**Improved community detection through data integration with the stochastic block model**

The study of gene networks relating to a given disease area often involves analysis of multiple sources of network data that feature weak and widespread signal and low signal to noise ratio. In this setting, interest commonly lies in detection of latent community structure in a given gene network. The stochastic block model (SBM) is a flexible and standard network model with the ability to perform community detection, though it suffers from poor performance in the case of weak and widespread signal. In many settings, data from multiple experiments on the same set of genes is available for use. Examples of such complimentary data sources are gene expression, DNA methylation, and more recently, literature mining experiments, each of which are concerned with measuring associations among a similar set of genes and often feature low signal to noise ratio. To address the issue of weak and widespread signal in network data, we propose a data integration framework for the SBM, whereby multiple available data sources are combined into a unified network model for a given gene set. We show through simulation studies that our proposed method offers improved community detection inference for a variety of settings when compared to SBMs fit to single data sources or under alternative data integration approaches. In future work, we plan to extend our data integration method to the Bayesian setting to allow for the use of prior information to guide community detection and further improve SBM performance in the case of weak and widespread signal.