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The Scalable Birth-Death MCMC Algorithm for Mixed Graphical Model Learning with Application to Genomic Data Integration

Recent advances in biological research have seen the emergence of high-throughput technologies with numerous applications. In cancer research, the challenge is now to perform integrative analyses of high-dimensional multi-omic data with the goal to better understand genomic processes that correlate with cancer outcomes. We propose here a novel mixed graphical model approach to analyze multi-omic data of different types (continuous, discrete and count) and perform model selection by extending the Birth-Death MCMC (BDMCMC) algorithm. We compare the performance of our method to the LASSO and the standard BDMCMC methods using simulations and found that our method is superior in terms of both computational efficiency and the accuracy of the model selection results. Finally, an application to the TCGA breast cancer data shows that integrating genomic information at different levels (mutation and expression data) leads to better subtyping of breast cancers.