Recent genetic studies have identified genes related to specific human diseases or traits. Besides marginal analysis of individual genes, analyzing biologically meaningful gene pathways, i.e., networks with nodes being genes and edges characterizing the presence/absence of the gene-gene interactions, may yield valuable insights. Identifying gene pathways that differ between conditions can be formulated as a multivariate hypothesis testing problem, but existing approaches handle the gene-gene correlations in inefficient ways, leading to inflated type I error rate and/or compromised power. Dr. Wang proposes a Hotelling’s T2-type statistic, named the T2-DAG test, which efficiently leverages the edge information in the gene pathway through a linear structural equation model. He investigates asymptotic properties of the T2-DAG test under pertinent assumptions and compare the T2-DAG test with six existing methods under various simulation settings. He also applies the T2-DAG test to a lung cancer gene expression data set, and identity several interesting gene pathways that are relevant to different stages of lung cancer.

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