



TMF: Novel Higher-Order Multi-View Network Analysis Pipeline for Multi-Omics Network Inference with Application to COPD Gene Data

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Abstract: Understanding relationships between molecular features in the context of a trait can give insight into biological mechanisms and move away from the reductionist approach of studying single genes or proteins at a time (Langfelder & Horvath, 2008). Constructing multi-omics networks with respect to the trait(s) of interest can be used to accomplish this goal but is also challenging due to multiple data sets with high dimensionality. SmCCNet (Shi et al., 2019) is a pioneering method in this area, which constructs multi-omics network modules by integrating 1 or 2 omics types and a single trait of interest. However, various issues and limitations are presented when conducting network inference with SmCCNet, which include but are not limited to (1) failing to consider the higher-order correlation between omics data, (2) computationally intensiveness and (3) limitations to only to 1 or 2 omics data types. In this project, we propose a novel and efficient multi-omics network analysis pipeline Sparse Generalized Tensor Canonical Correlation Network Analysis (SGTCCANet), an extension of tensor canonical correlation analysis (Luo et al., 2015), that shares the same stepwise structure as SmCCNet, but significantly elevates each step by addressing all issues and limitations of SmCCNet. A simulation study will be performed to demonstrate the superiority of SGTCCA-Net over SmCCNet in various settings, and the novel pipeline will be implemented to TOPMed data from COPDGene for network inference towards traits for chronic obstructive pulmonary disease (COPD) with omics data such as transcriptomics, proteomics, and metabolomics.

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