

Database, Display, and DevOps Improvements for GRNsight 7.2, a Web Application for Visualizing Gene Regulatory and Protein-Protein Interaction Network Models

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GRNsight is an open-source web application and service for visualizing models of gene regulatory networks (GRNs). A gene regulatory network consists of genes, transcription factors, and the regulatory connections between them, which govern the expression level of mRNA and protein from genes. GRNsight can now also display protein-protein physical interaction (PPI) networks. Whereas GRNs have directed edges, PPI networks have undirected edges to indicate protein binding. We have continued to integrate PPI networks so that users can display node coloring on a PPI with a choice of top or bottom datasets of expression data. GRNsight reads user-uploaded Microsoft Excel workbooks and automatically displays a graph. Users without their own data can use GRNsight's back-end PostgreSQL database to select a GRN or PPI based on yeast data from AllianceMine. Database loading scripts were ported to AllianceMine because YeastMine was discontinued. New graph functionality has been implemented that allows users to restrict the graph to viewport so that they can drag, zoom, and move the graph with the nodes staying within the application's bounding box. On the DevOps side, the project's continuous integration/development pipeline has been migrated from Travis CI to GitHub Actions, integrating workflows for automated builds, unit tests, and linting to streamline development processes and improve maintainability. Ongoing efforts prioritize bug resolution, user interface enhancements, and improved documentation. GRNsight is now positioned to comprehensively address GRNs and PPIs, offering a unified platform for visualizing diverse molecular interaction models. GRNsight is available at <https://dondi.github.io/GRNsight/>.