國立中山大學應用數學系
學術演講

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講　題：Deciphering Important Variables and Interactions via a Logic Tree-based Ensemble Algorithm

時　間：2023/11/23 (Thursday) 14:10~15:00

地　點：理 SC 4009-1 教室

茶　會：13:30

Abstract

Single Nucleotide Polymorphisms and their interactions play a crucial role in disease research within Genome-Wide Association Studies (GWAS). Traditional approaches in these studies utilize statistical and machine-learning methods. While statistical methods necessitate predefined interaction types, pinpointing precise interactions amidst a plethora of features becomes a considerable challenge. On the other hand, machine-learning approaches provide enhanced prediction accuracy and can detect varied interactions, but their intricate nature and lack of interpretability often hinder their applicability in biomedical fields where clear understanding is paramount.

Logic regression, a statistical method based on the logic tree, composed of Boolean operations on features. It is used to observe the interactions between features and can be represented as a tree structure that aligns with human intuition, making it easy to interpret. However, in the context of GWAS where features are abundant but only a few of them are truly important. Logic regression may struggle to reliably detect interactions, leading to decreased prediction accuracy. To address these limitations, we propose an algorithm that integrates concepts from statistics and machine-learning, named the iterative weighted Logic Forest (iwLF). This algorithm employs ensemble learning and uses the logic tree as the base learner model, incorporating two types of weights settings.

Through a thorough comparative analysis of both simulation and real data, it is evident that our proposed algorithm outperforms other models related to the logic tree in terms of predictive accuracy and stability. Moreover, it has shown better efficiency in correctly identifying significant features and their interactions.

敬 請 公 告！ 歡 迎 參 加！

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