

Applicant

Dr. Shelley Bull, Lunenfeld-Tanenbaum Research Institute

E-mail Address

bull@lunenfeld.ca

Project Title

Methods for region-based analysis of genome-wide association studies

Project Summary

Genome-wide association studies (GWAS) aim to detect statistical association between single nucleotide polymorphisms (SNP) variation and complex traits such as physiology or disease status. In discoveries facilitated by GWAS, it has been shown that many loci contribute to the genetic variation underlying trait differences between individuals in a population. In this study, we focus on development of a region-based approach (defined by sets of physically contiguous SNPs, including intergenic SNPs) to test the entire genome comprehensively and discover new regions. Compared to single-SNP analysis, region-based analysis reduces multiple testing, is more robust to population differences and more sensitive to complex genetic architectures. We will evaluate the efficiency and properties of the new methods using statistical simulation studies based on the CLSA data. We will apply the analysis methods to CLSA quantitative traits and compare the findings with those of single-SNP analysis.

Keywords

Statistical genetics, Complex traits, Fine-mapping