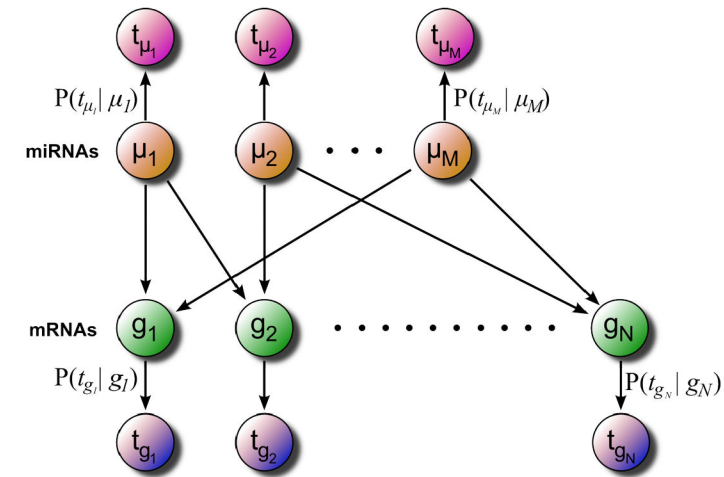
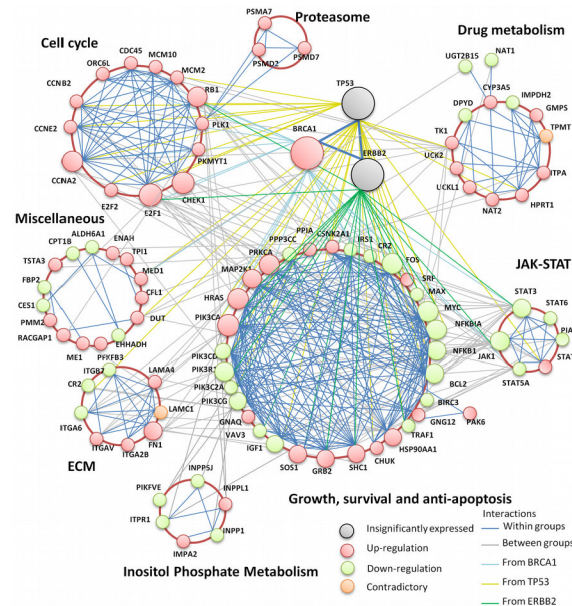



Bernie J. Daigle, Jr.

Departments of Biological Sciences and Computer Science

- Bioinformatics: My lab is developing computational tools for integrating genome-scale datasets to identify biomarkers for human disease. We are currently constructing a novel Bayesian network model for microarray data that leverages known interactions between messenger RNAs and microRNAs to more accurately characterize post-traumatic stress disorder (PTSD).



 Computational Systems Biology: My lab is performing modeling, simulation, and analysis of stochastic biological systems to infer detailed mechanisms of transcriptional regulation. We are currently developing parameter estimation and model selection techniques to characterize differences in mouse promoter architecture using single-cell gene expression data.

