Graduate Seminar in Statistics

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1:00-2:00pm, HH3017

Model the Complex Human Genome to Disease Association Using Information Theory and Network Science

Abstract:

With the fast development of genotyping techniques, scanning human whole genome is becoming feasible and affordable in the very near future. The increasing amount of genetics data imposes great promises and challenges for biomedical and health care research. Understanding the relationship between genetic variations and phenotypic traits has the potential to improve our ability to diagnose, treat, and prevent human diseases. One major contributor to this complex relationship is the non-additive effect of gene-gene interactions. The effect of a given gene on a trait can be dependent on one or more other genes. We used Information Gain from Information Theory to quantify the effect of gene-gene interaction and used networks to model the aggregation of those interaction effects in order to provide a global landscape of clustered interacting genes. We applied our framework to a large population-based bladder cancer data collected from New Hampshire, USA. We were able to identify a network of interacting genetic variants that possesses unique topological characteristics, which suggest the intricate and robust genetic architecture of bladder cancer that has not been described previously.