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A Moderated Trace Test for the Growth Curve Model and Its Application for Gene-Filtering in Time-Course Microarray Data

Traditional tests for analyzing longitudinal data are not applicable in high-dimensional setup (when $n < p$). We propose a moderated test using the Growth Curve Model, which is useful for analyzing high-dimensional longitudinal data. Extensive simulations demonstrated that our moderated test is unbiased, and is monotone with respect to sample size and parameter value, regardless of the covariance. We illustrated the application of our method for gene-filtering in time-course micro-array data using lung cancer data, where measurements were taken from normal and chemically treated human lung tissues. We were able to identify 1053 (4.7%) significant ones out of 22,227 genes.