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 magenta edges, repression is represented with cyan edges, and weight magnitudes below a certain threshold are represented with gray edges to denote weak activation or repression relationships. New features have been added that allow the comparison of up to two different time course gene expression data sets. The graphs generated by GRNsight may now be automatically laid out in a grid, for easy visualization purposes. Additionally, each node label is now cross-referenced with five databases and a webpage is generated with gene-pertinent information. Finally, a number of under the hood improvements were done to improve GRNsight’s architecture. Most notably, GRNsight now mostly falls the Model-View-Controller (MVC) software archetype. MVC calls for a consolidated store for the application’s state, from which every action is executed and derived. GRNsight 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.