

Animal	SNP1	...	SNPk	y
1	G ₁ G ₂	G ₁ G ₁		y ₁
2				y ₂
...				
N				y _N

Two different Models:

1. Marker Effect Model:

$$y = X\beta + Wq + e$$

Fixed Effects β

vector of marker effects for SNP1, ..., SNPk;

Linear fixed Effect Model

because $d=0$ for all SNPs q_j corresponds to the a -value of the single locus model for SNP position j

Problem with finding solutions for estimating \hat{q} :

- In most datasets: $k \gg N$

Least Squares cannot be used for finding \hat{q}

- Even, if $k < N$; most marker effects are assumed to be 0, and must therefore be excluded from the analysis, otherwise the standard error is inflated.