

國立中山大學應用數學系

學術演講

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講題：From whole genomes to brain signals: Natural
vector and multilinear discriminant analysis

時間：2019/07/01 (Monday) 11:10 ~ 12:00

地點：理學院四樓理 SC 4009-1 室

茶會：10:30 於理 SC 4010 室 (系辦公室)

Abstract

In this talk, I will introduce my recent research about classifying and clustering whole genome sequences and brain signals. Recently African swine fever virus (ASFV) has new mutated strains in China. Alignment-free methods have become popular in comparative genomic analyses for their top performance, less computation time and higher computation power compared to alignment-based methods. Our classification and clustering results are consistent with the biological categorization and verified by the fact that the new China strain is close to the Russia-Georgia strain. In the EEG analysis, we aim to establish feature extraction using wavelet spectral decomposition and multilinear discriminant analysis for classifying EEG data.

Discriminant analysis has been widely applied in the field of biomedical research for a long time. In some applications, covariates of interest have a natural structure, such as being a matrix, at the time of collection. The rows and columns of the covariate matrix then has certain physical meanings, and they must contain useful information regarding the response. If we simply stack the covariate

matrix as a vector and fit the conventional discriminant analysis model, relevant information can be lost, and the problem of inefficiency will arise. We propose in this paper the multilinear discriminant analysis (MDA) model. Advantages of MDA include the preservation of the inherent matrix structure of covariates and the parsimony of parameters needed. In the EEG Database Data Set, we successfully extract the structural effects of covariate matrix, and a high classification accuracy is achieved.

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