A Nanopublication Framework for Biological Networks using Cytoscape.js

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We leverage semantic technologies and Cytoscape.js to create a provenance-aware, probabilistic analysis platform for systems biology and evaluate its usefulness in discovering links between drugs and diseases. A number of databases have been developed that serve as a just one link across the landscape of systems biology, each focused on different experimental methods, many species, and a wide diversity of inclusion criteria. Systems biology has been used in the past to generate hypotheses for drug effects, but has become fragmented under the large number of disparate and disconnected databases. In this paper, we use a systematic approach to discovering new uses for existing data in the ReDrugS framework that can take data from nearly any database, connected or disconnected databases. In our efforts to create a systematic framework that can take data from nearly any database, connected or disconnected databases, in this paper, we use a systematic approach to discovering new uses for existing data in the ReDrugS framework that can take data from nearly any database, connected or disconnected databases.

Different databases can provide the same assertions. This might be by experimental replication! We model this with a composite z-score:

\[
P(x) = \left( \sum \frac{x}{\sqrt{n}} \right)
\]

The ReDrugS framework allows users to explore protein/protein, protein/disease, and drug/protein interactions using full text search, network expansion, and statistical aggregation. The edges are rendered with their width mapped to the probability that the link exists. These statin and topomate networks were built using a “disease finder” network expander.

Available: http://redrugs.tw.rpi.edu