

**MACQUARIE UNIVERSITY
STATISTICS DEPARTMENT SEMINAR**

Speaker: Professor Kim-Anh Do, Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Houston, USA

Date: Wednesday 20 June 2018, Time 2-3pm

Venue: 7 Wally's Walk, Room 149

Title: DINGO: Differential Network analysis in GenOmics

Abstract:

Motivation: Cancer progression and development are initiated by aberrations in various molecular networks through coordinated changes across multiple genes and pathways. It is important to understand how these networks change under different stress conditions and/or patient-specific groups to infer differential patterns of activation and inhibition. Existing methods are limited to correlation networks that are independently estimated from separate group-specific data and without due consideration of relationships that are conserved across multiple groups.

Method: We propose a pathway-based differential network analysis in genomics (DINGO) model for estimating group-specific networks and making inference on the differential networks. DINGO jointly estimates the group-specific conditional dependencies by decomposing them into global and group-specific components. The delineation of these components allows for a more refined picture of the major driver and passenger events in the elucidation of cancer progression and development.

Results: Simulation studies demonstrate that DINGO provides more accurate group-specific conditional dependencies than achieved by using separate estimation approaches. We apply DINGO to key signaling pathways in glioblastoma to build differential networks for long-term survivors and short-term survivors in The Cancer Genome Atlas. The hub genes found by mRNA expression, DNA copy number, methylation and microRNA expression reveal several important roles in glioblastoma progression.

(This is joint work with Min Jin Ha and Veerabhadran Baladandayuthapani)

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