PaIntDB: Visualizing Protein-protein interaction networks in *Pseudomonas aeruginosa*

CPSC 547 - Peer Review 2
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Objectives

- Create intuitive, user-friendly vis tool for biologists without a computational background to explore networks of protein interactions in *P. aeruginosa*.
- Deal with the “hairball” problem as networks get bigger.
Visualization

Dealing with the “hairball” problem:

- Create user-defined filters through the GUI to find specific nodes in the network, then generate smaller sub-network using only these genes.

**Filters:** Cellular location, experiment, associated GO term, fold change. Could add more? (Community detection, gene type)

**Example:** “Find all **up-regulated** genes identified through both TnSeq and RNASEq experiments associated with **DNA Repair** located in the **cytoplasm**.”
Visualization

Filter: GO term = RNA Processing
Future Work

● Finish visualization module (add GO term enrichment to the GUI, filters, new view for sub-networks).
● Implement algorithm to make minimally-connected networks out of first-order networks.
● Develop APIs to visualize generated networks in NetworkAnalyst or Cytoscape, if the user chooses.
● Add PseudoCyc pathways.
● Add sRNAs to database, possibly scrape more data to create additional filters.