**New layouts, data types, and architecture for GRNsight 3: a web application for visualizing gene regulatory networks**

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**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 accepts input files in the Excel, SIF, and GraphML formats and then produces weighted or unweighted network graphs by representing genes as nodes and regulatory connections as edges. Activation is represented with red edges, repression is represented with blue edges, and weight magnitudes below a certain threshold are represented with gray edges to denote weak activation or repression relationships. GRNsight now contains features to facilitate network comparison. Nodes on each graph show a heat map corresponding to gene expression levels over time; these nodes can be overlaid with up to two different data sets. The graphs generated by GRNsight may now be automatically laid out in a grid. When a user right-clicks on a gene, data requests are made to five public databases and a web page is dynamically populated with the data returned. Finally, a number of under the hood improvements were made to GRNsight’s architecture. Most notably, GRNsight was made to follow a strict Model-View-Controller (MVC) paradigm. MVC consolidates the application’s state into a single object, from which presentation and interaction are derived. GRNsight version 3.1.3 is freely available at http://dondi.github.io/GRNsight/; the code is available under the open source BSD license at https://github.com/dondi/GRNsight.