Gene-gene Interaction Screening by Kendall's Partial Correlation for Ultrahigh-dimensional Survival Data

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Abstract

Motivation: In genome-wide association studies, the identification of interaction effects is an important and challenging issue owing to its ultrahigh dimensional nature. In particular, contaminated data and right censored survival outcome make the associated feature screening even challenging.

Results: In this paper, we propose an inverse probability-of-censoring weighted Kendall's tau statistic to measure association of a survival trait with biomarkers, and a Kendall's partial correlation statistic to measure the relationship of a survival trait with an interaction variable conditional on main effects. The Kendall's partial correlation is then used to conduct interaction screening. Simulation studies under various scenarios are performed to compare the performance of our proposed method with current ones. In the real data application, we utilize our proposed method to identify epistasis that is associated with clinical survival outcome data of non-small-cell lung cancer patients. Both simulation and real data studies demonstrate that our method performs well and outperforms existing methods in identifying causal main and interaction biomarkers.