國立中山大學應用數學系
學術演講

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講　題：Association Study of Copy Number Variation via a Bayesian Procedure in Next Generation Sequencing

時　間：2019/12/5（Thursday）14:10 ~ 15:00

地　點：理學院四樓理 SC 4009-1 室

茶　會：15:00 於理 SC 4010 室（系辦公室)

Abstract

Copy number variations (CNVs) are genomic mutations consisting of abnormal numbers of gene fragment copies. Current algorithms for CNV association study for whole genome sequencing are restricted to a specific size or common / rare CNVs. We propose a Bayesian procedure to detect disease-associated CNVs. First, the absolute copy number of each window is estimated from sequencing read depths for every sample. And then the absolute copy numbers from case and control are compared to select candidate disease-associated windows. Finally, the information from neighboring windows is compared to identify the disease-associated copy number regions.

Key words: association study, Bayesian inference, copy number variation, next generation sequencing

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