Enhancing genetic discoveries with population-specific reference panels

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Stellingen behorend bij het proefschrift

Enhancing genetic discoveries with population-specific reference panels

1. **It took 10 years before the value of genome-wide association studies as drivers for gene discovery was fully recognized.**

2. **Genotype imputation saved thousands of dollars to small labs, helped to improve current technologies and gave real usable value to public, international efforts as HapMap and 1000 Genomes.**

3. **Population-specific reference panels are necessary to detect the full spectrum of genetic variation (this thesis).**

4. **Both the 'common disease-common variant (CDCV)' and the 'common-disease rare variant (CDRV)' hypotheses are true.**

5. **Large, isolated and founder populations are an ideal setting for genetic mapping of rare variants as genetic drift or selection may increase their frequency and therefore provide more statistical power (this thesis).**

6. **Association at very rare and private mutations detected in sequencing-based GWAS needs to be supported by functional studies.**

7. **Medical science today is collaboration among disciplines, among research groups, and between academia and industry.**

8. **The 'big data' explosion needs to be followed by 'data sharing' to turn it into valuable information.**

9. **The society needs to be educated on genomics to involve patients and volunteers in research decisions.**

10. **Unless you are a medical doctor, you cannot ignore the need for a PhD to pursue a career in research, even in a country where it is not necessary.**