, new ones being added, and others evolving in their functions). With such a large number of tools available, it would be reasonable to expect that one already existed that could fulfill our needs. However, our use case was narrow, and the tools we investigated out of this diverse set each had properties that limited their use for us.

Requirements of our tool:

- (1) Exist as a web application without the need to download and install specialized software;
- (2) Be simple and intuitive to use;
- (3) Automatically lay out and display small- to medium-scale, unweighted and weighted, directed network graphs in a way that is familiar to biologists and adds value to the interpretation of the modeling results.

Figure 2: Ferrari LaFerrari. (Image courtesy Flickr user “freeman23.”)

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2 MATERIALS AND METHODS

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$$P(t) = \frac{b^{\frac{t+1}{T+1}} - b^{\frac{t}{T+1}}}{b - 1}, \quad (1)$$

where $t = 0, \dots, T$, and b is a number greater than 1, litora torquent per conubia nostra, per inceptos himenaeos.

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hendrerit dui. Aenean semper eros non eros ornare, vitae efficitur nunc consequat.

$$L_o(x, \omega_o, \lambda, t) = L_e(x, \omega_o, \lambda, t) + \int_{\Omega} f_r(x, \omega_i, \omega_o, \lambda, t) L_i(x, \omega_i, \lambda, t) (\omega_i \cdot n) d\omega_i \quad (2)$$

(Yes, that's the Rendering Equation.) [?]. Aenean pharetra ipsum eu mi fermentum dictum. Maecenas vel dolor semper, efficitur elit eget, bibendum diam. Duis vitae varius nisl. Proin aliquet sapien enim, eu vehicula ipsum euismod ut. Curabitur quis luctus quam, at ultricies ligula. Etiam imperdiet efficitur ipsum eu feugiat. Maecenas quis laoreet eros. Morbi molestie ac dui ac vestibulum. Donec maximus ex at neque posuere, et blandit tellus iaculis.

Figure 3: A sample black and white graphic that has been resized with the includegraphics command.

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3 RESULTS AND DISCUSSION

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$$F = \{F_x \in F_c : (|S| > |C|) \cap (\minPixels < |S| < \maxPixels) \cap (|S_{connected}| > |S| - \epsilon)\} \quad (3)$$

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3.2 Another Subsection

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4 CONCLUSION AND FUTURE WORK

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Georgios A. Pavlopoulos, Dimitris Malliarakis, Nikolas Papanikolaou, Theodosios Theodosiou, Anton J. Enright, and Ioannis Iliopoulos. 2015. Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. *GigaScience* 4, 1 (2015), 1. <https://doi.org/10.1186/s13742-015-0077-2>