

Addition of SNP to the model

Along with the other terms in Eq.(2), SIRE allows for incorporation of a single SNP effect. This SNP is assumed to be bi-allelic with values A and B . When SNP data is added the model becomes

$$\begin{aligned} \mathbf{g} &= \mathbf{g}^{\text{SNP}} + \mathbf{X}\mathbf{b}_g + \mathbf{a}_g + \boldsymbol{\varepsilon}_g, \\ \mathbf{f} &= \mathbf{f}^{\text{SNP}} + \mathbf{X}\mathbf{b}_f + \mathbf{a}_f + \boldsymbol{\varepsilon}_f, \\ \mathbf{r} &= \mathbf{r}^{\text{SNP}} + \mathbf{X}\mathbf{b}_r + \mathbf{a}_r + \boldsymbol{\varepsilon}_r, \end{aligned} \tag{A1}$$

where $\mathbf{g}^{\text{SNP}}$, $\mathbf{f}^{\text{SNP}}$ and $\mathbf{r}^{\text{SNP}}$ give contributions from the SNP under investigation. These terms are parameterised by

$$\left. \begin{aligned} g_j^{\text{SNP}} &= \begin{matrix} h_g \\ h_g \Delta_g, \\ -h_g \end{matrix} & f_j^{\text{SNP}} &= \begin{matrix} h_f \\ h_f \Delta_f, \\ -h_f \end{matrix} & r_j^{\text{SNP}} &= \begin{matrix} h_r \\ h_r \Delta_r, \\ -h_r \end{matrix} \end{aligned} \right\} \begin{array}{l} \text{if } j \text{ is } AA \\ \text{if } j \text{ is } AB \\ \text{if } j \text{ is } BB \end{array} \tag{A2}$$

where h_g , h_f and h_r give half the difference in traits between the AA and BB homozygote genotypes and Δ_g , Δ_f and Δ_r represent the degree of dominance (a value of 1 corresponds to complete dominance of the A allele over the B allele and -1 when the reverse is true, whereas absence of dominance is represented by a value of 0) [74].