

Gene-set Integrative Omics Analysis Using Tensor-based Association Tests

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Abstract: Integrative multi-omics analyses integrate complementary level of information from different molecular events and have great potentials to detect novel disease genes and elucidate disease mechanisms. One major focus of integrative analysis has been on identifying gene-sets associated with clinical outcomes, and a common strategy is to regress clinical outcomes on all genomic variables in a gene set. However, such joint modeling methods encounter the challenges of high-dimensional inference, especially the sample size is usually moderate either due to research resources or missing data. In this work, we consider a tensor-based framework to enhance model efficiency for variable-wise inference. The tensor framework reduces the number of parameters by accounting for the inherent matrix structure of an individual's multi-omics data and naturally incorporates the relationship among omics variables. We study the variable-specific testing procedure under tensor regression framework and enhance computational efficiency of the omics tensor modeling. We evaluate the performance of the tensor-based test using simulations and real data application on the Uterine Corpus Endometrial Carcinoma dataset from the Cancer Genome Atlas (TCGA).