Recovering the missing heritability of complex diseases

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Abstract

Since 2005, genome-wide association studies (GWAS) have identified single nucleotide polymorphisms (SNPs) associated with complex diseases and traits. According to the NHGRI GWAS Catalog reports, up to the end of 2013, about 12 thousands of disease- or trait-associated SNPs from 1,750 curated publications have been reported. Nevertheless, “missing heritability” of complex diseases and traits is still a gap to be filled. In order to recover the missing heritability in GWAS, we developed statistical and bioinformatics tools to further enrich the collection of disease genes and mutations underlying complex diseases and traits. The developed analysis tools have been applied to study genetic mechanism and disease prognosis of hypertension, rheumatoid arthritis, schizophrenia, and acute lymphoblastic leukemia. The analyses include but are not limited to whole-genome sequencing data analysis, homozygosity disequilibrium analysis, gene- and pathway-based association and interaction analysis, copy number analysis, expression quantitative trait locus mapping, metabolomics data analysis, and integrative omics analysis. The analysis tools and some of their practical applications in biomedical research will be introduced in this talk.