

# Yale SCHOOL OF PUBLIC HEALTH

## *Biostatistics*

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### Presentation

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*"Integrative Analysis of Prognosis Data on Multiple Cancer Subtypes Using Compound Group Bridge"*

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**ABSTRACT:**

**In cancer research, profiling studies have been extensively conducted, searching for genes/SNPs associated with prognosis. Examining the similarity and difference in the genetic basis of multiple subtypes of the same cancer can lead to better understanding of their connections and distinctions. Integrative analysis approaches analyze the raw data on multiple subtypes simultaneously. In this study, prognosis data on multiple subtypes of the same cancer are analyzed. An AFT model is adopted to describe survival. The genetic basis of multiple subtypes is described using the heterogeneity model, which allows a gene/SNP to be associated with the prognosis of some subtypes but not the others. A compound penalization approach is developed to conduct gene-level analysis and identify genes that contain important SNPs associated with prognosis. The proposed approach has an intuitive formulation**

**and can be realized using an iterative algorithm. Asymptotic properties are rigorously established. Simulation shows that the proposed approach has satisfactory performance. An NHL (non-Hodgkin lymphoma) prognosis study with SNP measurements is analyzed.**

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