

Solution 1: Use LASSO instead of Least Squares
 \Rightarrow see Spring Semester 'Applied Statistical Methods'

Solution 2: Use a Linear Mixed Effect Model with q being a random effect with $E(q) = 0$ and $\text{var}(q) = I \cdot \sigma_q^2$

From marker effects \hat{q} , genomic breeding values \hat{g} are computed based on summation of marker effects for corresponding genotypes:

Animal	MP ₁	...	MP _k	
1				
i	G ₁₁	G ₁₂	G _{1k}	y _i

$$\left\{ \begin{aligned} \hat{g}_i &= 1 \cdot \hat{q}_1 + 0 \cdot \hat{q}_2 + (-1) \cdot \hat{q}_3 \\ &\quad + \dots + 0 \cdot \hat{q}_k \\ &= \underbrace{w_i}_{\substack{\text{i-th row of matrix} \\ W}} \cdot \hat{q} \end{aligned} \right.$$

$\underbrace{\begin{bmatrix} \hat{q}_1 & \hat{q}_2 & \dots & \hat{q}_k \end{bmatrix}}_{\hat{q}}$

To get to \hat{g}_i , all we need is \hat{q} and genotypes for animal $i \Rightarrow \hat{g}_i$ can be computed for animals right after birth.

2. Breeding Value Based Model

Genomic breeding values g as random Effects in a LME.

$$\Rightarrow y = X\beta + Zg + e$$

\rightarrow length of g corresponds to the number of animals with genotypes