

The Quantitative Genomic Analysis of Man

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ABSTRACT

KEYWORDS Quantitative genomics; ...

Some traits are influenced by many genes, each of small effect. Attempts to

Introduction

A quant...

The quantitative genetics approach

Prediction,

The single locus model

Holding the genotypes at other loci constant, then the relationship between genotype and phenotype at a single locus can be described by

$$z = a_i + a_j + d_{i,j} \quad (1)$$

For biallelic loci $a_j = -a_i$, and

More than one loci

This single locus model can be extended to allow mapping between a trait and any two loci by summing the single loci effects and adding a term to describe the , and then this relationship can be described . . .

$$z = a_i + a_j + d_{i,j} + a_k + a_l + d_{k,l} + l_{i,j,k,l} \quad (2)$$

Variance decomposition

$$\sigma_A^2 = 2 \sum_i p_i a_i^2 \quad (3)$$

$$\sigma_D^2 = \sum_i p_i^2 \delta_{ii}^2 + \sum_{i < j} 2 p_i p_j \delta_{ij}^2 \quad (4)$$

This implicitly assumes that each of the genotypes ii , ij and jj occur in the Hardy-Weinberg expectation. However, with

population structure and non-random mating this may not be the case, so two additional terms are needed.

$$\sigma_{ADI} = \sum_i \sum_j 4 x_i d_{ij} (p^3 q - p q^3) \quad (5)$$

$$\sigma_{DI}^2 = \sum_i \alpha_i^2 (p q^2 - p^2 q) \quad (6)$$

$$\sigma_{AA}^2 = \sum_i \sum_j \sum_k \sum_l \quad (7)$$

$$\sigma_{AD}^2 = \sum_i \sum_j \sum_k \quad (8)$$

$$\sigma_{DA}^2 = \sum_i \sum_k \sum_l \quad (9)$$

$$\sigma_{DD}^2 = \sum_i \sum_j \quad (10)$$

Epistasis and linkage

Variance decomposition revisited

IBD and genotypic correlations

Affine transformations, partitions, and genotypic correlations

zygosity correlations and runs of homozygosity

and inbreeding

Regression equation

population structure

The importance of priors

mating vectors

Comparison to other methods

GRML

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Simulation

Applications

Human data

Threshold characters

Correlated characters

Priors

covariance

$$\sigma_{AB} = \frac{A_1 B_1 + A_1 B_2 + A_2 B_1 + A_2 B_2}{4} - \mu$$
$$\sigma_{AB} = \frac{\langle AB - \langle A \rangle \langle B \rangle \rangle}{\sqrt{\langle A - \langle A \rangle \rangle \langle B - \langle B \rangle \rangle}}$$

Time Line

Jan 17th

- Run human data through mapgd [].
- Finish simulation pipeline [✓].
- Included linkage in simulations [✓].
- Send MAPGD manuscript to co-authors [].
- Analysis of the effect of priors [✓].
- Fix MPI [✓].
- Fix relatedness [].
- Spread causal SNPs throughout the genome [].
- Get Newton-Raphson working in allele.
- Set up mating vectors [].
- Edit genetics manuscript [].
- Make QQ plots [].

Literature Cited