1154-62-857 **Emily T Winn***, Box F, Brown University, Providence, RI 02906, and **Lorin Crawford**. *Unified Topological and Geometric Characterization of Genomic Networks Underlying Complex Traits in Genome-wide Association Studies.*

In many biological applications, graph-based methods have become widely used to represent large genomic data sets due to their ability to not only visualize sophisticated relationships between random variables, but also provide interpretable distance measures for comparing various populations. Unfortunately, current distance metrics are not flexible enough to reliably quantify differences between graphs in high-dimensional data settings where notable deviations can occur at either local or global scales. Here, we propose a novel Bayesian framework for estimating an optimal distance via a mixture of functions frequently used in the literature. Furthermore, to ensure both scalability and interpretability for our approach, the distances we compute are based on groups of nodes (features) defined by biologically relevant annotations (e.g. SNPs to genes, genes to signaling pathways). Our main contribution is a unified method which gives detailed insights about the sub-graphical structures driving the variation between classes of observations (such as case-control studies) and offers a new means of biological enrichment analyses with graphs. (Received September 11, 2019)