

Research Statement

Dr Zhang obtained his PhD in probability and statistics from Peking University in 1999 and joined the section of statistical genetics of University of Alabama at Birmingham as a research assistant professor in 2003. He has two related but different research areas: (1) to develop a new methods and designing novel algorithms to locate complex disease genes in genetic linkage analysis and linkage disequilibrium analysis using both population-based and family-based data; (2) to develop computational tools to understand molecular functions combining different data such as gene expression microarray data and protein-protein interaction data. The primary of his research is to develop mathematical, statistical and computational methods to help solve scientific problems in genetics and molecular biology.

Dr. Zhang and his colleagues have developed statistical methods to test linkage and association simultaneously for quantitative traits in general pedigrees and assessed the power of transmission disequilibrium tests for quantitative traits. He and his colleagues have developed a method to identify all compatible haplotypes in a general pedigree using genotype data at a set of tightly linked SNPs, which can be used in linkage and association studies to improve the power. Recently, he and his colleagues have developed a dynamic programming algorithm for haplotype block partitioning and tag SNP selection using haplotype data as well as genotype data, and studied the power of different association tests using tag SNPs. Dr. Zhang is also interested in microarray data analysis. He and his colleagues have developed a simulation-based approach to assessing the reliability of gene clusters identified from different clustering algorithms using microarray data. The method has been implemented in a software package to distribute to the scientific community.

Currently, Dr. Zhang is continuing his methodology developments for linkage, disequilibrium, and haplotype analysis and microarray analysis. He is very interested in collaborating with other investigators to apply these methods to their projects.