STELLINGEN

Behorend bij het proefschrift

APPROACHES TO DISSECT THE COMPLEX GENETIC ARCHITECTURE OF COMMON TRAITS

1. ProbABEL is an effective software tool for genome-wide association studies (this thesis).
2. Prediction of height using genetic data is a powerful approach, however current prediction accuracy is low (this thesis).
3. Variance heterogeneity analysis is currently the only method for detecting interacting genetic variants involved in a complex model consisting of many interacting genetic and environmental factors (this thesis).
4. Using collapsed genotypes in a genome-wide association study is more powerful than single-variant analysis for detecting the presence of multiple loss-of-function variants in the compound heterozygote state (this thesis).
5. A large part of the genetic component of total cholesterol is determined by common variants with additive effects, however, multiple rare variants play a role in the extreme total cholesterol levels (this thesis).
6. The genome-wide association study will probably remain an efficient way of investigating the remaining heritability (Teri A. Manolio 2009).
7. A highly polygenic model of disease susceptibility with causal variants across the entire range of the allele-frequency spectrum contributes to complex-trait variation (Peter M. Visscher 2012).
8. Dense genotyping and sequencing studies will facilitate discovering new genetic variants associated with various traits.
9. A sample of tens of millions of individuals is required to dissect the complex genetic architecture of many common traits.
10. Future investments in genome-wide association studies are fully justified by the great potential to use the discovered genetic variants for prediction of traits and diseases even if the biological meaning of those variants will remain undiscovered.
11. Similar to how genetic diversity is an important factor for the development of a species, the diversity of political, economical and cultural models is an important factor for the development of humanity.

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