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*A Hidden Markov Tree Model for Multiple Hypotheses Testing of Gene Ontology Gene Sets*

Testing predefined gene categories has become a common practice for scientists analyzing high throughput transcriptome data. A systematic way of testing gene categories leads to testing hundreds of null hypotheses that correspond to nodes in a directed acyclic graph. The relationships among gene categories induce logical restrictions among the corresponding null hypotheses. Under a hidden Markov tree model, we develop a computationally efficient method to incorporate the dependence information among the null hypotheses. Our method provides more powerful results than existing methods that honor the logical restrictions.