Principal Investigator

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Summary of research

Pleiotropy, phenotypic variability, GWAS, genomic prediction

Application Lay Summary:

1a: The aim of this project is to apply novel methods developed by the PI, in order to identify novel genes associated with obesity-related traits and improve prediction of individual-level phenotypes. The main methodology framework contains three parts: 1. multi-trait genome-wide association analysis for detecting pleiotropic loci, which boosts power for detecting novel loci associated with correlated traits and disease; 2. variance-heterogeneity genome-wide scan for identifying genes that regulate phenotypic variability, which prioritizes loci involved in gene-gene and gene-environment interactions; 3. multi-trait whole-genome regression analysis for prediction of multiple complex traits.

1b: A major purpose of UK Biobank is to contribute to deeper understanding of

health-related measurements and diseases in UK population, for which both gene discovery using genome-wide association studies and prediction of individual phenotypes using DNA information clearly play an important role. The proposed research here directly contributes to boost power of genome-wide association studies, hence improving discovery of genetic variants associated with obesity-related traits and disease in the UK population. High-throughput modeling of DNA data for multiple phenotypes has a great potential to improve prediction of many phenotypes.

1c: The PI will conduct three types of analyses using measured outcomes and DNA information in UK Biobank, in order to discover novel genes associated with obesity that control health and predict health-related traits in the UK population. The novel statistical analyses developed by the PI will detect new loci affecting multiple traits or affecting trait variation and hence enhance understanding of their interactions with other loci and environmental factors. The resulting improved disease understanding together with the ability to predict individual disease susceptibility will contribute to the implementation of precision medicine approaches that will increase treatment effectiveness.

1d: The full cohort of UK Biobank.

Project extension:

What we are interested in at present is which part of the brain (MRI info) is correlated or even genetically correlated with complex traits/ diseases. To answer this question, we would like to make use of the full resolution of the brain MRI scan. Certainly we will start with analyzing the derived fields e.g. the colume of the grey matter from the T1 scan, but we woud like to dig into smaller pixels as our phenotypes.

We do not see the necessity of deriving new fields for other researchers, however, if we do discover an interesting small piece of the brain to be genetically correlated with a particular trait/ disease, we are happy to share that particplar phenotype of the brain as a new field.