

Yale SCHOOL OF PUBLIC HEALTH

Biostatistics

Presentation

" Bayesian finite mixture of regression analysis for cancer based on histopathological imaging–environment interactions "

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ABSTRACT

Cancer is a heterogeneous disease. Finite mixture of regression (FMR)—as an important heterogeneity analysis technique when an outcome variable is present—has been extensively employed in cancer research, revealing important differences in the associations between a cancer outcome/phenotype and covariates. Cancer FMR analysis has been based on clinical, demographic, and omics variables. A relatively recent and alternative source of data comes from histopathological images. Recently, it has been shown that high-dimensional histopathological image features, which are extracted using automated digital image processing pipelines, are effective for modeling cancer outcomes/phenotypes. Histopathological imaging–environment interaction analysis has been further developed to expand the scope of cancer modeling and histopathological imaging-based analysis. Motivated by the significance of cancer FMR analysis and a still strong demand for more effective methods, in this study, we take the natural next step and conduct cancer FMR analysis based on models that incorporate low-dimensional clinical/demographic/environmental variables, high-dimensional imaging features, as well as their interactions. Complementary to many of the existing studies, we develop a Bayesian approach for accommodating high dimensionality, screening out noises, identifying signals, and respecting the “main effects, interactions” variable selection hierarchy. Simulation shows advantageous performance of the proposed approach. The analysis of The Cancer Genome Atlas data on lung squamous cell cancer leads to interesting findings.

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