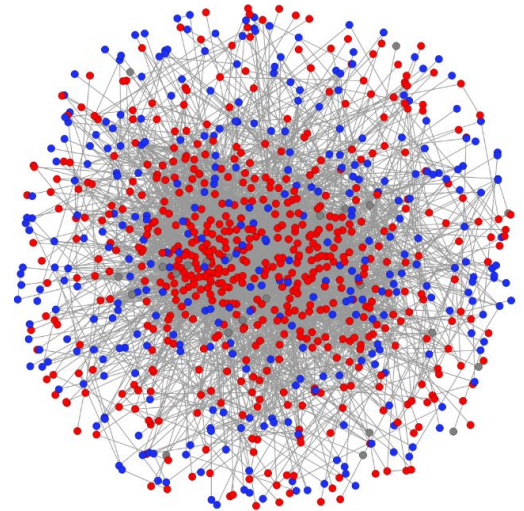
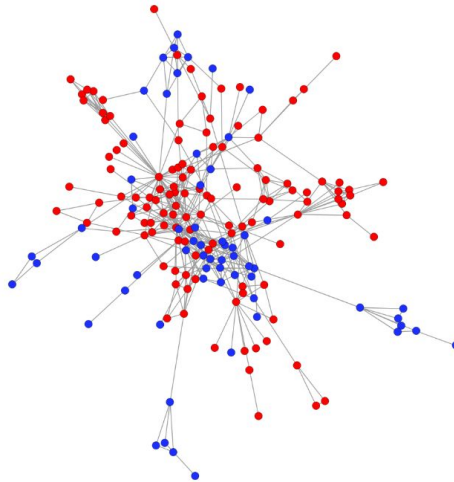
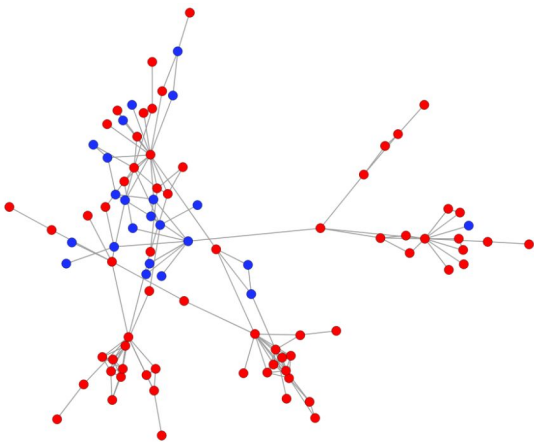


PaIntDB: Visualizing Protein-protein interaction networks in *Pseudomonas aeruginosa*

CPSC 547 - Peer Review 2
Javier J. Castillo-Arnemann
October 8, 2019

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.



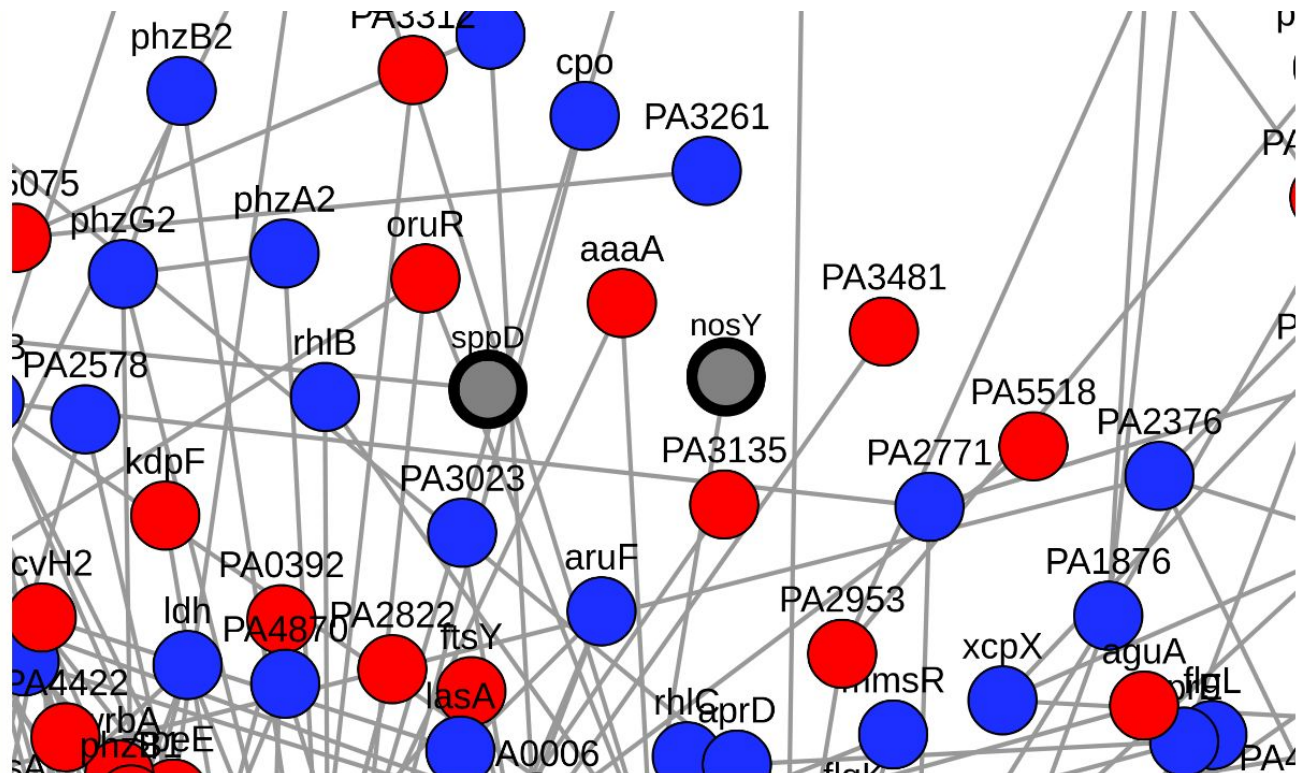
Color Mapping

- Significance Source
- Differential Expression

Select nodes

▼ By source of interest

- RNASeq
- TnSeq
- Both



Selected Node Details

shortName	description	log2FoldChange	padj	ncbi	uniprotkb
rplP	50S ribosomal protein L16		nan	NP_252946.1	Q9HWE2
rpsC	30S ribosomal protein S3		nan	NP_252947.1	Q9HWE1
ftsZ	cell division protein FtsZ		nan	NP_253897.1	P47204
hemB	delta-aminolevulinic		nan	NP_253930.1	Q59643

Visualization

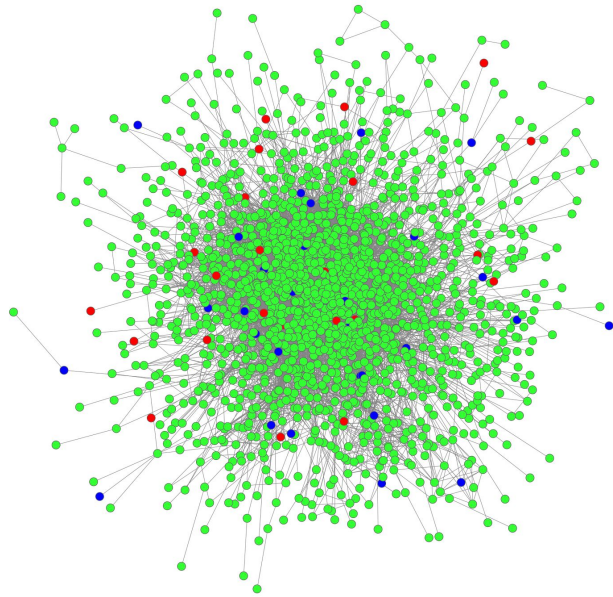
Dealing with the “hairball” problem:

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

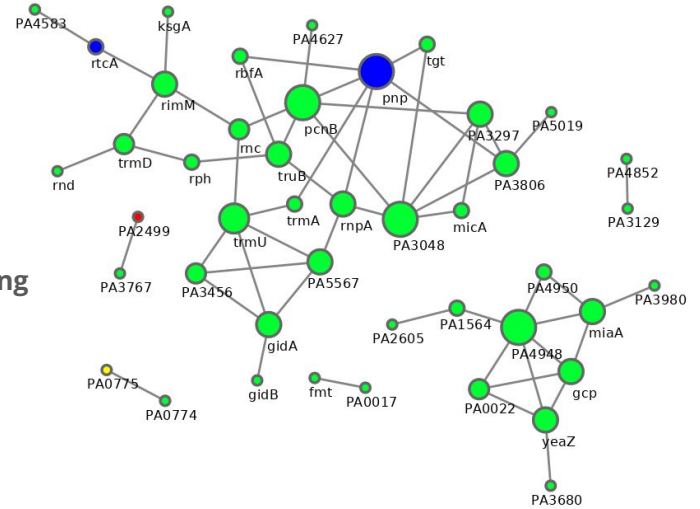
Filters: Cellular location, experiment, associated GO term, fold change. Could add more? (Community detection, gene type)

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.