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Jason E McDermott* (jason.mcdermott@pnnl.gov), **Jennifer Webster**, **Ryan McClure**, **Stephen J Young** and **Mahantesh Halappanavar**. *Biological graph analysis applications connecting molecular measurements with phenotype*. Preliminary report.

Biological graphs are commonly inferred from high-throughput measurements of biological molecules (mRNA, proteins, lipids, metabolites) from cells or tissues. Advances in ‘omics technologies have driven the generation of multi-omic datasets, and thus integrated multi-omic graphs. In these graphs nodes represent different molecular species (mRNA, protein, post-translational modifications, lipids, metabolites) and edges represent statistical and/or predictive relationships between molecules based on their abundance patterns over a range of different observations (time points, treatments, patients). Clusters of nodes in these graphs commonly represent important and coherent functional groups whose response to specific conditions lead to phenotypic outcomes of the overall system. In this talk I will describe the development of approaches for inferring multi-omic graphs, use of graph analytic clustering approaches to better characterize functional modules, and how these graphs can be used to formulate hypotheses about biological mechanisms in cancer, infectious disease, and soil ecosystems. (Received September 26, 2017)