敬請張貼

淡 江 大 學 統 計 學 系

學 術 演 講

講　題：Network-adjusted Kendall's tau measure for feature screening with application to high-dimensional survival genomic data

主講人：王价輝 助理教授(逢甲大學統計學系)

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地　點：B302A（淡水校園商管大樓）

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*實體與線上視訊同步進行(視疫情滾動式調整)

摘 要

Motivation: In high-dimensional genetic/genomic data, the identification of genes related to clinical survival trait is a challenging and important issue. In particular, right-censored survival outcomes and contaminated biomarker data make the relevant feature screening difficult. Several independence screening methods have been developed, but they fail to account for gene－gene dependency information, and may be sensitive to outlying feature data.

Results: We improve the inverse probability-of-censoring weighted (IPCW) Kendall' s tau statistic by using Google' s PageRank Markov matrix to incorporate feature dependency network information. Also, to tackle outlying feature data, the nonparanormal approach transforming the feature data to multivariate normal variates are utilized in the graphical lasso procedure to estimate the network structure in feature data. Simulation studies under various scenarios show that the proposed network-adjusted weighted Kendall' s tau approach leads to more accurate feature selection and survival prediction than the methods without accounting for feature dependency network information and outlying feature data. The applications on the clinical survival outcome data of The Cancer Genome Atlas cancer patients demonstrate clearly the advantages of the new proposal over the alternative methods.

Keywords: Feature screening, Graphical lasso, Google' s PageRank matrix, IPCW Kendall' s measure, Survival prediction

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