

Additional file 1

Conditional posterior densities BSSVS model

The conditional posterior density of α_j is:

$$N\left(\hat{\alpha}_j; \frac{\omega_j \hat{\sigma}_e^2}{\mathbf{x}_j' \mathbf{D}^{-1} \mathbf{x}_j + \lambda_j}\right)$$

where $\hat{\alpha}_j$ is the conditional mean of the allele substitution effect at locus j , $\lambda_j = \frac{\omega_j \hat{\sigma}_e^2}{\hat{\sigma}_\alpha^2}$, where

$\omega_j = 1$ (if $I_j = 1$) or $\omega_j = 100$ (if $I_j = 0$). The conditional posterior density of σ_α^2 was:

$\sigma_\alpha^2 | \alpha \sim \chi^{-2}(v_\alpha + n, S_\alpha^2 + \boldsymbol{\omega}' \hat{\boldsymbol{\alpha}}^2)$, where $\hat{\boldsymbol{\alpha}}^2$ is a vector of squares of the current estimates of the allele substitution effects of all loci, that is weighted by vector $\boldsymbol{\omega}$. The conditional posterior distribution of I_j was:

$$\Pr(I_j = 1) = \frac{f(r_j | I_j = 1)(1 - \pi)}{f(r_j | I_j = 0)\pi + f(r_j | I_j = 1)(1 - \pi)}$$

where $r_j = \mathbf{x}_j' \mathbf{D}^{-1} \mathbf{y}^* + \mathbf{x}_j' \mathbf{D}^{-1} \mathbf{x}_j \hat{\alpha}_j$ where \mathbf{y}^* are the conditional DRPs (i.e. for each SNP \mathbf{y}

minus the sum of the estimated SNP effects of the other SNPs), and $f(r_j | I_j = \delta)$ is the

probability density function, giving the probability that $I_j = 0$ ($\delta = 0$) or $I_j = 1$ ($\delta = 1$), and

is proportional to $\frac{1}{\sqrt{v}} e^{-\frac{r_j^2}{2v}}$, where $v = (\mathbf{x}_j' \mathbf{D}^{-1} \mathbf{x}_j)^2 \frac{\sigma_{\alpha_j}^2}{\omega_j} + \mathbf{x}_j' \mathbf{D}^{-1} \mathbf{x}_j \sigma_e^2$. The conditional posterior

density of σ_u^2 and σ_e^2 were inverse- χ^2 distributions, respectively $\sigma_u^2 | \mathbf{u} \sim \chi^{-2}(m - 2, \mathbf{u}' \mathbf{A}^{-1} \mathbf{u})$

and $\sigma_e^2 | \mathbf{e} \sim \chi^{-2}(m - 2, \mathbf{e}' \mathbf{D}^{-1} \mathbf{e})$, where m is the number of animals in the pedigree.