MCMC sampling strategies for each parameter and hyper-parameter

(1) Joint posterior densities of the SSGBLUP, SS-BayesA and SS-BayesB models

The joint posterior density for SSGBLUP was as below:

$$p(\boldsymbol{\beta}, \alpha_1, \alpha_2, ..., \alpha_m, \boldsymbol{\varepsilon}, \sigma_g^2, \sigma_\alpha^2, \sigma_e^2 \mid \mathbf{y}) \propto \left(\prod_{i=1}^{n} p(\mathbf{y} \mid \boldsymbol{\beta}, \alpha_1, \alpha_2, ..., \alpha_m, \boldsymbol{\varepsilon}, \sigma_e^2) \right)$$

$$\left(\prod_{j=1}^{m} p(\alpha_i \mid \sigma_\alpha^2) \right) p(\boldsymbol{\varepsilon} \mid \sigma_g^2) p(\sigma_\alpha^2 \mid \nu_\alpha, s_\alpha^2) p(\sigma_g^2 \mid \nu_g, s_g^2) p(\sigma_e^2 \mid \nu_e, s_e^2)$$

$$\propto (\sigma_e^2)^{-n/2} \exp\left(-\frac{1}{2\sigma_e^2} \sum_{i=1}^{n} (y_i - \mathbf{x}_i^{'}\boldsymbol{\beta} - \mathbf{w}_i^{'}\boldsymbol{\alpha} - \mathbf{u}_i^{'}\boldsymbol{\varepsilon})^2 \right) (\sigma_g^2)^{-q_1/2} \exp\left(-\frac{1}{2\sigma_g^2} \boldsymbol{\varepsilon}^{'} \mathbf{A}^{\mathbf{11}} \boldsymbol{\varepsilon} \right) (\sigma_\alpha^2)^{-m/2} \exp\left(-\frac{1}{2\sigma_\alpha^2} \sum_{j=1}^{m} \alpha_j^2 \right)$$

$$\sigma_\alpha^{2^{-\left(\frac{\nu_\alpha}{2}+1\right)}} e^{-\frac{\nu_\alpha s_\alpha^2}{2\sigma_\alpha^2}} \sigma_g^{2^{-\left(\frac{\nu_g}{2}+1\right)}} e^{-\frac{\nu_g s_g^2}{2\sigma_g^2}} \sigma_e^{2^{-\left(\frac{\nu_e}{2}+1\right)}} e^{-\frac{\nu_e s_e^2}{2\sigma_e^2}}.$$

Here, $\mathbf{y}$ was the vector of phenotype of all animals, $\boldsymbol{\beta}$ was the fixed effects vector, α_j was the marker effects of the *j*th marker, $\boldsymbol{\varepsilon}$ was the imputation residuals vector for the non-genotyped animals, σ_g^2 and σ_α^2 were the polygenic variance and SNP effects' variance, σ_e^2 was the residual variance, ν_α and s_α^2 were degree of freedom and scale of the scaled inverse chi-square prior of the SNP effects' variance, ν_g and s_g^2 were degree of freedom and scale of the scaled inverse chi-square prior for the polygenic variance, ν_e and s_e^2 were degree of freedom and scale of the scaled inverse chi-square prior for the residual variance. $\mathbf{x}$, $\mathbf{w}$ and $\mathbf{u}$ were the corresponding design matrices or vectors for fixed effects, SNP effects and imputation residuals, n was the total number of genotyped and non-genotyped animals, m was the total number of markers, q_1 was the number of non-genotyped animals, and $\mathbf{A}^{11} = \left(\mathbf{A}_{11} - \mathbf{A}_{12}\mathbf{A}_{22}^{-1}\mathbf{A}_{12}'\right)^{-1}$.

The joint posterior density of SS-BayesA was

$$p(\boldsymbol{\beta},\alpha_1,\alpha_2,...,\alpha_m,\boldsymbol{\varepsilon},\sigma_g^2,\sigma_{\alpha_1}^2,\sigma_{\alpha_2}^2,...,\sigma_{\alpha_m}^2,\sigma_e^2,\nu_\alpha,s_\alpha^2\mid\mathbf{y})\propto\left(\prod_{i=1}^{n}p(\mathbf{y}\mid\boldsymbol{\beta},\alpha_1,\alpha_2,...,\alpha_m,\boldsymbol{\varepsilon},\sigma_e^2)\right)$$
$$\left(\prod_{j=1}^{m}p\left(\alpha_i\mid\sigma_{\alpha_j}^2\right)\right)p\left(\boldsymbol{\varepsilon}\mid\sigma_g^2\right)\left(\prod_{j=1}^{m}p\left(\sigma_{\alpha_j}^2\mid\nu_\alpha,s_\alpha^2\right)\right)p\left(\sigma_g^2\mid\nu_g,s_g^2\right)p\left(\sigma_e^2\mid\nu_e,s_e^2\right)p(\nu_\alpha)p\left(s_\alpha^2\right)$$
$$\propto\left(\sigma_e^2\right)^{-n/2}\exp\left(-\frac{1}{2\sigma_e^2}\sum_{i=1}^{n}\left(y_i-\mathbf{x}_\mathbf{i}'\boldsymbol{\beta}-\mathbf{w}_\mathbf{i}'\boldsymbol{\alpha}-\mathbf{u}_\mathbf{i}'\boldsymbol{\varepsilon}\right)^2\right)\left(\sigma_g^2\right)^{-q_1/2}\exp\left(-\frac{1}{2\sigma_g^2}\boldsymbol{\varepsilon}'\mathbf{A}^{\mathbf{11}}\boldsymbol{\varepsilon}\right)\left(\prod_{j=1}^{m}\sigma_{\alpha_j}^2\right)^{-1/2}\exp\left(-\frac{1}{2}\sum_{j=1}^{m}\frac{\alpha_j^2}{\sigma_{\alpha_j}^2}\right)$$
$$\left(\prod_{j=1}^{m}\sigma_{\alpha_j}^{2\;-\left(\frac{\nu_\alpha}{2}+1\right)}e^{-\frac{\nu_\alpha s_\alpha^2}{2\sigma_{\alpha_j}^2}}\right)\sigma_g^{2^{-\left(\frac{\nu_g}{2}+1\right)}}e^{-\frac{\nu_g s_g^2}{2\sigma_g^2}}\sigma_e^{2^{-\left(\frac{\nu_e}{2}+1\right)}}e^{-\frac{\nu_e s_e^2}{2\sigma_e^2}}\frac{1}{\left(1+\nu_\alpha\right)^2}s_\alpha^{2^{-\left(\frac{\nu_s}{2}+1\right)}}e^{-\frac{\nu_s s_s^2}{2s_\alpha^2}}.$$

Here, $\sigma_{\alpha_j}^2$ was the jth marker's marker-specific effect variance, the prior for the degree of freedom (ν_α) was $p(\nu_\alpha)=\frac{1}{\left(1+\nu_\alpha\right)^2}$ [1], and the prior of scale (s_α^2) was a scaled inverse chi-square distribution $p\left(s_\alpha^2\right)=s_\alpha^{2^{-\left(\frac{\nu_s}{2}+1\right)}}e^{-\frac{\nu_s s_s^2}{2s_\alpha^2}}$.

The joint posterior density of SS-BayesB was

$$p(\boldsymbol{\beta},\alpha_1,\alpha_2,...,\alpha_m,\boldsymbol{\varepsilon},\sigma_g^2,\sigma_{\alpha_1}^2,\sigma_{\alpha_2}^2,...,\sigma_{\alpha_m}^2,\sigma_e^2,\nu_\alpha,s_\alpha^2,\pi_m\mid\mathbf{y})\propto\left(\prod_{i=1}^{n}p(\mathbf{y}\mid\boldsymbol{\beta},\alpha_1,\alpha_2,...,\alpha_m,\boldsymbol{\varepsilon},\sigma_e^2)\right)$$
$$\left(\prod_{j=1}^{m_1}p\left(\alpha_i\mid\sigma_{\alpha_j}^2\right)\right)p\left(\boldsymbol{\varepsilon}\mid\sigma_g^2\right)\left(\prod_{j=1}^{m_1}p\left(\sigma_{\alpha_j}^2\mid\nu_\alpha,s_\alpha^2\right)\right)p\left(\sigma_g^2\mid\nu_g,s_g^2\right)p\left(\sigma_e^2\mid\nu_e,s_e^2\right)p(\nu_\alpha)p\left(s_\alpha^2\right)p(\pi_m)$$
$$\propto\left(\sigma_e^2\right)^{-n/2}\exp\left(-\frac{1}{2\sigma_e^2}\sum_{i=1}^{n}\left(y_i-\mathbf{x}_\mathbf{i}'\boldsymbol{\beta}-\mathbf{w}_\mathbf{i}'\boldsymbol{\alpha}-\mathbf{u}_\mathbf{i}'\boldsymbol{\varepsilon}\right)^2\right)\left(\sigma_g^2\right)^{-q_1/2}\exp\left(-\frac{1}{2\sigma_g^2}\boldsymbol{\varepsilon}'\mathbf{A}^{\mathbf{11}}\boldsymbol{\varepsilon}\right)\left(\prod_{j=1}^{m_1}\sigma_{\alpha_j}^2\right)^{-1/2}\exp\left(-\frac{1}{2}\sum_{j=1}^{m_1}\frac{\alpha_j^2}{\sigma_{\alpha_j}^2}\right)$$
$$\left(\prod_{j=1}^{m_1}\sigma_{\alpha_j}^{2\;-\left(\frac{\nu_\alpha}{2}+1\right)}e^{-\frac{\nu_\alpha s_\alpha^2}{2\sigma_{\alpha_j}^2}}\right)\sigma_g^{2^{-\left(\frac{\nu_g}{2}+1\right)}}e^{-\frac{\nu_g s_g^2}{2\sigma_g^2}}\sigma_e^{2^{-\left(\frac{\nu_e}{2}+1\right)}}e^{-\frac{\nu_e s_e^2}{2\sigma_e^2}}\frac{1}{\left(1+\nu_\alpha\right)^2}\left(s_\alpha^2\right)^{\alpha_\alpha-1}e^{-\beta_\alpha s_\alpha^2}\pi_m{}^{m_1+\alpha_\pi-1}\left(1-\pi_m\right)^{m-m_1+\beta_\pi-1}.$$

Here, π_m was the proportion of markers which had non-zero effects, m_1 was the number of non-zero effect SNP, π_m had a beta distribution prior with $p(\pi_m)=\pi_m{}^{\alpha_\pi-1}\left(1-\pi_m\right)^{\beta_\pi-1}$, and s_α^2 had a gamma prior of

$$p\left(s_{\alpha}^{2} \mid \alpha_{\alpha}, \beta_{\alpha}\right)=\frac{\beta_{\alpha}{}^{\alpha_{\alpha}}}{\Gamma\left(\alpha_{\alpha}\right)}\left(s_{\alpha}^{2}\right)^{\alpha_{\alpha}-1} e^{-\beta_{\alpha} s_{\alpha}^{2}}.$$

(2) Sampling of polygenic variance for all three single-step models

Fernando et al. [2] assumed that the polygenic variance was independent with marker effects' variances. They used a scaled inverse chi-square prior on the polygenic variance. The full conditional density (FCD) of polygenic variance then also followed a scaled inverse chi-square distribution:

$$p\left(\sigma_{g}^{2} \mid ELSE\right) \propto \left(\sigma_{g}^{2}\right)^{-\left(\frac{q_{1}+v_{g}}{2}+1\right)} \exp\left(-\frac{1}{2\sigma_{g}^{2}}\left(\boldsymbol{\varepsilon}^{'}\mathbf{A}^{\mathbf{11}}\boldsymbol{\varepsilon}+v_{g} s_{g}^{2}\right)\right)$$

where v_{g} and s_{g}^{2} were the degree of freedom and scale of the prior, and q_{1} was the total number of ungenotyped animals. This FCD of polygenic variance was used for all the three models (SSGBLUP, SS-BayesA and SS-BayesB).

(3) Sampling of imputation residuals for all three single-step models

The FCD of imputation residuals are the same for SSGBLUP, SS-BayesA and SS-BayesB models. The joint FCD of the imputation residuals can be written as follow:

$$p\left(\boldsymbol{\varepsilon} \mid ELSE\right) \propto N\left(\boldsymbol{\mu}_{\boldsymbol{\varepsilon}}, \boldsymbol{\Sigma}_{\boldsymbol{\varepsilon}}\right)$$

where $\boldsymbol{\mu}_{\boldsymbol{\varepsilon}}=\left(\mathbf{Z}_{1}^{'}\mathbf{Z}_{1}+\mathbf{A}^{11}\lambda_{g}\right)^{-1}\mathbf{Z}_{1}^{'}\mathbf{y}_{1}*$, and $\boldsymbol{\Sigma}_{\boldsymbol{\varepsilon}}=\left(\mathbf{Z}_{1}^{'}\mathbf{Z}_{1}+\mathbf{A}^{11}\lambda_{g}\right)^{-1}\sigma_{e}^{2}$.

where $\mathbf{y}_{1}*=\left(\mathbf{y}_{1}-\mathbf{X}_{1}\boldsymbol{\beta}-\mathbf{W}_{1}\boldsymbol{\alpha}\right)$, $\lambda_{g}=\sigma_{e}^{2}/\sigma_{g}^{2}$, and y_{1} is the vector of phenotype of ungenotyped animals. The block-Gibbs sampler could be used to sample from this multivariate normal distribution [2, 3].

(4) Sampling of marker effects and their variance for SSGBLUP and SS-BayesA

With a scaled inverse chi-square prior $\chi^{-2}\left(\nu_\alpha, s_\alpha^2\right)$, the FCD of marker effects' variance for the SSGBLUP model is

$$
\begin{aligned}
p\left(\alpha_\alpha^2 \mid ELSE\right) &\propto \left(\alpha_\alpha^2\right)^{-m/2} \exp\left(-\frac{1}{2\alpha_\alpha^2}\sum_{j=1}^{m}\alpha_j^2\right)\alpha_\alpha^{2^{-\left(\frac{\nu_\alpha}{2}+1\right)}} e^{-\frac{\nu_\alpha s_\alpha^2}{2\alpha_\alpha^2}} \\
&\propto \left(\alpha_\alpha^2\right)^{-\left(\frac{\nu_\alpha+m}{2}+1\right)} \exp\left(-\frac{1}{2\alpha_\alpha^2}\left(\sum_{j=1}^{m}\alpha_j^2 + \nu_\alpha s_\alpha^2\right)\right)
\end{aligned}
$$

which is also a scaled inverse chi-square distribution. For the SS-BayesA model, each marker has its specific effect's variance. The FCD of $\sigma_{\alpha_j}^2$ for the j^{th} marker in the SS-BayesA model is

$$
\begin{aligned}
p\left(\alpha_{\alpha_j}^2 \mid ELSE\right) &\propto \left(2\pi\alpha_{\alpha_j}^2\right)^{-1/2} \exp\left(-\frac{1}{2\alpha_{\alpha_j}^2}\alpha_j^2\right)\alpha_{\alpha_j}^{2^{-\left(\frac{\nu_\alpha}{2}+1\right)}} e^{-\frac{\nu_\alpha s_\alpha^2}{2\alpha_{\alpha_j}^2}} \\
&\propto \left(\alpha_{\alpha_j}^2\right)^{-\left(\frac{\nu_\alpha+1}{2}+1\right)} \exp\left(-\frac{1}{2\alpha_{\alpha_j}^2}\left(\alpha_j^2 + \nu_\alpha s_\alpha^2\right)\right)
\end{aligned} \tag{A1}
$$

This is also a scaled inverse chi-square distribution. The FCD of markers effects for both SSGBLUP and SS-BayesA follow normal distributions [2] with

$$
p\left(\alpha_j \mid ELSE\right) \sim N\left(\tilde{\alpha}_j \;\; \tilde{v}_{\alpha_j}\right) \tag{A2}
$$

where j = 1,2,…,*m*, $\tilde{\alpha}_j = \dfrac{\sum_{i=1}^{n} w_{ij}e_i + \left(\sum_{i=1}^{n} w_{ij}^2\right)g_j}{\left(\sum_{i=1}^{n} w_{ij}^2 + \dfrac{\sigma_e^2}{\sigma_{\alpha_j}^2}\right)}$ and $\tilde{v}_{\alpha_j} = \left(\dfrac{\sum_{i=1}^{n}\left(w_{ij}\right)^2}{\sigma_e^2} + \sigma_{\alpha_j}^{-2}\right)^{-1}$

where w_{ij} is the ith row and jth column of the incidence matrix **W** of (3). For the SSGBLUP model, marker effects variance $\sigma^2_{\alpha_j}$ is the same for all markers. For the SS-BayesA and model, $\sigma^2_{\alpha_j}$ are unequal for different markers.

(5) Sampling of marker effects and their variance for SS-BayesB

The FCD of marker effects' variance for the jth marker in the SS-BayesB model is

$$p\left(\sigma^2_{\alpha_j} \mid ELSE \text{ except } \alpha_j\right) \propto \left|\mathbf{V}_j\right|^{-1/2} \exp\left(-\frac{1}{2}\mathbf{y}*'\mathbf{V}_j^{-1}\mathbf{y}*\right) p\left(\sigma^2_{\alpha_j} \mid \nu_\alpha, s^2_\alpha, \pi_m\right)$$

where $\mathbf{y}* = \left\{y_i - \mathbf{X}_i\boldsymbol{\beta} - \sum_{k\neq j}^{m} w_{ik}\alpha_k\right\}_{i=1}^{n}$, $\mathbf{V}_j = \mathbf{w}_j\mathbf{w}_j'\sigma^2_{\alpha_j} + \mathbf{I}\sigma^2_e$ and $p\left(\sigma^2_{\alpha_j} \mid \nu_\alpha, s^2_\alpha, \pi_m\right)$ is the prior density. This FCD is not recognizable, and we adopted the Metropolis-Hasting algorithm. We used the prior $p\left(\sigma^2_{\alpha_j} \mid \nu_\alpha, s^2_\alpha, \pi_m\right)$ as the proposal (driver) density [4], where the prior is a scaled inverse chi-square distribution. Then, the Metropolis-Hastings acceptance ratio (for jth marker) of the new proposal $\sigma^{2*}_{\alpha_j}$ is:

$$\alpha\left(\sigma^2_{\alpha_{j[t-1]}}, \sigma^{2*}_{\alpha_j}\right) = \min\left(\frac{p\left(\sigma^{2*}_{\alpha_j} \mid ELSE \text{ except } \alpha_j\right) p\left(\sigma^2_{\alpha_{j[t-1]}} \mid \nu_\alpha, s^2_\alpha, \pi_m\right)}{p\left(\sigma^2_{\alpha_{j[t-1]}} \mid ELSE \text{ except } \alpha_j\right) p\left(\sigma^{2*}_{\alpha_j} \mid \nu_\alpha, s^2_\alpha, \pi_m\right)}, 1\right)$$

This ratio is further equal to:

$$\begin{aligned}\alpha\left(\sigma^2_{\alpha_{j[t-1]}}, \sigma^{2*}_{\alpha_j}\right) &= \min\left(\frac{\left|\mathbf{V}_j^*\right|^{-1/2} \exp\left(-\frac{1}{2}\mathbf{y}*'\mathbf{V}_j^{*-1}\mathbf{y}*\right)}{\left|\mathbf{V}_j^{[t-1]}\right|^{-1/2} \exp\left(-\frac{1}{2}\mathbf{y}*'\left(\mathbf{V}_j^{[t-1]}\right)^{-1}\mathbf{y}*\right)}, 1\right) \\ &= \min\left(\frac{v_j^{*-1/2} \exp\left(-\frac{r_j^2}{2v_j*}\right)}{v_j^{[t-1]-1/2} \exp\left(-\frac{r_j^2}{2v_j^{[t-1]}}\right)}, 1\right)\end{aligned}$$

where $r_j = \mathbf{w}_j'\mathbf{y}*$, $v_j = \left(\mathbf{w}_\mathbf{j}'\mathbf{w}_\mathbf{j}\right)^2\sigma^2_{\alpha_i} + \mathbf{w}_\mathbf{j}'\mathbf{w}_\mathbf{j}\sigma^2_e$, and the proposal density is

$$p\left(\sigma^2_{\alpha_j} \mid v_\alpha, s^2_\alpha, \pi_m\right) \propto \begin{cases} 0 & \text{with probability of } (1-\pi_m) \\ \chi^{-2}\left(v_\alpha, s^2_\alpha\right) & \text{with probability of } \pi_m \end{cases}.$$

Then, we can accept $\sigma^{2*}_{\alpha_j}$ with the probability of $\alpha\left(\sigma^2_{\alpha_{j[t-1]}}, \sigma^{2*}_{\alpha_j}\right)$. If the accepted $\sigma^{2*}_{\alpha_j}$ is not zero, then SNP effect of marker *j* is sampled from its FCD, which is the same as in the SS-BayesA model; if the new accepted $\sigma^{2*}_{\alpha_j}$ is zero, then SNP effect of marker *j* is also zero. During the MCMC sampling procedure, the latest estimates of $v_\alpha, s^2_\alpha, \pi_m$ were used in the proposal density.

(6) Sampling of scale (s^2_α) and degree of freedom (v_α)) in SS-BayesA

Sampling of scale (s^2_α)

For s^2_α, we used a scaled inverse chi-square prior $\chi^{-2}(v_s = -1, s^2_s = 0)$. Then, the FCD of s^2_α is:

$$\begin{aligned} p\left(s^2_\alpha \mid ELSE\right) &\propto \left(\prod_{j=1}^{m} p\left(\sigma^2_{\alpha_j} \mid v_\alpha, s^2_\alpha\right)\right) p\left(s^2_\alpha\right) \\ &\propto \left(\prod_{j=1}^{m} \frac{\left(v_\alpha s^2_\alpha\right)^{\frac{v_\alpha}{2}}}{\Gamma\left(\frac{v_\alpha}{2}\right)} \sigma^{2\,-\left(\frac{v_\alpha}{2}+1\right)}_{\alpha_j} e^{-\frac{v_\alpha s^2_\alpha}{2\sigma^2_{\alpha_j}}}\right) s_\alpha^{2\,-\left(\frac{v_s}{2}+1\right)} e^{-\frac{v_s s_s^2}{2 s_\alpha^2}} \end{aligned}$$

It can be further simplified by integrating out marker effects' variances [5], then

$$p(s^2_\alpha \mid ELSE) \propto \left(\prod_{j=1}^{m} \frac{\Gamma\left(\frac{v_\alpha+1}{2}\right)}{\Gamma\left(\frac{v_\alpha}{2}\right)} \left(\frac{1}{\pi v_\alpha s^2_\alpha}\right)^{1/2} \left(1 + \frac{\alpha_j^{\,2}}{v_\alpha s^2_\alpha}\right)^{-\frac{v_\alpha+1}{2}}\right) s_\alpha^{2\,-\left(\frac{v_s}{2}+1\right)} e^{-\frac{v_s s_s^2}{2 s_\alpha^2}}.$$

This FCD is not recognizable. Therefore, we used the Metropolis-Hasting sampling strategy with a truncated normal distribution as the proposal density to draw samples on s_α^2 [6].

Sampling of degree of freedom (ν_α)

The FCD of ν_α with a vaguely informative prior of $p(\nu_\alpha)=\frac{1}{(1+\nu_\alpha)^2}$ [1] is as follow:

$$
\begin{aligned}
p(\nu_\alpha \mid ELSE) &\propto \left(\prod_{j=1}^{m} p\left(\sigma_{\alpha_j}^2 \mid \nu_\alpha, s_\alpha^2\right)\right) p(\nu_\alpha) \\
&\propto \left(\prod_{j=1}^{m} \frac{\Gamma\left(\frac{\nu_\alpha+1}{2}\right)}{\Gamma\left(\frac{\nu_\alpha}{2}\right)} \left(\frac{1}{\pi \nu_\alpha s_\alpha^2}\right)^{1/2} \left(1+\frac{\alpha_j^2}{\nu_\alpha s_\alpha^2}\right)^{-\frac{\nu_\alpha+1}{2}}\right) \frac{1}{(1+\nu_\alpha)^2}
\end{aligned},
$$

where *m* is the total number of markers. As this FCD is not recognizable, we also used Metropolis-Hasting sampling strategy with a truncated normal distribution as the proposal density to sample ν_α.

(7) Sampling of hyper-parameters (s_α^2, ν_α and π_m) in SS-BayesB

Sampling of sacle (s_α^2)

We used a conjugate gamma prior $p\left(s_\alpha^2 \mid \alpha_\alpha = 0.1, \beta_\alpha = 0.1\right) = \frac{(\beta_\alpha)^{\alpha_\alpha}}{\Gamma(\alpha_\alpha)}\left(s_\alpha^2\right)^{\alpha_\alpha - 1} e^{-\beta_\alpha s_\alpha^2}$ on s_α^2 of SS-BayesB, then the FCD was

$$
\begin{aligned}
p(s_\alpha^2 \mid ELSE) &\propto \left(\prod_{j=1}^{m_1} p\left(\sigma_{\alpha_j}^2 \mid \nu_\alpha, s_\alpha^2\right)\right) p\left(s_\alpha^2\right) \\
&\propto \left(\prod_{j=1}^{m} I\left(\sigma_{\alpha_j}^2 \neq 0\right) \frac{\left(\frac{\nu_\alpha s_\alpha^2}{2}\right)^{\frac{\nu_\alpha}{2}}}{\Gamma\left(\frac{\nu_\alpha}{2}\right)} {\sigma_{\alpha_j}^2}^{-\left(\frac{\nu_\alpha}{2}+1\right)} e^{-\frac{\nu_\alpha s_\alpha^2}{2\sigma_{\alpha_j}^2}}\right) \left(s_\alpha^2\right)^{\alpha_\alpha - 1} e^{-\beta_\alpha s_\alpha^2} \propto \left(s_\alpha^2\right)^{\frac{m_1 \nu_\alpha}{2}+\alpha_\alpha - 1} e^{-\left(\frac{\nu_\alpha}{2\sum_{j=1}^{m}\sigma_{\alpha_j}^2 I\left(\sigma_{\alpha_j}^2 \neq 0\right)}+\beta_\alpha\right)s_\alpha^2}
\end{aligned}
$$

where m_1 is the number of markers with non-zero effects. It is again a gamma distribution. A Gibbs sampler was applied here to draw MCMC samples.

Sampling of degree of freedom (ν_α)

For ν_α of SS-BayesB, its FCD was

$$p(\nu_\alpha \mid ELSE) \propto \left(\prod_{j=1}^{m} I(\alpha_j \neq 0) p\left(\sigma^2_{\alpha_j} \mid \nu_\alpha, s^2_\alpha\right)\right) p(\nu_\alpha)$$

$$\propto \left(\prod_{j=1}^{m} I(\alpha_j \neq 0) \frac{\Gamma\left(\frac{\nu_\alpha + 1}{2}\right)}{\Gamma\left(\frac{\nu_\alpha}{2}\right)} \left(\frac{1}{\pi \nu_\alpha s^2_\alpha}\right)^{1/2} \left(1 + \frac{\alpha_j^2}{\nu_\alpha s^2_\alpha}\right)^{-\frac{\nu_\alpha+1}{2}}\right) \frac{1}{(1+\nu_\alpha)^2}.$$

Similar to SS-BayesA, Metropolis-Hasting sampling strategy with a normal distribution proposal density was used to sample ν_α.

Sampling of π_m

A beta prior $beta(\alpha_\pi = 1, \beta_\pi = 10)$ was used for π_m, and its FCD was

$$p(\pi_m) \propto \pi_m^{m_1 + \alpha_\pi - 1} (1 - \pi_m)^{m - m_1 + \beta_\pi - 1}.$$

It was still a beta distribution, and Gibbs sampling was used here to sample from this beta distribution.

We used $\left(s^2_\alpha\right)^{\frac{m_1 \nu_\alpha}{2} + \alpha_\alpha - 1} e^{-\left(\sum_{j=1}^{m} I\left(\sigma^2_{\alpha_j} \neq 0\right) \frac{\nu_\alpha}{2\sigma^2_{\alpha_j}} + \beta_\alpha\right) s^2_\alpha}$ (a gamma density distribution) as the proposal density in the Metropolis-Hasting sampling strategy for s^2_α here.

References:

1. Kizilkaya K and Tempelman RJ. 2005. A general approach to mixed effects modeling of residual variances in generalized linear mixed models. Genetics Selection Evolution 37: 31-56.
2. Fernando RL, Dekkers JCM and Garrick DJ. 2014. A class of Bayesian methods to combine large numbers of genotyped and non-genotyped animals for whole-genome analyses. Genetics Selection Evolution. 46:50.
3. Sorensen D and Gianola D. 2002. Likelihood, Bayesian, and MCMC methods in quantitative

genetics. Springer Science & Business Media.
4. Meuwissen TH, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps. Genetics, 2001, 157(4):1819-1829.
5. Gianola D, Campos GDL, Hill WG, et al. Additive genetic variability and the Bayesian alphabet. Genetics, 2009, 183(1):347-63.
6. Yang W and Tempelman RJ 2011. A Bayesian antedependence model for whole genome prediction. Genetics. 2012 Apr; 190(4):1491-501.