國 立 東 華 大 學 應 用 數 學 系
專 題 演 講

主 講 人 ：楊郁成博士/國立成功大學統計學系博士後研究員

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講　　題：楊郁成博士/ Extending t linear mixed models for longitudinal data with non-ignorable dropout applied to AIDS studies

龔一鴻博士/ Statistical Methods for Infectious Disease Risk and Transmission

時　　間：115年09月16日(星期三) 10:10-12:00

地　　點：理工一館A318教室

摘　要

楊郁成博士： One typical missing pattern in longitudinal data is dropout in the sense that some participants may withdraw prematurely and never return. Dropout is generally regarded as a non-ignorable mechanism when the probability of the occurrence of missing values is related to both observed and unobserved data. This paper aims at extending the t linear mixed models to cope with the problem of non-ignorable dropout for modeling continuous longitudinal data in the situation where outliers or heavy-tailed noises may be present. We consider the selection modeling strategy with a logistic link function to describe the relationship between the probability of missing process and some possible factors, including responses and extra covariates. A Monte Carlo expectation conditional maximization algorithm is developed to simultaneously compute maximum likelihood (ML) estimates of the missingness indexing parameters within the logistic link function and mixed-effects parameters of the full-data t linear mixed-effects (tLME) model that are of scientific interest. Additionally, the standard errors of the ML estimates can be calculated using the Monte Carlo version of the empirical information matrix. Two simulation studies are conducted to assess the capability of the tLME model in the presence of non-ignorable dropout and outliers. The performance is compared to its normal counterpart on the basis of information criteria indices, the precision of estimation for fixed effects and missingness indexing parameters, and the predictive accuracy of missing responses. The proposed methodology is demonstrated through a real-world example from an AIDS clinical trial, which provides practical implications when the non-ignorable dropout is considered in the analysis.

龔一鴻博士：Understanding the geographic variation and risk factors of infectious diseases is important for disease surveillance and public health decision-making. However, infectious disease data often exhibit complex spatial features, such as spatial autocorrelation, geographic clustering, excess zeros, nonlinear relationships, and interactions among multiple risk factors. These features pose considerable challenges for traditional statistical modeling and analysis.

In this talk, I will introduce several spatial statistical approaches for investigating infectious disease risk and transmission, with a particular focus on dengue fever in Taiwan. Spatial regression models are first applied to examine climatic, environmental, urbanization, and socioeconomic factors associated with disease risk. Geographic cluster detection methods, including mixture scan statistics and ellipse-shaped transmission hotspots, are then presented to identify high-risk areas while considering covariate effects, spatial dependence, and excess zeros.

I will further introduce a spatial regression tree framework that combines spatial dependence with the flexibility and interpretability of tree-based models. This approach aims to identify important risk factors while capturing spatial autocorrelation, nonlinear relationships, and interaction effects that may not be adequately characterized by conventional regression models. Dengue fever data from southern Taiwan are used to demonstrate the proposed framework and to investigate how climatic, environmental, and socioeconomic factors jointly influence disease risk.

Overall, these studies illustrate how spatial statistics and statistical learning can complement each other in understanding infectious disease transmission. The proposed approaches provide interpretable tools for identifying important risk factors and geographic hotspots and may contribute to more effective disease surveillance, targeted interventions, and public health decision-making.

Keywords: spatial statistics, statistical learning, spatial epidemiology, spatial autocorrelation, regression tree

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