

中央研究院統計科學研究所

博士後演講

講題：Massively parallel multi-mediator analyses with integrative genomic application

演講人：Dr. En-Yu Lai (賴恩語 博士後研究學者)

Institute of Statistical Sciences, Academia Sinica, Taipei, Taiwan (中央研究院統計科學研究所)

時間：2022年1月12日(星期三) 下午 14:00-15:00

地點：中央研究院統計科學研究所 B1F 演講廳

※茶會：下午 15:00 開始

※實體與線上直播同步進行

Abstract

Mediation analysis is performed to evaluate the effects of a hypothetical causal mechanism that marks the progression from an exposure, through mediators, to an outcome. Conventional methods for assessing mediation effects are not applicable to a massively parallel analysis and lose statistical power when the signals are sparse. To address this, Huang (2019) proposed an adjustment procedure, which unfortunately is limited to single-mediator analyses. Our contribution is to extend the method to the setting of multiple mediators that is more realistic and commonly encountered in genomic studies. We propose a series of approaches that enables large scale multi-mediator analyses integrating Huang's method and various multivariate non-mediation tests such as Hotelling's t-test, variance component test, minimum p-value method, Berk-Jones test, and higher-criticism test. Our methods can be categorized into global approaches that favor dense and diverse mediation effects, and local approaches that favor sparse and consistent effects. We also provide a method-selecting guideline supported by comprehensive simulation studies. Our analysis suite has been implemented as an R package `MACTest`. The utility is demonstrated by an application study of The Cancer Genome Atlas Lung Adenocarcinoma data set to investigate genes and networks whose expression may be regulated by smoking-induced DNA methylation aberration.

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