

Estimating the genetic correlation between populations

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AIM

Estimate genetic correlations:

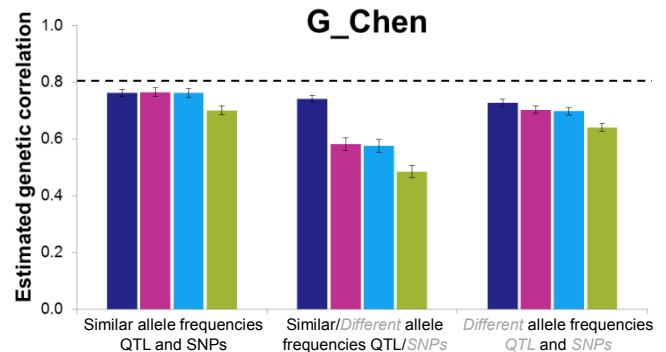
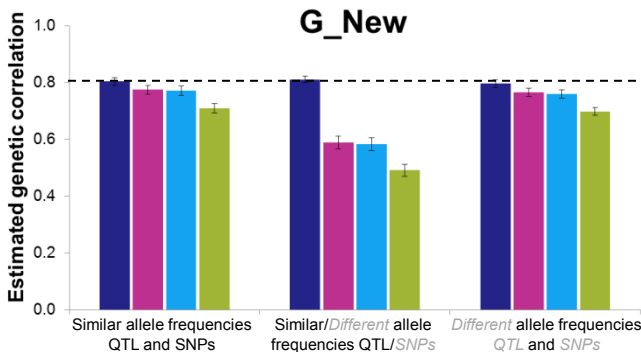
- How to calculate **G**?
- Effect of differences in linkage disequilibrium (LD) and allele frequencies across populations?

CONCLUSION

Accurate estimation of genetic correlations between populations:

- Using **G_{New}**
- When **SNP** characteristics represent **QTL** characteristics
- **Differences in LD** between populations have a **minor** effect

GENETIC CORRELATION BETWEEN POPULATIONS (r_G) = CORRELATION BETWEEN ADDITIVE GENETIC VALUES OF TWO POPULATIONS



QTL: 2 000 QTL; **High Density:** 200 000 SNPs; **Low Density:** 20 000 SNPs; **Very Low Density:** 2 000 SNPs

METHODS

Genomic relationship matrix between populations

G_{New}

$$\frac{\mathbf{Z}_A \mathbf{Z}_B'}{2\sqrt{p_A(1-p_A)}\sqrt{p_B(1-p_B)}}$$

G_{Chen}

$$\frac{\mathbf{Z}_A \mathbf{Z}_B'}{2\sqrt{p_A(1-p_A)}p_B(1-p_B)}$$

Genetic correlation

- True: Correlation allele substitution effects of QTL
- Estimated: Multi-trait GREML model in ASReml

Simulations

- Genotypes: QMSim
- 50 generations of separation
- Differences in LD pattern
- 50 replicates
- 2000 individuals per population

Genome

- 10 chromosomes of 1 M
- Allele frequencies QTL: U-shape
- Allele frequencies SNPs: Uniform
- Allele frequencies similar or different across populations



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