Presentation title: Mixed linear model analyses of human complex traits using SNP data

Abstract:
Most traits and common diseases in humans, such as height, cognitive ability, psychiatric disorders and obesity, are influenced by many genes and their interplay with environmental factors. These diseases/traits are called "complex" traits to differentiate them from "Mendelian" traits that are caused by single genes. Understanding the genetic architecture of human complex traits, e.g. how much of the difference between people's susceptibilities to diseases are accounted for by their difference in DNA sequence, how many genes are involved in the etiology of diseases, where the genes are located and how much effects of the genes are on the disease risks, is essential to diagnosis, discovery of new drug targets and prevention. To date, thousands gene loci as represented by single nucleotide polymorphisms (SNPs) have been identified to be associated with hundreds of human complex traits by the genome-wide association study (GWAS) technique. In this lecture, I will be introducing the use of mixed linear model in the analyses of GWAS data, to estimate the proportion of variance for a trait that can be explained by all SNPs (or called SNP heritability), to quantify the extent to which two traits (or diseases) share a common genetic basis (genetic correlation) using all SNPs, and to control for population structure in genome-wide association analyses of individuals SNPs.