

# Heritability

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## 1 SNP Heritability

These derivations are based on the Methods of [Yang et al., 2010].

### 1.1 Phenotype model

We can define a quantitative phenotype  $y$  as:

$$y = Z\beta + \epsilon$$

Where:

- $y$ : phenotypes.  $N \times 1$  vector. Centered so that  $E[y] = 0$ .
  - $N$ : number of samples.
- $Z$ : normalized genotypes for causal SNPs.  $N \times M$  matrix.
  - $M$ : number of causal SNPs.
  - Normalized according to  $Z_i = \frac{Z'_i - 2f_i}{\sqrt{2f_i(1-f_i)}}$ .
    - $Z'$ : allele dosages, taking on values of 0, 1, 2.
    - $f_i$ : true population allele frequency for SNP  $i$ .
    - Such that for each row (SNP),  $E[Z_i] = 0$  and  $Var[Z_i] = 1$ .
- $\beta$ : per-normalized-genotype causal effects.  $M \times 1$  vector.
  - Assume infinitesimal model.
  - Drawn from  $\beta \sim \mathcal{N}(0, I\sigma_\beta^2)$ .
    - $I$ :  $M \times M$  identity matrix.
    - $\sigma_\beta^2$ : variance of causal effects.
- $\epsilon$ : residual effects (i.e. error or noise term).  $N \times 1$  vector.
  - Drawn from  $\epsilon \sim \mathcal{N}(0, I\sigma_\epsilon^2)$ .
    - $I$ :  $N \times N$  identity matrix.
    - $\sigma_\epsilon^2$ : residual variance.

We assume  $Z$ ,  $\beta$ , and  $\epsilon$  are all independent from each other. We can define the genetic effects as a single term,  $g = Z\beta$ , meaning that:

$$y = g + \epsilon \quad \text{where} \quad g \sim \mathcal{N}(0, I\sigma_g^2) \quad \text{where} \quad \sigma_g^2 = M\sigma_\beta^2$$

We interpret  $\sigma_g^2$  as variance of total additive genetic effects on the phenotype.

## 1.2 Variance of the phenotype

By making use of the independence between terms, we can define the variance-covariance matrix of  $y$  as:

$$\begin{aligned} \text{Var}[y] &= \text{Var}[Z\beta + \epsilon] \\ &= \text{Var}[Z]\text{Var}[\beta] + \text{Var}[\epsilon] \\ &= (ZZ^\top)\sigma_\beta^2 + I\sigma_\epsilon^2 \\ &= (ZZ^\top)\frac{\sigma_g^2}{M} + I\sigma_\epsilon^2 \\ &= G\sigma_g^2 + I\sigma_\epsilon^2 \end{aligned}$$

Where we define  $G = \frac{ZZ^\top}{M}$  as the  $N \times N$  genetic relationship matrix (GRM) between individuals. The  $G_{ii}$  element is the variance of individual  $i$ 's normalized genotype vector, while the  $G_{ij}$  element is the covariance of individuals  $i$  and  $j$ 's normalized genotype vectors.

Narrow-sense heritability is defined as the proportion of phenotypic variance,  $\sigma_P^2$ , explained by additive genetic effects:

$$h^2 = \frac{\sigma_g^2}{\sigma_P^2} = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_\epsilon^2}$$