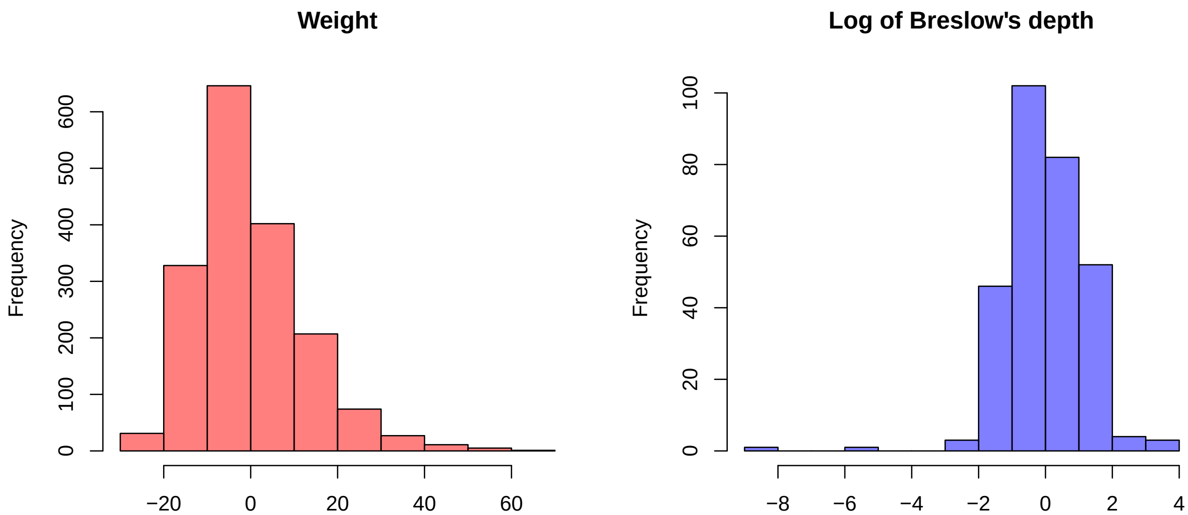
Supporting Information for "Robust Bayesian variable selection for gene-environment interactions" by Jie Ren, Fei Zhou, Xiaoxi Li, Shuangge Ma, Yu Jiang and Cen Wu

1 Web Appendix A



Web Figure 1: Distribution of the residuals for the NHS (left) and SKCM (right) data.

1.1 A remark for the Bayesian LAD regression

The Laplace distribution in Bayesian LAD regression can be treated as a special case of the asymmetric Laplace distribution (ALD) in Bayesian quantile regression (Yu and Moyeed (2001); Yu and Zhang (2005)). In Bayesian quantile regression, ϵ_i follows the asymmetric Laplace distribution with density

$$f(\epsilon_i|\tau, \nu) = \tau(1-\tau)\nu \exp\left\{-\nu\rho_\tau(\epsilon_i)\right\}, \quad i = 1, \ldots, n, \tag{1}$$

where the check loss function is $\rho_\tau(\epsilon_i) = \epsilon_i \left\{\tau - I(\epsilon_i < 0)\right\}$ for the τth quantile $(0 < \tau < 1)$. Note that, when $\tau = 0.5$, the ALD in (1) reduces to a symmetric Laplace distribution. Yu and Moyeed (Yu and Moyeed (2001)) have shown that maximizing a likelihood function under the asymmetric Laplace error distribution (1) is equivalent to minimizing the check loss function in quantile regression. Kozumi and Kobayashi (2011) have proposed a Gibbs sampler for Bayesian quantile regression based on a location-scale mixture representation of the ALD. In particular, with $\widetilde{u}$ and z defined as above, the asymmetric Laplace error in (1) can be represented as

$$\epsilon = \nu^{-1}\psi z + \nu^{-1}\kappa\sqrt{\widetilde{u}}z, \tag{2}$$

where

$$\psi = \frac{1-2\tau}{\tau(1-\tau)} \quad \text{and} \quad \kappa = \sqrt{\frac{2}{\tau(1-\tau)}}.$$

When $\tau = 0.5$, we have $\psi = 0$ and $\kappa = \sqrt{8}$, and equation (2) reduces to the Laplace error.

1.2 A summary of proposed and alternative methods

All the methods under comparison can be grouped according to three criteria: with or without robustness, with or without spike-and-slab priors, and the types of structured sparsity (individual-, group- and bi-level) accommodated through variable selection. We first describe the robust Bayesian methods with spike-and-slab priors: RBSG–SS, RBG–SS and RBL–SS, which have all been proposed for the first time. Among them, RBSG–SS is the "golden" method developed for conducting robust sparse group variable selection for G×E interactions with spike-and-slab priors on both the group and individual levels. Besides, RBG–SS and RBL–SS are robust Bayesian group level and individual level selection with spike–and–slab priors, respectively. The spike–and–slab prior has only been imposed on the group level in RBG–SS. Compared to RBSG–SS, it does not induce within group sparsity. On the other hand, RBL–SS conducts individual-level selection without accounting for group structure. An immediate family of robust methods related to the three are RBSG, RBG and RBL, which do not adopt spike–and–slab priors and cannot shrink coefficients corresponding to the main and interaction effects to zero exactly. While RBG and RBL can be directly derived based on Li et al. (2010), RBSG, robust Bayesian sparse group selection, has not been investigated in existing studies so far.

We have also included six non-robust methods for comparison. Among them, BSG–SS, BG–SS and BL–SS are the non–robust counterparts of RBSG–SS, RBG–SS and RBL–SS, respectively. In particular, the BSG–SS conducts (non–robust) Bayesian sparse group selection with spike-and-slab priors on the group and individual level simultaneously, while variable selection has only been conducted on group (individual) level through RBG–SS (RBL–SS) under the spike–and–slab priors. In addition, BSG, BG and BL can be viewed as the benchmarks without incorporating spike–and–slab priors corresponding to BSG–SS, BG–SS and BL–SS. They can also be considered as the non–robust counterpart corresponding to RBSG, RBG and RBL. All the six non–robust alternatives can be readily derived based on existing studies.

For clarification, we list all the methods under comparison in Web Table (1) and Web Table (2) in the Appendix. Our contribution includes developing the 4 robust Bayesian variable selection approaches, RBSG–SS, RBG–SS, RBL–SS and RBSG among the first time. For all the rest of the approaches, a modification to the methods from the references provided in Web Table (1) by including clinical covariates is necessary. Otherwise, these methods cannot be adopted for a direct comparison with the four newly developed ones.

Web Table 1: Summary of the proposed and alternative methods.

		Methods	Reference
Robust	**RBSG-SS**	Robust Bayesian sparse group selection with spike–and–slab priors	proposed for the first time
	RBG-SS	Robust Bayesian group selection with spike–and–slab priors	proposed for the first time
	RBL-SS	Robust Bayesian Lasso with spike–and–slab priors	proposed for the first time
	RBSG	Robust Bayesian sparse group selection	proposed for the first time
	RBG	Robust Bayesian group Lasso	Li et al. (2010)
	RBL	Robust Bayesian Lasso	Li et al. (2010)
Non-robust	**BSG-SS**	Bayesian sparse group Lasso with spike–and–slab priors	Xu and Ghosh (2015)
	BG-SS	Bayesian group Lasso with spike–and–slab priors	Xu and Ghosh (2015); Zhang et al. (2014)
	BL-SS	Bayesian Lasso with spike–and–slab priors	Xu and Ghosh (2015); Zhang et al. (2014)
	BSG	Bayesian sparse group Lasso	Xu and Ghosh (2015)
	BG	Bayesian group Lasso	Kyung et al. (2010)
	BL	Bayesian Lasso	Park and Casella (2008)

Note: The models in the references are modified to be applicable to G×E settings.

Web Table 2: Summary of comparisons between the proposed and alternative methods.

Methods	**Robustness**	**Likelihood**	**Variable Selection**	**Structure**	**Identification**
RBSG-SS	Yes	Laplacian	Spike-and-slab prior	Bi-level	MPM
RBG-SS	Yes	Laplacian	Spike-and-slab prior	Group level	MPM
RBL-SS	Yes	Laplacian	Spike-and-slab prior	Individual level	MPM
RBSG	Yes	Laplacian	Laplacian shrinkage	Bi-level	Credible interval
RBG	Yes	Laplacian	Laplacian shrinkage	Group level	Credible interval
RBL	Yes	Laplacian	Laplacian shrinkage	Individual level	Credible interval
BSG-SS	No	Gaussian	Spike-and-slab prior	Bi-level	MPM
BG-SS	No	Gaussian	Spike-and-slab prior	Group level	MPM
BL-SS	No	Gaussian	Spike-and-slab prior	Individual level	MPM
BSG	No	Gaussian	Laplacian shrinkage	Bi-level	Credible interval
BG	No	Gaussian	Laplacian shrinkage	Group level	Credible interval
BL	No	Gaussian	Laplacian shrinkage	Individual level	Credible interval

Bi-level: both the group and individual level.

MPM: Median Probability Model.

1.3 Posterior inference of the proposed method (RBSG-SS)

1.3.1 Hierarchical model specification

The joint posterior distribution of all the unknown parameters conditional on data can be expressed as

$$
\begin{aligned}
&\pi(\boldsymbol{\alpha}, \boldsymbol{\theta}, \boldsymbol{b_j}, \omega_{jl}, \nu, u_i, \pi_0, \pi_1, s^2 | \boldsymbol{Y}) \\
&\qquad \propto \prod_{i=1}^{n} (2\pi\kappa^2\nu^{-1}u_i)^{-\frac{1}{2}} \exp\left\{ -\frac{\left(Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \sum_{j=1}^{p} \boldsymbol{U_{ij}}^\top \boldsymbol{\beta_j}\right)^2}{2\kappa^2\nu^{-1}u_i} \right\} \\
&\qquad \times \prod_{i=1}^{n} \nu \exp(-\nu u_i)\; \nu^{c-1} \exp\left(-d\nu\right) \\
&\qquad \times \exp\left(-\frac{1}{2}\boldsymbol{\theta}^\top \boldsymbol{\Sigma}_{\boldsymbol{\theta 0}}^{-1}\boldsymbol{\theta}\right) \exp\left(-\frac{1}{2}\boldsymbol{\alpha}^\top \boldsymbol{\Sigma}_{\boldsymbol{\alpha 0}}^{-1}\boldsymbol{\alpha}\right) \\
&\qquad \times \prod_{j=1}^{p} \left\{ \pi_0 (2\pi)^{-\frac{L}{2}} \exp\left(-\frac{1}{2}\boldsymbol{b_j}^\top \boldsymbol{b_j}\right) \mathbf{I}_{\{\boldsymbol{b_j} \neq \mathbf{0}\}} + (1-\pi_0)\delta_0(\boldsymbol{b_j}) \right\} \\
&\qquad \times \prod_{j=1}^{p} \prod_{l=1}^{L} \left\{ \pi_1 2 (2\pi s^2)^{-\frac{1}{2}} \exp\left(-\frac{\omega_{jl}^2}{2s^2}\right) \mathbf{I}_{\{\omega_{jl} > 0\}} + (1-\pi_1)\delta_0(\omega_{jl}) \right\} \\
&\qquad \times \pi_0^{a_0-1}(1-\pi_0)^{b_0-1} \\
&\qquad \times \pi_1^{a_1-1}(1-\pi_1)^{b_1-1} \\
&\qquad \times (s^2)^{-2} \exp(-\frac{\eta}{s^2}).
\end{aligned}
$$

1.3.2 Gibbs sampler

Define the coefficient vector without the jth group as $\boldsymbol{\beta_{(j)}} = (\boldsymbol{\beta_1}^\top, \dots, \boldsymbol{\beta_{j-1}}^\top, \boldsymbol{\beta_{j+1}}^\top, \dots, \boldsymbol{\beta_p}^\top)$ and the corresponding part of the design matrix as $\boldsymbol{U_{(j)}}$. Likewise, define the coefficient vector without the lth element in the jth group as $\boldsymbol{\beta_{(jl)}}$ and the corresponding design matrix as $\boldsymbol{U_{(jl)}}$. Let $l_j^b = p(\boldsymbol{b_j} \neq \mathbf{0}|\text{rest})$, then the conditional posterior distribution of $\boldsymbol{b_j}$ is a multivariate spike–and–slab distribution:

$$\boldsymbol{b_j}|\text{rest} \sim l_j^b \, \mathrm{N}_L(\boldsymbol{\mu_{b_j}}, \, \boldsymbol{\Sigma_{b_j}}) + (1 - l_j^b) \, \delta_0(\boldsymbol{b_j}), \tag{3}$$

where $\boldsymbol{\Sigma_{b_j}} = \left(\nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{V_j}^{\frac{1}{2}} \boldsymbol{U_{ij}} \boldsymbol{U_{ij}}^\top \boldsymbol{V_j}^{\frac{1}{2}} + \mathbf{I}_L\right)^{-1}$, $\boldsymbol{\mu_{b_j}} = \boldsymbol{\Sigma_{b_j}} \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{V_j}^{\frac{1}{2}} \boldsymbol{U_{ij}} \widetilde{y}_{ij}$ and $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_{(j)}}^\top \boldsymbol{\beta_{(j)}}$. The l_j^b can be derived as

$$l_j^b = \frac{\pi_0}{\pi_0 + (1 - \pi_0)|\boldsymbol{\Sigma_{b_j}}|^{-\frac{1}{2}} \exp\left\{-\frac{1}{2} \|\boldsymbol{\Sigma}_{\boldsymbol{b_j}}^{\frac{1}{2}} \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{V_j}^{\frac{1}{2}} \boldsymbol{U_{ij}} \widetilde{y}_{ij}\|_2^2\right\}}.$$

The posterior distribution (3) is a mixture of a multivariate normal and a point mass at $\mathbf{0}$. Specifically, at the gth iteration of MCMC, $\boldsymbol{b_j}^{(g)}$ is drawn from $N(\boldsymbol{\mu_{b_j}}, \, \boldsymbol{\Sigma_{b_j}})$ with probability l_j^b and is set to $\mathbf{0}$ with probability $1 - l_j^b$. If $\boldsymbol{b_j}^{(g)}$ is set to $\mathbf{0}$, we have $\phi_j^{b(g)} = 0$, which suggests that the jth genetic variant is not associated with the phenotype at the gth iteration. Otherwise, $\phi_j^{b(g)} = 1$.

In addition to the multivariate spike–and–slab distribution on the group level, on the individual level, the conditional posterior distribution of ω_{jl} is also spike-and-slab. Let $l_{jl}^w = p(\omega_{jl} \neq 0|\text{rest})$, we have

$$\omega_{jl}|\text{rest} \sim l_{jl}^w \, \mathrm{N}^+(\mu_{\omega_{jl}}, \, \sigma_{\omega_{jl}}^2) + (1 - l_{jl}^w)\delta_0(\omega_{jl}),$$

where $\sigma_{\omega_{jl}}^2 = \left(\frac{1}{s^2} + \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} U_{ijl}^2 b_{jl}^2\right)^{-1}$, $\mu_{\omega_{jl}} = \sigma_{\omega_{jl}}^2 \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} b_{jl} U_{ijl} \widetilde{y}_{ijl}$ and $\widetilde{y}_{ijl} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_{(jl)}}^\top \boldsymbol{\beta_{(jl)}}$. It can be shown that

$$l_{jl}^w = \frac{\pi_1}{\pi_1 + (1 - \pi_1)\frac{1}{2} s (\sigma_{\omega_{jl}}^2)^{-\frac{1}{2}} \exp\left\{-\frac{1}{2} \sigma_{\omega_{jl}}^2 \left(\nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} b_{jl} U_{ijl} \widetilde{y}_{ijl}\right)^2\right\} \left[\Phi\left(\frac{\mu_{\omega_{jl}}}{\sigma_{\omega_{jl}}}\right)\right]^{-1}},$$

where $\Phi(\cdot)$ is the cumulative distribution function of the standard normal random variable. At the gth iteration, the value of $\phi_{jl}^{w(g)}$ can be determined by whether the $\omega_{jl}^{(g)}$ is set to 0 or not. Recall that $\phi_{jl}^{w(g)} = 0$ implies that the jth genetic variant does not have the main effect (if l=1) or the interaction effect with the $(l-1)$th E factor (if $l > 1$).

The full conditional distribution for u_i is Inverse-Gaussian:

$$u_i|\text{rest} \sim \text{Inverse-Gaussian}(\mu_{u_i}, \, \lambda_{u_i}),$$

where the shape parameter $\lambda_{u_i} = 2\nu$, mean parameter $\mu_{u_i} = \sqrt{\frac{2\kappa^2}{(Y_i - \widetilde{y}_i)^2}}$ and $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.

With the conjugate Inverse–Gamma prior, the posteriors of s^2 is still an Inverse–Gamma distribution

$$s^2|\text{rest} \sim \text{Inv-Gamma}\left(1 + \frac{1}{2}\sum_{j,l} \mathbf{I}_{\{\omega_{jl}\neq 0\}},\ \eta + \frac{1}{2}\sum_{j,l} \omega_{jl}^2\right).$$

With conjugate Beta priors, π_0 and π_1 have beta posterior distributions

$$\pi_0|\text{rest} \sim \text{Beta}\left(a_0 + \sum_{j=1}^{p} \mathbf{I}_{\{\boldsymbol{b_j}\neq\mathbf{0}\}},\ b_0 + \sum_{j=1}^{p} \mathbf{I}_{\{\boldsymbol{b_j}=\mathbf{0}\}}\right),$$

$$\pi_1|\text{rest} \sim \text{Beta}\left(a_1 + \sum_{j,l} \mathbf{I}_{\{\omega_{jl}\neq 0\}},\ b_1 + \sum_{j,l} \mathbf{I}_{\{\omega_{jl}=0\}}\right).$$

Last, the full conditional distribution for ν is Gamma distribution

$$\nu|\text{rest} \sim \text{Gamma}\left(s_\nu,\ r_\nu\right),$$

where the shape parameter $s_\nu = c + \frac{3n}{2}$ and the rate parameter $r_\nu = d + \sum_{i=1}^n u_i + (2\kappa^2)^{-1}\sum_{i=1}^n u_i^{-1}\widetilde{y}_i^2$. Under our prior setting, conditional posterior distributions of all unknown parameters have closed forms by conjugacy. Therefore, efficient Gibbs sampler can be constructed for the posterior distribution.

1.4 Posterior inference of RBG-SS

1.4.1 Hierarchical model specification

$$
\begin{gathered}
Y_i = \boldsymbol{W_i}^\top\boldsymbol{\alpha} + \boldsymbol{E_i}^\top\boldsymbol{\theta} + \boldsymbol{U_i}^\top\boldsymbol{\beta} + \nu^{-\frac{1}{2}}\kappa\sqrt{u_i}z_i, \quad i = 1, \dots, n,\\
u_i|\nu \overset{ind}{\sim} \text{Exp}(\nu), \quad i = 1, \dots, n,\\
z_i \overset{ind}{\sim} \text{N}(0,\ 1), \quad i = 1, \dots, n,\\
\nu \sim \text{Gamma}\left(c_1,\ c_2\right),\\
\boldsymbol{\alpha} \sim \text{N}_q(\mathbf{0},\ \boldsymbol{\Sigma_{\alpha 0}}),\\
\boldsymbol{\theta} \sim \text{N}_k(\mathbf{0},\ \boldsymbol{\Sigma_{\theta 0}}),\\
\boldsymbol{\beta_j}|\phi_j, s_j \overset{ind}{\sim} \phi_j\,\text{N}_L\left(\mathbf{0},\ s_j\mathbf{I}_L\right) + (1-\phi_j)\delta_0(\boldsymbol{\beta_j}), \quad j = 1, \dots, p,\\
\phi_j|\pi_0 \overset{ind}{\sim} \text{Bernoulli}(\pi_0), \quad j = 1, \dots, p,\\
\pi_0 \sim \text{Beta}\left(a_0,\ b_0\right),\\
s_j|\eta \sim \text{Gamma}\left(\frac{L+1}{2}, \frac{\eta}{2}\right), \quad j = 1, \dots, p,\\
\eta \sim \text{Gamma}\left(d_1,\ d_2\right).
\end{gathered}
$$

1.4.2 Gibbs Sampler

- $u_i|\text{rest} \sim$ Inverse-Gaussian$(\mu_{u_i},\ \lambda_{u_i})$, where the shape parameter $\lambda_{u_i} = 2\nu$, mean parameter $\mu_{u_i} = \sqrt{\frac{2\kappa^2}{(Y_i - \widetilde{y_i})^2}}$ and $\widetilde{y_i} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.

- $\nu|\text{rest} \sim$ Gamma $(s_\nu,\ r_\nu)$, where the shape parameter $s_\nu = c_1 + \frac{3n}{2}$ and the rate parameter $r_\nu = c_2 + \sum_{i=1}^n u_i + (2\kappa^2)^{-1} \sum_{i=1}^n u_i^{-1} \widetilde{y_i}^2$.

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i} \boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}} \right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i} \boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}} \right)^{-1}.$$

- $\boldsymbol{\beta_j}|\text{rest} \sim l_j \mathrm{N}(\boldsymbol{\mu_{\beta_j}},\ \boldsymbol{\Sigma_{\beta_j}}) + (1 - l_j)\delta_0(\boldsymbol{\beta_j})$ where

$$\boldsymbol{\mu_{\beta_j}} = \boldsymbol{\Sigma_{\beta_j}} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{U_{ij}} \widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{\beta_j}} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{U_{ij}} \boldsymbol{U_{ij}}^\top + \frac{1}{s_j} \mathbf{I}_L \right)^{-1},$$

$$l_j = \frac{\pi_0}{\pi_0 + (1 - \pi_0) s_j^{\frac{L}{2}} |\boldsymbol{\Sigma_{\beta_j}}|^{-\frac{1}{2}} \exp\left\{ -\frac{1}{2} \|\boldsymbol{\Sigma_{\beta_j}^{\frac{1}{2}}} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{U_{ij}} \widetilde{y}_{ij}\|_2^2 \right\}}.$$

  and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_{(j)}^\top} \boldsymbol{\beta_{(j)}}$.

- The posterior of s_j is

$$s_j^{-1}|\text{rest} \sim \begin{cases} \text{Inverse-Gamma}(\frac{L+1}{2},\ \frac{\eta}{2}), & \text{if } \boldsymbol{\beta_j} = \mathbf{0}, \\ \text{Inverse-Gaussian}(\eta,\ \sqrt{\frac{\eta}{\|\boldsymbol{\beta_j}\|_2^2}}), & \text{if } \boldsymbol{\beta_j} \neq \mathbf{0} \end{cases}$$

- $\pi_0|\text{rest} \sim$ Beta $\left(a_0 + \sum_{j=1}^p \mathbf{I}_{\{\boldsymbol{\beta_j} \neq \mathbf{0}\}},\ b_0 + \sum_{j=1}^p \mathbf{I}_{\{\boldsymbol{\beta_j} = \mathbf{0}\}} \right)$.

- $\eta|\text{rest} \sim$ Gamma $(s_\eta,\ r_\eta)$, where $s_\eta = \frac{p + p \times L}{2} + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j=1}^p s_j}{2} + d_2$.

1.5 Posterior inference of RBL-SS

1.5.1 Hierarchical model specification

$$
\begin{gathered}
Y_i = \boldsymbol{W_i}^\top \boldsymbol{\alpha} + \boldsymbol{E_i}^\top \boldsymbol{\theta} + \boldsymbol{U_i}^\top \boldsymbol{\beta} + \nu^{-\frac{1}{2}} \kappa \sqrt{u_i} z_i, \\
u_i|\nu \overset{ind}{\sim} \mathrm{Exp}(\nu), \quad i = 1, \ldots, n, \\
z_i \overset{ind}{\sim} \mathrm{N}(0,\ 1), \\
\nu \sim \mathrm{Gamma}\left(c_1,\ c_2\right), \\
\boldsymbol{\alpha} \sim \mathrm{N}_q(\mathbf{0},\ \boldsymbol{\Sigma}_{\boldsymbol{\alpha}\mathbf{0}}), \\
\boldsymbol{\theta} \sim \mathrm{N}_k(\mathbf{0},\ \boldsymbol{\Sigma}_{\boldsymbol{\theta}\mathbf{0}}), \\
\beta_{jl}|\phi_{jl}, s_{jl} \overset{ind}{\sim} \phi_{jl}\, \mathrm{N}\left(0,\ s_{jl}\right) + (1 - \phi_{jl})\delta_0(\beta_{jl}), \quad j = 1, \ldots, p;\ l = 1, \ldots, L, \\
\phi_{jl}|\pi_1 \overset{ind}{\sim} \mathrm{Bernoulli}(\pi_1), \quad j = 1, \ldots, p;\ l = 1, \ldots, L, \\
s_{jl}|\eta \sim \mathrm{Gamma}\left(1, \frac{\eta}{2}\right), \quad j = 1, \ldots, p;\ l = 1, \ldots, L, \\
\pi_1 \sim \mathrm{Beta}\left(a_1,\ b_1\right), \\
\eta \sim \mathrm{Gamma}\left(d_1,\ d_2\right).
\end{gathered}
$$

1.5.2 Gibbs Sampler

- $u_i|\text{rest} \sim \text{Inverse-Gaussian}(\mu_{u_i},\ \lambda_{u_i})$, where the shape parameter $\lambda_{u_i} = 2\nu$, mean parameter $\mu_{u_i} = \sqrt{\frac{2\kappa^2}{(Y_i - \widetilde{y}_i)^2}}$ and $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.
- $\nu|\text{rest} \sim \mathrm{Gamma}\left(s_\nu,\ r_\nu\right)$, where the shape parameter $s_\nu = c_1 + \frac{3n}{2}$ and the rate parameter $r_\nu = c_2 + \sum_{i=1}^n u_i + (2\kappa^2)^{-1} \sum_{i=1}^n u_i^{-1} \widetilde{y}_i^{\,2}$.
- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$
\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i} (Y_i - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),
$$

$$
\boldsymbol{\Sigma_\alpha} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i} \boldsymbol{W_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\alpha}\mathbf{0}}^{-1} \right)^{-1}.
$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$
\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i} (Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),
$$

$$
\boldsymbol{\Sigma_\theta} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i} \boldsymbol{E_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\theta}\mathbf{0}}^{-1} \right)^{-1}.
$$

- $\beta_{jl}|\text{rest} \sim l_{jl}\mathrm{N}(\mu_{\beta_{jl}},\, \sigma^2_{\beta_{jl}}) + (1-l_{jl})\delta_0(\beta_{jl})$ where

$$\mu_{\beta_{jl}} = \sigma^2_{\beta_{jl}}\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}U_{ijl}\widetilde{y}_{ijl},$$

$$\sigma^2_{\beta_{jl}} = \left(\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}U^2_{ijl} + \frac{1}{s_{jl}}\right)^{-1},$$

$$l_{jl} = \frac{\pi_1}{\pi_1 + (1-\pi_1)s_{jl}^{\frac{1}{2}}(\sigma^2_{\beta_{jl}})^{-\frac{1}{2}}\exp\left\{-\frac{1}{2}\sigma^2_{\beta_{jl}}(\nu\kappa^{-2}\sum_{i=1}^{n}u_i^{-1}U_{ijl}\widetilde{y}_{ijl})^2\right\}}.$$

  and $\widetilde{y}_{ijl}$ is defined as $\widetilde{y}_{ijl} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U}^\top_{\boldsymbol{(jl)}}\boldsymbol{\beta_{(jl)}}$.

- The posterior of s_{jl} is

$$s_{jl}^{-1}|\text{rest} \sim \begin{cases}\text{Inverse-Gamma}(1,\ \frac{\eta}{2}), & \text{if } \beta_{jl} = 0,\\ \text{Inverse-Gaussian}(\eta,\ \sqrt{\frac{\eta}{\beta^2_{jl}}}), & \text{if } \beta_{jl} \neq 0.\end{cases}$$

- $\pi_1|\text{rest} \sim \text{Beta}\left(a_1 + \sum_{j,l}\mathbf{I}_{\{\beta_{jl}\neq 0\}},\ b_1 + \sum_{j,l}\mathbf{I}_{\{\beta_{jl}=0\}}\right)$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\, r_\eta)$, where $s_\eta = p\times L + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j,l}s_{jl}}{2} + d_2$.

1.6 Posterior inference of RBSG

1.6.1 Hierarchical model specification

$$Y_i = \boldsymbol{W_i}^\top\boldsymbol{\alpha} + \boldsymbol{E_i}^\top\boldsymbol{\theta} + \boldsymbol{U_i}^\top\boldsymbol{\beta} + \nu^{-\frac{1}{2}}\kappa\sqrt{u_i}z_i,$$

$$u_i|\nu \overset{ind}{\sim} \text{Exp}(\nu), \quad i = 1, \dots, n,$$

$$z_i \overset{ind}{\sim} \mathrm{N}(0,\ 1),$$

$$\nu \sim \text{Gamma}\,(c_1,\ c_2)\,,$$

$$\boldsymbol{\alpha} \sim \mathrm{N}_q(\mathbf{0},\ \boldsymbol{\Sigma_{\alpha 0}}),$$

$$\boldsymbol{\theta} \sim \mathrm{N}_k(\mathbf{0},\ \boldsymbol{\Sigma_{\theta 0}}),$$

$$\boldsymbol{\beta_j}|r_j, \omega_{jl} \overset{ind}{\sim} \mathrm{N}_L(\mathbf{0},\ \boldsymbol{V_j}),\ \text{where } \boldsymbol{V_j} = \text{diag}\left\{(\frac{1}{r_j} + \frac{1}{\omega_{jl}})^{-1},\ l = 1, 2, \dots, L\right\},$$

$$r_j, \omega_{j1}, \dots, \omega_{jL}|\eta_1, \eta_2 \propto \prod_{l=1}^{L}\left[(\omega_{jl})^{-\frac{1}{2}}\left(\frac{1}{r_j} + \frac{1}{\omega_{jl}}\right)^{-\frac{1}{2}}\right](r_j)^{-\frac{1}{2}}\exp\left(-\frac{\eta_1}{2}r_j - \frac{\eta_2}{2}\sum_{l=1}^{L}\omega_{jl}\right),$$

$$\eta_1, \eta_2 \propto \eta_1^{\frac{p}{2}}\eta_2^{pL}\exp\left\{-d_1\eta_1 - d_2\eta_2\right\},$$

$$\sigma^2 \sim 1/\sigma^2.$$

1.6.2 Gibbs Sampler

- $u_i|\text{rest} \sim$ Inverse-Gaussian$(\mu_{u_i}, \lambda_{u_i})$, where the shape parameter $\lambda_{u_i} = 2\nu$, mean parameter $\mu_{u_i} = \sqrt{\frac{2\kappa^2}{(Y_i - \widetilde{y}_i)^2}}$ and $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.

- $\nu|\text{rest} \sim$ Gamma(s_ν, r_ν), where the shape parameter $s_\nu = c_1 + \frac{3n}{2}$ and the rate parameter $r_\nu = c_2 + \sum_{i=1}^n u_i + (2\kappa^2)^{-1} \sum_{i=1}^n u_i^{-1} \widetilde{y}_i^2$.

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha}, \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha} \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i} \boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}} \right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta}, \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta} \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i} \boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}} \right)^{-1}.$$

- $\boldsymbol{\beta_j}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_{\beta_j}}, \boldsymbol{\Sigma_{\beta_j}})$ where

$$\boldsymbol{\mu_{\beta_j}} = \boldsymbol{\Sigma_{\beta_j}} \nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{U_{ij}} \widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{\beta_j}} = \left(\nu\kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{U_{ij}} \boldsymbol{U_{ij}^\top} + \boldsymbol{V_j^{-1}} \right)^{-1},$$

  and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_{(j)}^\top} \boldsymbol{\beta_{(j)}}$.

- $r_j^{-1}|\text{rest} \sim$ Inv-Gaussian$(\eta_1, \sqrt{\frac{\eta_1 \sigma^2}{\|\boldsymbol{\beta_j}\|_2^2}})$.

- $\omega_{jl}^{-1}|\text{rest} \sim$ Inv-Gaussian$(\eta_2, \sqrt{\frac{\eta_2 \sigma^2}{\beta_{jl}^2}})$.

- $\eta_1|\text{rest} \sim$ Gamma(s_{η_1}, r_{η_1}), where $s_{\eta_1} = \frac{p}{2} + 1$ and the rate parameter $r_{\eta_1} = \frac{\sum_{j=1}^p r_j}{2} + d_1$.

- $\eta_2|\text{rest} \sim$ Gamma(s_{η_2}, r_{η_2}), where $s_{\eta_2} = p \times L + 1$ and the rate parameter $r_{\eta_2} = \frac{\sum_{j,l} \omega_{jl}}{2} + d_2$.

1.7 Posterior inference of RBG

1.7.1 Hierarchical model specification

$$
\begin{gathered}
Y_i = \boldsymbol{W_i}^\top \boldsymbol{\alpha} + \boldsymbol{E_i}^\top \boldsymbol{\theta} + \boldsymbol{U_i}^\top \boldsymbol{\beta} + \nu^{-\frac{1}{2}} \kappa \sqrt{u_i} z_i, \quad i = 1, \ldots, n, \\
u_i | \nu \overset{ind}{\sim} \operatorname{Exp}(\nu), \quad i = 1, \ldots, n, \\
z_i \overset{ind}{\sim} \mathrm{N}(0,\ 1), \quad i = 1, \ldots, n, \\
\nu \sim \operatorname{Gamma}\left(c_1,\ c_2\right), \\
\boldsymbol{\alpha} \sim \mathrm{N}_q(\mathbf{0},\ \boldsymbol{\Sigma_{\alpha 0}}), \\
\boldsymbol{\theta} \sim \mathrm{N}_k(\mathbf{0},\ \boldsymbol{\Sigma_{\theta 0}}), \\
\boldsymbol{\beta_j} | s_j \overset{ind}{\sim} \mathrm{N}_L\left(0,\ s_j \mathbf{I}_L\right), \quad j = 1, \ldots, p, \\
s_j | \eta \sim \operatorname{Gamma}\left(\frac{L+1}{2}, \frac{\eta}{2}\right), \quad j = 1, \ldots, p, \\
\eta \sim \operatorname{Gamma}\left(d_1,\ d_2\right).
\end{gathered}
$$

1.7.2 Gibbs Sampler

- $u_i|\text{rest} \sim \text{Inverse-Gaussian}(\mu_{u_i},\ \lambda_{u_i})$, where the shape parameter $\lambda_{u_i} = 2\nu$, mean parameter $\mu_{u_i} = \sqrt{\frac{2\kappa^2}{(Y_i - \widetilde{y}_i)^2}}$ and $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.
- $\nu|\text{rest} \sim \operatorname{Gamma}\left(s_\nu,\ r_\nu\right)$, where the shape parameter $s_\nu = c_1 + \frac{3n}{2}$ and the rate parameter $r_\nu = c_2 + \sum_{i=1}^n u_i + (2\kappa^2)^{-1} \sum_{i=1}^n u_i^{-1} \widetilde{y}_i^{\,2}$.
- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$
\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i} (Y_i - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),
$$

$$
\boldsymbol{\Sigma_\alpha} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{W_i} \boldsymbol{W_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\alpha 0}}^{-1} \right)^{-1}.
$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$
\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta} \nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i} (Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{U_i}^\top \boldsymbol{\beta}),
$$

$$
\boldsymbol{\Sigma_\theta} = \left(\nu \kappa^{-2} \sum_{i=1}^n u_i^{-1} \boldsymbol{E_i} \boldsymbol{E_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\theta 0}}^{-1} \right)^{-1}.
$$

- $\boldsymbol{\beta_j}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_{\beta_j}},\, \boldsymbol{\Sigma_{\beta_j}})$ where

$$\boldsymbol{\mu_{\beta_j}} = \boldsymbol{\Sigma_{\beta_j}} \nu\kappa^{-2} \sum_{i=1}^{n} u_i^{-1} \boldsymbol{U_{ij}} \widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{\beta_j}} = \left(\nu\kappa^{-2} \sum_{i=1}^{n} u_i^{-1} \boldsymbol{U_{ij}} \boldsymbol{U_{ij}}^\top + \frac{1}{s_j} \mathbf{I}_L \right)^{-1},$$

and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_{(j)}}^\top \boldsymbol{\beta_{(j)}}$.

- $s_j^{-1}|\text{rest} \sim \text{Inverse-Gaussian}(\eta,\, \sqrt{\frac{\eta}{\|\boldsymbol{\beta_j}\|_2^2}})$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\, r_\eta)$, where $s_\eta = \frac{p+p\times L}{2} + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j=1}^{p} s_j}{2} + d_2$.

1.8 Posterior inference of RBL

1.8.1 Hierarchical model specification

$$\begin{aligned}
Y_i &= \boldsymbol{W_i}^\top \boldsymbol{\alpha} + \boldsymbol{E_i}^\top \boldsymbol{\theta} + \boldsymbol{U_i}^\top \boldsymbol{\beta} + \nu^{-\frac{1}{2}} \kappa \sqrt{u_i} z_i, \\
u_i|\nu &\overset{ind}{\sim} \mathrm{Exp}(\nu), \quad i = 1, \dots, n, \\
z_i &\overset{ind}{\sim} \mathrm{N}(0,\ 1), \\
\nu &\sim \mathrm{Gamma}\,(c_1,\ c_2)\,, \\
\boldsymbol{\alpha} &\sim \mathrm{N}_q(\mathbf{0},\, \boldsymbol{\Sigma_{\alpha 0}}), \\
\boldsymbol{\theta} &\sim \mathrm{N}_k(\mathbf{0},\, \boldsymbol{\Sigma_{\theta 0}}), \\
\beta_{jl}|s_{jl} &\overset{ind}{\sim} \mathrm{N}\,(0,\, s_{jl})\,, \quad j = 1, \dots, p;\ l = 1, \dots, L, \\
s_{jl}|\eta &\sim \mathrm{Gamma}\left(1, \frac{\eta}{2}\right), \quad j = 1, \dots, p;\ l = 1, \dots, L, \\
\eta &\sim \mathrm{Gamma}\,(d_1,\ d_2)\,.
\end{aligned}$$

1.8.2 Gibbs Sampler

- $u_i|\text{rest} \sim \text{Inverse-Gaussian}(\mu_{u_i},\, \lambda_{u_i})$, where the shape parameter $\lambda_{u_i} = 2\nu$, mean parameter $\mu_{u_i} = \sqrt{\frac{2\kappa^2}{(Y_i - \widetilde{y}_i)^2}}$ and $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.

- $\nu|\text{rest} \sim \text{Gamma}\,(s_\nu,\, r_\nu)$, where the shape parameter $s_\nu = c_1 + \frac{3n}{2}$ and the rate parameter $r_\nu = c_2 + \sum_{i=1}^{n} u_i + (2\kappa^2)^{-1} \sum_{i=1}^{n} u_i^{-1} \widetilde{y}_i^{\,2}$.

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\, \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}\boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}\boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\alpha 0}}^{-1}\right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\, \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}\boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}\boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\theta 0}}^{-1}\right)^{-1}.$$

- $\beta_{jl}|\text{rest} \sim \mathrm{N}(\mu_{\beta_{jl}},\, \sigma^2_{\beta_{jl}})$ where

$$\mu_{\beta_{jl}} = \sigma^2_{\beta_{jl}}\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}U_{ijl}\widetilde{y}_{ijl},$$

$$\sigma^2_{\beta_{jl}} = \left(\nu\kappa^{-2}\sum_{i=1}^{n} u_i^{-1}U_{ijl}^2 + \frac{1}{s_{jl}}\right)^{-1},$$

  and $\widetilde{y}_{ijl}$ is defined as $\widetilde{y}_{ijl} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U}_{\boldsymbol{(jl)}}^\top\boldsymbol{\beta}_{\boldsymbol{(jl)}}$.

- $s_j^{-1}|\text{rest} \sim \text{Inverse-Gaussian}(\eta,\, \sqrt{\frac{\eta}{\beta_{jl}^2}})$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\, r_\eta)$, where $s_\eta = p \times L + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j,l} s_{jl}}{2} + d_2$.

1.9 Posterior inference of BSG-SS

1.9.1 Hierarchical model specification

$$\boldsymbol{Y}|\boldsymbol{\alpha},\boldsymbol{\theta},\boldsymbol{\beta},\sigma^2 \propto (\sigma^2)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^{n}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta})^2\right\},$$

$$\boldsymbol{\alpha} \sim \mathrm{N}_q(\mathbf{0},\, \boldsymbol{\Sigma}_{\boldsymbol{\alpha}\mathbf{0}}),$$

$$\boldsymbol{\theta} \sim \mathrm{N}_k(\mathbf{0},\, \boldsymbol{\Sigma}_{\boldsymbol{\theta}\mathbf{0}}),$$

$$\boldsymbol{\beta_j} = \boldsymbol{V_j}^{\frac{1}{2}}\boldsymbol{b_j}, \quad \text{where } \boldsymbol{V_j}^{\frac{1}{2}} = \mathrm{diag}\{\omega_{j1},\ldots,\omega_{jL}\},$$

$$\boldsymbol{b_j}|\phi_j^b \overset{ind}{\sim} \phi_j^b\,\mathrm{N}_L\,(0,\,\mathbf{I}_L) + (1-\phi_j^b)\delta_0(\boldsymbol{b_j}),$$

$$\phi_j^b|\pi_0 \overset{ind}{\sim} \mathrm{Bernoulli}(\pi_0),$$

$$\pi_0 \sim \mathrm{Beta}\,(a_0,\, b_0)\,,$$

$$\omega_{jl}|\phi_{jl}^w \overset{ind}{\sim} \phi_{jl}^w\,\mathrm{N}^+\left(0,\, s^2\right) + (1-\phi_{jl}^w)\delta_0(\omega_{jl}),$$

$$\phi_{jl}^w|\pi_1 \overset{ind}{\sim} \mathrm{Bernoulli}(\pi_1),$$

$$\pi_1 \sim \mathrm{Beta}\,(a_1,\, b_1)\,,$$

$$s^2 \sim \text{Inverse-Gamma}\,(1,\eta)\,,$$

$$\sigma^2 \sim 1/\sigma^2.$$

1.9.2 Gibbs Sampler

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\, \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\alpha}\mathbf{0}}^{-1}\right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\, \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma}_{\boldsymbol{\theta}\mathbf{0}}^{-1}\right)^{-1}.$$

- $\boldsymbol{b_j}|\text{rest} \sim l_j \mathrm{N}(\boldsymbol{\mu_{b_j}}, \boldsymbol{\Sigma_{b_j}}) + (1-l_j)\delta_0(\boldsymbol{b_j})$ where

$$\boldsymbol{\mu_{b_j}} = \boldsymbol{\Sigma_{b_j}}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{V_j}^{\frac{1}{2}}\boldsymbol{U_{ij}}\widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{b_j}} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{V_j}^{\frac{1}{2}}\boldsymbol{U_{ij}}\boldsymbol{U_{ij}}^\top\boldsymbol{V_j}^{\frac{1}{2}} + \mathbf{I}_L\right)^{-1},$$

$$l_j^b = \frac{\pi_0}{\pi_0 + (1-\pi_0)|\boldsymbol{\Sigma_{b_j}}|^{-\frac{1}{2}}\exp\left\{-\frac{1}{2\sigma^4}\|\boldsymbol{\Sigma}_{\boldsymbol{b_j}}^{\frac{1}{2}}\sum_{i=1}^{n}\boldsymbol{V_j}^{\frac{1}{2}}\boldsymbol{U_{ij}}\widetilde{y}_{ij}\|_2^2\right\}},$$

and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_{(j)}}^\top\boldsymbol{\beta_{(j)}}$.

- $\omega_{jl}|\text{rest} \sim l_{jl}^w\, \mathrm{N}^+(\mu_{\omega_{jl}}, \sigma_{\omega_{jl}}^2) + (1-l_{jl}^w)\delta_0(\omega_{jl})$ where

$$\mu_{\omega_{jl}} = \sigma_{\omega_{jl}}^2(\sigma^2)^{-1}\sum_{i=1}^{n}b_{jl}U_{ijl}\widetilde{y}_{ijl},$$

$$\sigma_{\omega_{jl}}^2 = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}U_{ijl}^2 b_{jl}^2 + \frac{1}{s^2}\right)^{-1},$$

$$l_{jl}^w = \frac{\pi_1}{\pi_1 + (1-\pi_1)\frac{1}{2}s(\sigma_{\omega_{jl}}^2)^{-\frac{1}{2}}\exp\left\{-\frac{\sigma_{\omega_{jl}}^2}{2\sigma^4}\left(\sum_{i=1}^{n}b_{jl}U_{ijl}\widetilde{y}_{ijl}\right)^2\right\}\left[\Phi\left(\frac{\mu_{\omega_{jl}}}{\sigma_{\omega_{jl}}}\right)\right]^{-1}}.$$

and $\widetilde{y}_{ijl}$ is defined as $\widetilde{y}_{ijl} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_{(jl)}}^\top\boldsymbol{\beta_{(jl)}}$.

- $s^2|\text{rest} \sim \text{Inv-Gamma}\left(1 + \frac{1}{2}\sum_{j,l}\mathbf{I}_{\{\omega_{jl}\neq 0\}},\ \eta + \frac{1}{2}\sum_{j,l}\omega_{jl}^2\right)$.

- $\pi_0|\text{rest} \sim \text{Beta}\left(a_0 + \sum_{j=1}^{p}\mathbf{I}_{\{\boldsymbol{\beta_j}\neq\mathbf{0}\}},\ b_0 + \sum_{j=1}^{p}\mathbf{I}_{\{\boldsymbol{\beta_j}=\mathbf{0}\}}\right)$.

- $\pi_1|\text{rest} \sim \text{Beta}\left(a_1 + \sum_{j,l}\mathbf{I}_{\{\omega_{jl}\neq 0\}},\ b_1 + \sum_{j,l}\mathbf{I}_{\{\omega_{jl}=0\}}\right)$.

- η is estimated with the EM approach used in the proposed method. For the gth EM update $\eta^{(g)} = \frac{1}{E_{\eta^{(g-1)}}\left[\frac{1}{s^2}|\boldsymbol{Y}\right]}$.

- $\sigma^2|\text{rest} \sim \text{Inv-Gamma}(\frac{n}{2},\ \frac{\sum_{i=1}^{n}\widetilde{y}_i^{\,2}}{2})$, where $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}$.

1.10 Posterior inference of BGL-SS

1.10.1 Hierarchical model specification

$$\boldsymbol{Y}|\boldsymbol{\alpha},\boldsymbol{\theta},\boldsymbol{\beta},\sigma^2 \propto (\sigma^2)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^{n}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta})^2\right\},$$

$$\boldsymbol{\alpha} \sim \mathrm{N}_q(\mathbf{0},\ \boldsymbol{\Sigma_{\alpha 0}}),$$

$$\boldsymbol{\theta} \sim \mathrm{N}_k(\mathbf{0},\ \boldsymbol{\Sigma_{\theta 0}}),$$

$$\boldsymbol{\beta_j}|\phi_j,\sigma^2,s_j \overset{ind}{\sim} \phi_j\,\mathrm{N}_L\left(\mathbf{0},\ \sigma^2 s_j \mathbf{I}_L\right) + (1-\phi_j)\delta_0(\boldsymbol{\beta_j}), \quad j=1,\dots,p,$$

$$\phi_j|\pi_0 \overset{ind}{\sim} \mathrm{Bernoulli}(\pi_0), \quad j=1,\dots,p,$$

$$\pi_0 \sim \mathrm{Beta}\left(a_0,\ b_0\right),$$

$$s_j|\eta \overset{ind}{\sim} \mathrm{Gamma}\left(\frac{L+1}{2}, \frac{\eta}{2}\right), \quad j=1,\dots,p,$$

$$\eta \sim \mathrm{Gamma}\left(d_1,\ d_2\right),$$

$$\sigma^2 \sim 1/\sigma^2.$$

1.10.2 Gibbs Sampler

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\beta_j}|\text{rest} \sim l_j \mathrm{N}(\mu_{\beta_j},\, \sigma^2 \Sigma_{\beta_j}) + (1-l_j)\delta_0(\boldsymbol{\beta_j})$ where

$$\boldsymbol{\mu_{\beta_j}} = \boldsymbol{\Sigma_{\beta_j}} \sum_{i=1}^{n} \boldsymbol{U_{ij}} \widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{\beta_j}} = \left(\sum_{i=1}^{n} \boldsymbol{U_{ij}} \boldsymbol{U_{ij}}^\top + \frac{1}{s_j} \mathbf{I}_L \right)^{-1},$$

$$l_j = \frac{\pi_0}{\pi_0 + (1-\pi_0) s_j^{\frac{L}{2}} |\boldsymbol{\Sigma_{\beta_j}}|^{-\frac{1}{2}} \exp\left\{ -\frac{1}{2\sigma^2} \|\boldsymbol{\Sigma}_{\boldsymbol{\beta_j}}^{\frac{1}{2}} \sum_{i=1}^{n} \boldsymbol{U_{ij}} \widetilde{y}_{ij}\|_2^2 \right\}}.$$

  and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U}_{\boldsymbol{(j)}}^\top \boldsymbol{\beta_{(j)}}$.

- The posterior of s_j is

$$s_j^{-1}|\text{rest} \sim \begin{cases} \text{Inverse-Gamma}(\frac{L+1}{2},\ \frac{\eta}{2}), & \text{if } \boldsymbol{\beta_j} = \mathbf{0}, \\ \text{Inverse-Gaussian}(\eta,\ \sqrt{\frac{\eta\sigma^2}{\|\boldsymbol{\beta_j}\|_2^2}}), & \text{if } \boldsymbol{\beta_j} \neq \mathbf{0}. \end{cases}$$

- $\pi_0|\text{rest} \sim \text{Beta}\left(a_0 + \sum_{j=1}^{p} \mathbf{I}_{\{\boldsymbol{\beta_j} \neq \mathbf{0}\}},\ b_0 + \sum_{j=1}^{p} \mathbf{I}_{\{\boldsymbol{\beta_j} = \mathbf{0}\}} \right)$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\, r_\eta)$, where $s_\eta = \frac{p + p\times L}{2} + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j=1}^{p} s_j}{2} + d_2$.

- $\sigma^2|\text{rest} \sim \text{Inv-Gamma}(\frac{n + L\sum_{j=1}^{p} \mathbf{I}_{\{\boldsymbol{\beta_j} \neq \mathbf{0}\}}}{2},\ \frac{\sum_{i=1}^{n} \widetilde{y}_i{}^2 + \sum_{j=1}^{p} (s_j)^{-1} \boldsymbol{\beta_j}^\top \boldsymbol{\beta_j}}{2})$, where $\widetilde{y}_i = Y_i - \boldsymbol{W_i}^\top \boldsymbol{\alpha} - \boldsymbol{E_i}^\top \boldsymbol{\theta} - \boldsymbol{U_i}^\top \boldsymbol{\beta}$.

1.11 Posterior inference of BL-SS

1.11.1 Hierarchical model specification

$$\boldsymbol{Y}|\boldsymbol{\alpha},\boldsymbol{\theta},\boldsymbol{\beta},\sigma^2 \propto (\sigma^2)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^{n}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta})^2\right\},$$

$$\boldsymbol{\alpha} \sim \mathrm{N}_q(\boldsymbol{0},\ \boldsymbol{\Sigma_{\alpha 0}}),$$

$$\boldsymbol{\theta} \sim \mathrm{N}_k(\boldsymbol{0},\ \boldsymbol{\Sigma_{\theta 0}}),$$

$$\beta_{jl}|\phi_{jl},\sigma^2,s_{jl} \overset{ind}{\sim} \phi_{jl}\,\mathrm{N}\left(0,\ \sigma^2 s_{jl}\right) + (1-\phi_{jl})\delta_0(\beta_{jl}), \quad j=1,\ldots,p;\ l=1,\ldots,L,$$

$$\phi_{jl}|\pi_1 \overset{ind}{\sim} \mathrm{Bernoulli}(\pi_1), \quad j=1,\ldots,p;\ l=1,\ldots,L,$$

$$s_{jl}|\eta \overset{ind}{\sim} \mathrm{Gamma}\left(1,\frac{\eta}{2}\right), \quad j=1,\ldots,p;\ l=1,\ldots,L,$$

$$\pi_1 \sim \mathrm{Beta}\left(a_1,\ b_1\right),$$

$$\eta \sim \mathrm{Gamma}\left(d_1,\ d_2\right),$$

$$\sigma^2 \sim 1/\sigma^2.$$

1.11.2 Gibbs Sampler

- $\boldsymbol{\alpha}|\mathrm{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\theta}|\mathrm{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}}\right)^{-1}.$$

- $\beta_{jl}|\text{rest} \sim l_{jl}\text{N}(\mu_{\beta_{jl}},\, \sigma^2_{\beta_{jl}}) + (1-l_{jl})\delta_0(\beta_{jl})$ where

$$\mu_{\beta_{jl}} = \sigma^2_{\beta_{jl}}(\sigma^2)^{-1}\sum_{i=1}^{n} U_{ijl}\widetilde{y}_{ijl},$$

$$\sigma^2_{\beta_{jl}} = \sigma^2\left(\sum_{i=1}^{n} U^2_{ijl} + \frac{1}{s_{jl}}\right)^{-1},$$

$$l_{jl} = \frac{\pi_0}{\pi_0 + (1-\pi_0)s_{jl}^{\frac{1}{2}}(\sigma^2_{\beta_{jl}})^{-\frac{1}{2}}(\sigma^2)^{-\frac{1}{2}}\exp\left\{-\frac{\sigma^2_{\beta_{jl}}}{2\sigma^4}\left(\sum_{i=1}^{n} U_{ijl}\widetilde{y}_{ijl}\right)^2\right\}}.$$

and $\widetilde{y}_{ijl}$ is defined as $\widetilde{y}_{ijl} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U}^\top_{\boldsymbol{(jl)}}\boldsymbol{\beta_{(jl)}}$.

- The posterior of s_{jl} is

$$s_{jl}^{-1}|\text{rest} \sim \begin{cases}\text{Inverse-Gamma}(1,\ \frac{\eta}{2}), & \text{if } \beta_{jl} = 0,\\ \text{Inverse-Gaussian}(\eta,\ \sqrt{\frac{\eta\sigma^2}{\beta^2_{jl}}}), & \text{if } \beta_{jl} \neq 0.\end{cases}$$

- $\pi_1|\text{rest} \sim \text{Beta}\left(a_1 + \sum_{j,l}\mathbf{I}_{\{\beta_{jl}\neq 0\}},\ b_1 + \sum_{j,l}\mathbf{I}_{\{\beta_{jl}=0\}}\right)$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\, r_\eta)$, where $s_\eta = p\times L + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j,l} s_{jl}}{2} + d_2$.

- $\sigma^2|\text{rest} \sim \text{Inv-Gamma}(\frac{n+\sum_{j,l}\mathbf{I}_{\{\beta_{jl}\neq 0\}}}{2},\ \frac{\sum_{i=1}^{n}\widetilde{y_i}^2 + \sum_{j,l}(s_{jl}^{-1})\beta^2_{jl}}{2})$, where $\widetilde{y_i} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}$.

1.12 Posterior inference of BSG

1.12.1 Hierarchical model specification

$$\boldsymbol{Y}|\boldsymbol{\alpha},\boldsymbol{\theta},\boldsymbol{\beta},\sigma^2 \propto (\sigma^2)^{-\frac{n}{2}}\exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^{n}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta})^2\right\},$$

$$\boldsymbol{\alpha} \sim \text{N}_q(\mathbf{0},\ \boldsymbol{\Sigma_{\alpha 0}}),$$

$$\boldsymbol{\theta} \sim \text{N}_k(\mathbf{0},\ \boldsymbol{\Sigma_{\theta 0}}),$$

$$\boldsymbol{\beta_j}|\omega_{jl}, r_j \overset{ind}{\sim} \text{N}_L(0,\ \sigma^2\boldsymbol{V_j}),\ \text{where } \boldsymbol{V_j} = \text{diag}\left\{(\frac{1}{r_j} + \frac{1}{\omega_{jl}})^{-1},\ l = 1,2,\ldots,L\right\}$$

$$r_j, \omega_{j1},\ldots,\omega_{jL}|\eta_1,\eta_2 \propto \prod_{l=1}^{L}\left[(\omega_{jl})^{-\frac{1}{2}}\left(\frac{1}{r_j} + \frac{1}{\omega_{jl}}\right)^{-\frac{1}{2}}\right](r_j)^{-\frac{1}{2}}\exp\left(-\frac{\eta_1}{2}r_j - \frac{\eta_2}{2}\sum_{l=1}^{L}\omega_{jl}\right),$$

$$\eta_1,\eta_2 \propto \eta_1^{\frac{p}{2}}\eta_2^{pL}\exp\left\{-d_1\eta_1 - d_2\eta_2\right\},$$

$$\sigma^2 \sim 1/\sigma^2.$$

1.12.2 Gibbs Sampler

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha}, \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta}, \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\beta_j}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_{\beta_j}}, \boldsymbol{\Sigma_{\beta_j}})$ where

$$\boldsymbol{\mu_{\beta_j}} = \boldsymbol{\Sigma_{\beta_j}}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{U_{ij}}\widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{\beta_j}} = \sigma^2\left(\sum_{i=1}^{n}\boldsymbol{U_{ij}}\boldsymbol{U_{ij}^\top} + \boldsymbol{V_j^{-1}}\right)^{-1}.$$

  and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_{(j)}^\top}\boldsymbol{\beta_{(j)}}$.

- $r_j^{-1}|\text{rest} \sim \text{Inv-Gaussian}(\eta_1, \sqrt{\frac{\eta_1\sigma^2}{\|\boldsymbol{\beta_j}\|_2^2}})$.

- $\omega_{jl}^{-1}|\text{rest} \sim \text{Inv-Gaussian}(\eta_2, \sqrt{\frac{\eta_2\sigma^2}{\beta_{jl}^2}})$.

- $\eta_1|\text{rest} \sim \text{Gamma}\,(s_{\eta_1}, r_{\eta_1})$, where $s_{\eta_1} = \frac{p}{2}+1$ and the rate parameter $r_{\eta_1} = \frac{\sum_{j=1}^{p} r_j}{2}+d_1$.

- $\eta_2|\text{rest} \sim \text{Gamma}\,(s_{\eta_2}, r_{\eta_2})$, where $s_{\eta_2} = p \times L + 1$ and the rate parameter $r_{\eta_2} = \frac{\sum_{j,l}\omega_j}{2} + d_2$.

- $\sigma^2|\text{rest} \sim \text{Inv-Gamma}(\frac{n+p\times L}{2}, \frac{\sum_{i=1}^{n}\widetilde{y_i}^2+\sum_{j=1}^{p}\boldsymbol{\beta_j^\top}\boldsymbol{V_j}^{-1}\boldsymbol{\beta_j}}{2})$, where $\widetilde{y_i} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}$.

1.13 Posterior inference of BGL

1.13.1 Hierarchical model specification

$$\boldsymbol{Y}|\boldsymbol{\alpha},\boldsymbol{\theta},\boldsymbol{\beta},\sigma^2 \propto (\sigma^2)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^{n}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta})^2\right\},$$

$$\boldsymbol{\alpha} \sim \mathrm{N}_q(\boldsymbol{0},\ \boldsymbol{\Sigma_{\alpha 0}}),$$

$$\boldsymbol{\theta} \sim \mathrm{N}_k(\boldsymbol{0},\ \boldsymbol{\Sigma_{\theta 0}}),$$

$$\boldsymbol{\beta_j}|\sigma^2, s_j \overset{ind}{\sim} \mathrm{N}_L\left(\boldsymbol{0},\ \sigma^2 s_j \mathbf{I}_L\right), \quad j = 1,\ldots,p,$$

$$s_j|\eta \overset{ind}{\sim} \mathrm{Gamma}\left(\frac{L+1}{2}, \frac{\eta}{2}\right), \quad j = 1,\ldots,p,$$

$$\eta \sim \mathrm{Gamma}\left(d_1,\ d_2\right),$$

$$\sigma^2 \sim 1/\sigma^2.$$

1.13.2 Gibbs Sampler

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\alpha} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}(\sigma^2)^{-1}\sum_{i=1}^{n}\boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),$$

$$\boldsymbol{\Sigma_\theta} = \left(\frac{1}{\sigma^2}\sum_{i=1}^{n}\boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}}\right)^{-1}.$$

- $\boldsymbol{\beta_j}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_{\beta_j}},\ \sigma^2\boldsymbol{\Sigma_{\beta_j}})$ where

$$\boldsymbol{\mu_{\beta_j}} = \boldsymbol{\Sigma_{\beta_j}}\sum_{i=1}^{n}\boldsymbol{U_{ij}}\widetilde{y}_{ij},$$

$$\boldsymbol{\Sigma_{\beta_j}} = \left(\sum_{i=1}^{n}\boldsymbol{U_{ij}}\boldsymbol{U_{ij}}^\top + \frac{1}{s_j}\mathbf{I}_L\right)^{-1}$$

  and $\widetilde{y}_{ij}$ is defined as $\widetilde{y}_{ij} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_{(j)}}^\top\boldsymbol{\beta_{(j)}}$.

- $s_j^{-1}|\text{rest} \sim \text{Inverse-Gaussian}(\eta,\ \sqrt{\frac{\eta\sigma^2}{\|\boldsymbol{\beta_j}\|_2^2}})$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\ r_\eta)$, where $s_\eta = \frac{p+p\times L}{2} + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j=1}^p s_j}{2} + d_2$.

- $\sigma^2|\text{rest} \sim \text{Inv-Gamma}(\frac{n+p\times L}{2},\ \frac{\sum_{i=1}^n \widetilde{y_i}^2 + \sum_{j=1}^p (s_j)^{-1}\boldsymbol{\beta_j}^\top\boldsymbol{\beta_j}}{2})$, where $\widetilde{y_i} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}$.

1.14 Posterior inference of BL

1.14.1 Hierarchical model specification

$$
\begin{gathered}
\boldsymbol{Y}|\boldsymbol{\alpha},\boldsymbol{\theta},\boldsymbol{\beta},\sigma^2 \propto (\sigma^2)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^n (Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta})^2\right\}, \\
\boldsymbol{\alpha} \sim \mathrm{N}_q(\mathbf{0},\ \boldsymbol{\Sigma_{\alpha 0}}), \\
\boldsymbol{\theta} \sim \mathrm{N}_k(\mathbf{0},\ \boldsymbol{\Sigma_{\theta 0}}), \\
\beta_{jl}|\sigma^2, s_{jl} \overset{ind}{\sim} \mathrm{N}\left(0,\ \sigma^2 s_{jl}\right), \quad j = 1,\dots,p;\ l = 1,\dots,L, \\
s_{jl}|\eta \overset{ind}{\sim} \text{Gamma}\left(1, \frac{\eta}{2}\right), \quad j = 1,\dots,p;\ l = 1,\dots,L, \\
\eta \sim \text{Gamma}\,(d_1,\ d_2)\,, \\
\sigma^2 \sim 1/\sigma^2.
\end{gathered}
$$

1.14.2 Gibbs Sampler

- $\boldsymbol{\alpha}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\alpha},\ \boldsymbol{\Sigma_\alpha})$, where

$$
\boldsymbol{\mu_\alpha} = \boldsymbol{\Sigma_\alpha}(\sigma^2)^{-1}\sum_{i=1}^n \boldsymbol{W_i}(Y_i - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),
$$

$$
\boldsymbol{\Sigma_\alpha} = \left(\frac{1}{\sigma^2}\sum_{i=1}^n \boldsymbol{W_i}\boldsymbol{W_i}^\top + \boldsymbol{\Sigma_{\alpha 0}^{-1}}\right)^{-1}.
$$

- $\boldsymbol{\theta}|\text{rest} \sim \mathrm{N}(\boldsymbol{\mu_\theta},\ \boldsymbol{\Sigma_\theta})$, where

$$
\boldsymbol{\mu_\theta} = \boldsymbol{\Sigma_\theta}(\sigma^2)^{-1}\sum_{i=1}^n \boldsymbol{E_i}(Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{U_i}^\top\boldsymbol{\beta}),
$$

$$
\boldsymbol{\Sigma_\theta} = \left(\frac{1}{\sigma^2}\sum_{i=1}^n \boldsymbol{E_i}\boldsymbol{E_i}^\top + \boldsymbol{\Sigma_{\theta 0}^{-1}}\right)^{-1}.
$$

- $\beta_{jl}|\text{rest} \sim \mathrm{N}(\mu_{\beta_{jl}},\, \sigma^2_{\beta_{jl}})$ where

$$\mu_{\beta_{jl}} = \sigma^2_{\beta_{jl}}(\sigma^2)^{-1}\sum_{i=1}^{n} U_{ijl}\widetilde{y}_{ijl},$$

$$\sigma^2_{\beta_{jl}} = \sigma^2\left(\sum_{i=1}^{n} U^2_{ijl} + \frac{1}{s_{jl}}\right)^{-1}.$$

  and $\widetilde{y}_{ijl}$ is defined as $\widetilde{y}_{ijl} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U}^\top_{\boldsymbol{(jl)}}\boldsymbol{\beta}_{\boldsymbol{(jl)}}$.

- $s_j^{-1}|\text{rest} \sim \text{Inverse-Gaussian}(\eta,\, \sqrt{\frac{\eta\sigma^2}{\beta^2_{jl}}})$.

- $\eta|\text{rest} \sim \text{Gamma}\,(s_\eta,\, r_\eta)$, where $s_\eta = p\times L + d_1$ and the rate parameter $r_\eta = \frac{\sum_{j,l} s_{jl}}{2} + d_2$.

- $\sigma^2|\text{rest} \sim \text{Inv-Gamma}(\frac{n+p\times L}{2},\, \frac{\sum_{i=1}^{n}\widetilde{y_i}^2 + \sum_{j,l} s_{jl}^{-1}\beta^2_{jl}}{2})$, where $\widetilde{y_i} = Y_i - \boldsymbol{W_i}^\top\boldsymbol{\alpha} - \boldsymbol{E_i}^\top\boldsymbol{\theta} - \boldsymbol{U_i}^\top\boldsymbol{\beta}$.

2 Web Appendix B

2.1 Simulation results for Examples 2, 3 and 4

Web Table 3: Simulation results in Example 2 for methods with spike–and–slab priors. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
Error 1	TP	24.87(0.35)	25.00(0.00)	24.53(0.51)	24.83(0.38)	25.00(0.00)	24.53(0.51)
N	FP	1.63(1.16)	31.40(3.38)	2.30(1.86)	1.13(1.04)	29.20(1.10)	0.60(0.85)
	Pred	0.85(0.03)	0.86(0.03)	0.86(0.03)	1.09(0.06)	1.13(0.06)	1.10(0.07)
Error 2	TP	22.23(1.76)	24.67(0.76)	19.23(1.72)	19.97(1.63)	24.47(0.90)	15.27(1.91)
L	FP	1.90(1.30)	35.73(7.83)	2.10(1.40)	2.33(1.42)	34.13(7.44)	1.73(1.39)
	Pred	2.24(0.14)	2.18(0.11)	2.38(0.16)	10.21(1.27)	9.13(0.94)	11.30(1.83)
Error 3	TP	21.50(1.48)	25.00(0.00)	17.43(2.13)	18.73(2.02)	25.00(0.00)	13.10(1.54)
Mix.L	FP	2.13(1.14)	35.20(6.77)	1.90(1.37)	2.90(1.71)	34.00(6.88)	1.37(0.96)
	Pred	2.39(0.18)	2.29(0.11)	2.52(0.22)	12.46(1.67)	10.40(0.94)	13.04(1.35)
Error 4	TP	23.58(1.49)	25.00(0.00)	21.04(2.29)	15.94(5.34)	23.18(3.50)	12.08(4.60)
t2	FP	0.80(0.93)	30.32(3.27)	0.78(1.07)	7.46(27.02)	53.50(58.05)	3.56(8.91)
	Pred	1.85(0.16)	1.82(0.13)	1.92(0.17)	25.65(55.13)	25.63(67.60)	30.67(87.77)
Error 5	TP	24.12(1.00)	25.00(0.00)	21.82(1.90)	18.04(3.64)	24.24(1.88)	13.12(2.99)
logNor	FP	0.90(1.02)	29.48(1.64)	0.82(0.90)	2.72(1.75)	36.12(12.21)	1.48(1.25)
	Pred	1.81(0.13)	1.82(0.12)	1.89(0.15)	14.85(6.53)	12.87(5.94)	15.19(6.43)

Web Table 4: Simulation results in Example 2 for methods without spike–and–slab priors. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP) and prediction errors (Pred) based on 100 replicates.

		RBSG	RBG	RBL	BSG	BG	BL
Error 1	TP	24.20(0.61)	25.00(0.00)	24.23(0.57)	24.33(0.61)	25.00(0.00)	24.30(0.60)
N	FP	2.93(1.86)	54.80(17.34)	3.30(1.97)	1.87(1.61)	56.20(10.30)	5.77(2.56)
	Pred	1.14(0.05)	1.32(0.06)	1.15(0.05)	1.74(0.12)	2.13(0.14)	2.01(0.15)
Error 2	TP	14.00(2.27)	22.20(2.33)	13.63(2.66)	13.70(2.29)	23.63(1.61)	14.20(1.97)
L	FP	0.60(0.85)	31.40(12.07)	0.83(1.05)	1.33(1.18)	62.77(24.90)	8.80(4.54)
	Pred	2.57(0.13)	2.77(0.14)	2.58(0.14)	12.18(1.15)	14.42(1.40)	14.91(1.43)
Error 3	TP	12.40(2.03)	22.47(1.17)	12.27(1.87)	12.43(1.77)	23.20(1.49)	13.37(2.13)
Mix.L	FP	0.57(0.77)	29.33(5.54)	0.60(0.93)	1.47(1.31)	59.80(13.17)	8.17(3.04)
	Pred	2.69(0.11)	2.86(0.11)	2.69(0.10)	13.59(1.05)	16.32(1.46)	16.93(1.60)
Error 4	TP	15.98(2.92)	23.04(2.78)	16.10(3.12)	10.20(5.31)	20.52(5.81)	11.08(5.00)
t2	FP	0.26(0.53)	27.36(6.21)	0.30(0.65)	2.34(3.56)	65.04(30.70)	9.38(6.26)
	Pred	2.19(0.16)	2.35(0.16)	2.21(0.17)	26.27(53.26)	34.08(78.47)	34.95(79.04)
Error 5	TP	16.48(2.69)	23.48(1.58)	16.30(2.63)	11.96(3.66)	22.26(3.70)	12.70(3.50)
logNor	FP	0.32(0.59)	28.72(5.89)	0.34(0.59)	1.40(1.21)	62.34(20.52)	8.34(3.77)
	Pred	2.20(0.14)	2.41(0.14)	2.20(0.13)	15.79(5.97)	18.90(6.61)	19.53(6.65)

Web Table 5: Simulation results in Example 3 for methods with spike–and–slab priors. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
Error 1	TP	24.00(0.91)	25.00(0.00)	22.13(1.57)	24.33(0.66)	25.00(0.00)	22.83(1.37)
N	FP	1.85(1.46)	33.40(5.21)	1.87(1.36)	1.27(1.34)	29.60(1.83)	0.77(1.04)
	Pred	0.86(0.03)	0.86(0.03)	0.89(0.03)	1.11(0.07)	1.13(0.07)	1.17(0.10)
Error 2	TP	17.63(2.37)	24.73(0.69)	14.37(2.54)	15.00(2.32)	23.73(1.46)	11.00(1.95)
L	FP	2.50(1.41)	33.27(5.14)	2.67(1.99)	2.60(1.43)	30.67(6.69)	1.87(1.53)
	Pred	2.33(0.12)	2.15(0.10)	2.40(0.17)	10.37(1.01)	9.01(0.81)	10.71(0.94)
Error 3	TP	17.23(1.77)	24.80(0.61)	14.47(2.21)	15.10(2.29)	23.67(1.77)	11.03(1.38)
Mix.L	FP	2.27(1.78)	32.20(6.94)	1.63(1.43)	2.13(1.70)	30.93(5.48)	1.17(1.34)
	Pred	2.39(0.13)	2.24(0.10)	2.45(0.13)	11.98(1.45)	10.32(1.04)	12.37(1.41)
Error 4	TP	23.63(1.19)	24.67(0.92)	20.13(2.19)	15.07(4.69)	22.67(3.68)	11.40(4.01)
t2	FP	1.30(1.12)	29.13(2.67)	1.17(0.95)	3.37(1.88)	29.93(9.48)	2.37(1.97)
	Pred	1.48(0.13)	1.45(0.11)	1.55(0.14)	12.66(12.40)	10.10(8.77)	12.75(11.83)
Error 5	TP	24.80(0.48)	25.00(0.00)	23.57(1.43)	20.30(2.83)	24.87(0.51)	15.87(2.32)
logNor	FP	0.33(0.55)	29.60(1.83)	0.40(1.04)	3.00(1.66)	32.93(5.86)	2.33(1.63)
	Pred	1.19(0.10)	1.21(0.10)	1.21(0.11)	6.055(1.77)	5.47(1.73)	6.54(1.75)

Web Table 6: Simulation results in Example 3 for methods without spike–and–slab priors. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP) and prediction errors (Pred) based on 100 replicates.

		RBSG	RBG	RBL	BSG	BG	BL
Error 1	TP	21.27(1.17)	25.00(0.00)	21.30(1.06)	22.23(0.94)	25.00(0.00)	22.13(1.28)
N	FP	1.97(1.56)	45.40(11.68)	2.03(1.56)	1.23(1.33)	43.60(10.41)	3.37(2.03)
	Pred	1.08(0.04)	1.21(0.05)	1.07(0.04)	1.57(0.12)	1.87(0.13)	1.79(0.13)
Error 2	TP	8.40(1.87)	18.67(2.68)	8.27(2.02)	8.07(1.57)	20.73(2.65)	8.73(2.15)
L	FP	0.43(0.63)	20.73(4.93)	0.57(0.77)	0.67(0.66)	36.27(11.59)	3.83(2.05)
	Pred	2.44(0.13)	2.58(0.13)	2.44(0.12)	10.97(1.05)	12.78(1.31)	13.02(1.33)
Error 3	TP	8.43(2.18)	16.70(3.29)	8.70(2.00)	7.97(2.04)	18.60(3.07)	8.27(1.78)
Mix.L	FP	0.33(0.71)	17.70(4.60)	0.43(0.73)	0.60(0.72)	33.60(10.63)	3.70(2.34)
	Pred	2.54(0.11)	2.69(0.12)	2.55(0.11)	12.33(1.15)	14.30(1.40)	14.55(1.40)
Error 4	TP	13.77(2.18)	21.20(2.06)	13.67(2.04)	9.67(3.74)	20.60(4.79)	9.77(3.76)
t2	FP	0.43(0.63)	22.80(3.98)	0.57(0.63)	1.03(1.13)	38.00(12.21)	4.47(2.50)
	Pred	1.73(0.12)	1.85(0.13)	1.73(0.13)	11.78(9.05)	13.94(11.84)	14.22(12.41)
Error 5	TP	19.10(1.86)	24.87(0.73)	19.10(1.60)	15.27(2.94)	24.07(1.70)	15.07(2.88)
logNor	FP	0.20(0.48)	31.13(5.96)	0.23(0.57)	1.10(1.16)	43.93(11.82)	3.83(2.21)
	Pred	1.45(0.08)	1.61(0.09)	1.46(0.08)	6.13(1.13)	7.19(1.24)	7.16(1.29)

Web Table 7: Simulation results in Example 4 for methods with spike–and–slab priors. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP) and prediction errors (Pred) based on 100 replicates.

		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
Error 1	TP	24.93(0.37)	25.00(0.00)	24.93(0.25)	25.00(0.00)	25.00(0.00)	24.90(0.31)
N	FP	1.33(0.99)	30.60(3.84)	1.47(1.25)	1.00(1.02)	29.20(1.10)	0.33(0.61)
	Pred	0.84(0.02)	0.88(0.02)	0.85(0.03)	1.10(0.04)	1.20(0.06)	1.11(0.05)
Error 2	TP	20.80(2.65)	23.60(1.47)	17.24(2.96)	18.58(3.46)	23.04(1.64)	14.08(3.26)
L	FP	1.32(1.22)	30.76(4.93)	1.66(1.29)	1.98(1.53)	27.72(5.49)	1.42(1.25)
	Pred	2.25(0.11)	2.22(0.08)	2.37(0.12)	10.32(1.25)	9.53(0.75)	11.43(1.20)
Error 3	TP	20.56(2.73)	23.69(1.38)	16.53(3.20)	17.56(3.49)	22.80(1.65)	12.67(3.39)
Mix.L	FP	1.40(1.30)	30.04(5.46)	1.78(1.82)	1.76(1.28)	27.60(5.24)	1.22(1.43)
	Pred	2.38(0.13)	2.35(0.10)	2.51(0.16)	12.04(1.40)	11.12(0.96)	13.32(1.44)
Error 4	TP	24.60(0.93)	24.67(0.92)	23.77(1.57)	20.10(6.38)	22.27(5.10)	15.63(6.69)
t2	FP	0.40(0.56)	29.13(2.97)	0.47(0.73)	1.83(1.90)	28.13(9.22)	1.17(1.15)
	Pred	1.48(0.09)	1.52(0.09)	1.51(0.11)	11.54(6.94)	11.33(6.95)	12.64(6.74)
Error 5	TP	23.16(1.68)	24.96(0.28)	19.60(2.14)	15.64(3.76)	23.44(1.83)	11.60(2.75)
logNor	FP	1.08(1.16)	29.16(1.33)	0.72(0.83)	2.20(1.83)	30.56(7.43)	1.48(1.43)
	Pred	1.56(0.14)	1.53(0.13)	1.63(0.15)	10.98(5.80)	9.45(5.38)	11.38(6.03)

Web Table 8: Simulation results in Example 4 for methods without spike–and–slab priors. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP) and prediction errors (Pred) based on 100 replicates.

		RBSG	RBG	RBL	BSG	BG	BL
Error 1	TP	21.47(1.87)	24.40(1.07)	21.67(1.81)	22.70(1.64)	24.87(0.51)	22.53(1.85)
N	FP	3.17(2.51)	56.00(20.03)	3.33(2.59)	2.30(1.66)	66.33(14.04)	6.57(2.62)
	Pred	1.26(0.06)	1.44(0.07)	1.27(0.06)	2.40(0.27)	2.83(0.24)	2.75(0.30)
Error 2	TP	9.08(2.54)	19.38(3.12)	9.20(2.60)	9.68(2.41)	20.82(2.93)	10.80(2.65)
L	FP	0.78(0.86)	30.30(10.26)	0.84(0.89)	2.18(1.48)	65.94(19.60)	8.62(3.38)
	Pred	2.67(0.08)	2.89(0.09)	2.67(0.09)	13.54(0.87)	16.38(1.19)	16.87(1.27)
Error 3	TP	8.51(2.31)	18.71(3.37)	8.62(2.33)	9.02(2.33)	20.60(2.76)	10.58(2.50)
Mix.L	FP	0.56(0.69)	25.29(7.94)	0.56(0.66)	1.87(1.36)	56.87(15.55)	7.38(2.91)
	Pred	2.79(0.11)	3.00(0.12)	2.79(0.12)	15.34(1.29)	18.66(1.69)	19.30(1.88)
Error 4	TP	13.30(3.32)	21.93(2.72)	13.47(3.33)	10.93(4.30)	20.97(4.76)	11.97(4.43)
t2	FP	0.50(0.57)	29.07(9.28)	0.40(0.50)	1.70(1.39)	60.03(20.56)	7.90(3.92)
	Pred	2.03(0.12)	2.22(0.12)	2.03(0.12)	15.20(7.98)	18.61(12.19)	19.41(13.39)
Error 5	TP	14.38(2.64)	22.36(2.22)	14.40(2.70)	10.12(3.53)	20.84(3.74)	10.56(3.39)
logNor	FP	0.30(0.58)	25.16(4.36)	0.22(0.46)	0.88(1.12)	36.52(12.60)	3.70(2.57)
	Pred	1.84(0.15)	1.99(0.17)	1.84(0.15)	11.23(5.54)	13.02(5.80)	13.18(5.90)

2.2 Hyper-parameters sensitivity analysis

We demonstrate the sensitivity of RBSG-SS for variable selection to the choice of the hyper-parameters for π_0 and π_1. We consider five different Beta priors: (1) Beta(0.5, 0.5) which is a U-shape curve between $(0, 1)$; (2) Beta(1, 1) which is a essentially a uniform prior; (3) Beta(2, 2) which is a quadratic curve; (4) Beta(1, 5) which is highly right-skewed; (5) Beta(5, 1) which is highly left-skewed. As a demonstrating example, we use the same setting of Example 1 to generate data under Error 2. Web Table 9 shows the identification performance of the median thresholding model (MPM) with different Beta priors. For all choices of Beta priors, the MPM model is very stable. Also, RBSG-SS correctly identifies most of the true effects with low false positives in all cases. Therefore, we simply use Beta$(1, 1)$ as the prior for π_0, and π_1 in this study.

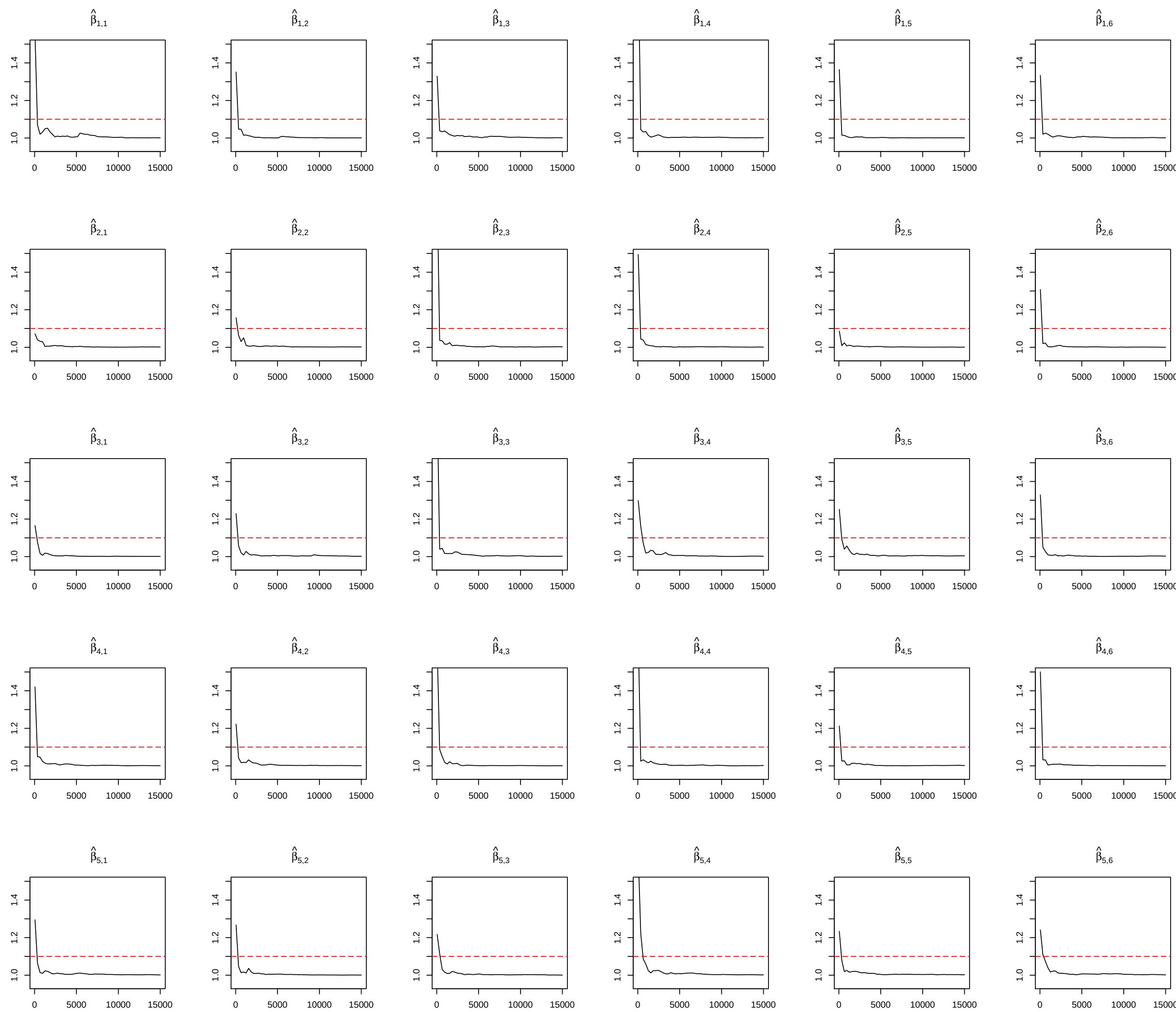
In addition, we evaluate the sensitivity of RBSG-SS to the choice of the Gamma hyperprior on ν. We test the shape parameter of the Gamma prior for five different values: $\{0.1, 0.5, 1, 2, 5\}$, ranging from highly skewed exponential shape to highly diffuse unimodal shape. The rate parameter is fixed at $\{1, 2, 5\}$. We test different combinations of shape and rate parameters on a two-dimensional grid. In Web Table 9, we show the simulation results of some representative cases under the scenarios of Example 1. RBSG-SS model has stable performance with high TP and low FP for different Gamma priors. Similar patterns are observed for all other cases. In this study, we use Gamma(1, 1) for ν under all scenarios.

Web Table 9: Sensitivity analysis for RBSG-SS under Example 1 for Beta hyperprior (upper panel) and Gamma hyperprior (lower panel). mean(sd) of true positives (TP), false positives (FP) and prediction errors (Pred) based on 100 replicates.

	TP	FP	Pred
Beta(0.5, 0.5)	21.31(1.67)	1.71(1.50)	2.19(0.11)
Beta(1, 1)	21.66(1.72)	1.32(1.33)	2.17(0.10)
Beta(2, 2)	21.13(2.10)	1.47(1.16)	2.18(0.10)
Beta(1, 5)	20.82(1.71)	1.38(1.30)	2.17(0.10)
Beta(5, 1)	21.58(1.75)	2.22(1.52)	2.19(0.09)
	TP	FP	Pred
Gamma(0.1, 1)	20.95(2.06)	1.38(1.19)	2.19(0.12)
Gamma(0.5, 2)	20.93(1.95)	1.70(1.30)	2.19(0.10)
Gamma(1, 1)	21.66(1.72)	1.32(1.33)	2.17(0.10)
Gamma(1, 5)	20.91(2.10)	1.52(1.40)	2.18(0.12)
Gamma(2, 5)	20.81(1.88)	1.48(1.30)	2.18(0.10)
Gamma(5, 1)	20.89(2.06)	1.78(1.40)	2.18(0.10)

2.3 Assessment of the convergence of MCMC chains

Following Li et al. Li et al. (2015), we assess the convergence of the MCMC chains by the potential scale reduction factor (PSRF).Brooks and Gelman (1998); Gelman and Rubin (1992) PSRF values close to 1 indicate that chains converge to the stationary distribution. Gelman et al. Gelman et al. (2004) recommend using PSRF$\leq$ 1.1 as the cutoff for convergence, which has been adopted in our study. We compute the PSRF for each parameter and find all chains converge after the burn-ins. For the purpose of demonstration, Web Figure 2 shows the pattern of PSRF of the first five groups of coefficients in Example 1 under Error 2. The figure clearly shows the convergence of the proposed Gibbs sampler.



Web Figure 2: Potential scale reduction factor (PSRF) against iterations for the first five groups of coefficients in Example 1. Black line: the PSRF. Red line: the threshold of 1.1. The $\widehat{\beta}_{j1}$ to $\widehat{\beta}_{j6}$ represent the six estimated coefficients for the main and interaction effects in the jth group, $(j = 0, \ldots, 5)$, respectively.

2.4 Computational cost

We examine the computational cost of the proposed and alternative methods. As a demonstrating example, Web Table 10 shows the CPU time of different methods for finishing 15,000 MCMC iterations under the setting of Example 1.

	Time (seconds)		Time (seconds)
RBSG-SS	64.29	BSG-SS	55.35
RBG-SS	44.94	BG-SS	55.08
RBL-SS	28.79	BL-SS	29.26
RBSG	40.14	BSG	36.01
RBG	19.33	BG	35.15
RBL	10.50	BL	11.18

Web Table 10: Computational cost analysis under the setting of Example 1. time: CPU time (in seconds) for 15,000 MCMC iterations.

2.5 Estimation results for data analysis

Web Table 11: Analysis of the NHS T2D data using RBSG-SS.

SNP	Gene		chol	act	gl	ceraf	alcohol
			3.503	-3.447	0.752	-3.364	-2.639
rs10741150	DOCK1		-0.948				
rs10765059	TCERG1L	-0.531					0.877
rs10786611	RF00019	0.668	0.723		0.530		
rs10884466	RNA5SP326	-0.466		0.643			
rs10885423	NRG3				-0.715		
rs10886442	GRK5		0.805				
rs11196539	NRG3				-0.608		-0.801
rs11198590	CACUL1	-0.494				0.994	-0.687
rs11259039	FRMD4A	1.016					
rs1194657	THAP12P3				0.798		
rs1219508	RPS15AP5	-0.742					
rs12265854	SLC16A12	0.397					
rs12414552	TCERG1L	0.667		0.470	0.585		-0.690
rs12767723	SLC25A18P1	0.820				-0.515	
rs12772559	TACR2				0.938	0.510	
rs12774333	LRMDA	-0.599					
rs12775160	FOXI2	-0.651	-0.501				0.647
rs16916794	SLC39A12	-0.552	0.511	0.455			
rs16920092	PLXDC2						-0.843
rs17094114	GFRA1	-0.615					
rs2492664	OR6L1P	0.695			-0.737		
rs2784767	PLAC9	-0.540					
rs2814322	GRID1				-0.830		
rs3740063	ABCC2				-0.966		
rs3763722	LARP4B	0.332	-1.156				0.866
rs4411238	PRKG1	0.537					
rs4578341	CHST15		-0.822			0.602	
rs4747517	ITIH5		-1.468			0.920	
rs4749926	IL2RA	-0.840	-0.815				
rs4917817	PYROXD2	-0.624		0.594			
rs4918904	XRCC6P1					0.997	
rs6482836	DOCK1	-0.957		1.067			
rs7070789	GPAM				-1.245		-0.791
rs7072255	ANTXRLP1		0.800				
rs7077721	SNRPD2P1	0.858		0.774			
rs7896554	NACAP2	0.840		-0.630	-0.565		
rs7897847	LGI1						0.962
rs870753	CFAP58				-0.783		

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Web Table 11: Continued from the previous page.

SNP	Gene		chol	act	gl	ceraf	alcohol
rs881726	GFRA1						1.001

Web Table 12: Analysis of the NHS T2D data using RBL-SS.

SNP	Gene		chol	act	gl	ceraf	alcohol
			1.354	-0.430	-0.778	-2.424	-4.000
rs1041168	PLPP4	0.463					
rs10741150	DOCK1		-1.126				
rs10786611	RF00019	0.632					
rs10794069	ADAM12	0.524					
rs10824802	MBL2	0.553					
rs10884466	RNA5SP326	-0.439		0.503			
rs10885423	NRG3				-1.060		
rs10886047	MIR3663HG						-0.410
rs10886442	GRK5		1.087				
rs10998780	ATP5MC1P7				0.150		
rs11003665	RNA5SP318		0.632				
rs11013740	KIAA1217						0.852
rs11196539	NRG3						-0.624
rs11198590	CACUL1	-0.628					
rs11202221	BMPR1A				0.815		
rs11259039	FRMD4A	1.021					
rs11595123	AKR1E2			1.079			
rs11813505	KIAA1217					1.301	
rs1194657	THAP12P3				0.663		
rs1219508	RPS15AP5	-0.886					
rs12265854	SLC16A12	0.596					
rs12269237	RF00017					0.884	
rs12414552	TCERG1L	0.594					
rs12414627	PNLIPRP1				-0.551		
rs12767723	SLC25A18P1	0.962					
rs12772559	TACR2				0.906		
rs12774333	LRMDA	-0.449					
rs12775160	FOXI2	-0.560					
rs1573137	SORCS3				0.615		
rs16916794	SLC39A12	-0.803	0.528				
rs16920092	PLXDC2						-0.655
rs17094114	GFRA1	-0.563					
rs2291314	PLPP4	0.536					
rs2420979	TACC2					-1.091	
rs2492664	OR6L1P	0.655			-0.363		

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Web Table 12: Continued from the previous page.

SNP	Gene		chol	act	gl	ceraf	alcohol
rs2664339	RNU6-543P	-0.501					
rs2666236	IATPR					0.689	
rs2784767	PLAC9	-0.452	0.730				
rs2814322	GRID1				-0.806		
rs2842129	DYNC1I2P1	-0.662					
rs2900814	SNRPD2P1	-0.643					
rs3740063	ABCC2				-0.885		
rs3763722	LARP4B						1.036
rs4411238	PRKG1	0.399					
rs4578341	CHST15		-0.582			0.479	
rs4747009	LRRC20						0.710
rs4747517	ITIH5		-0.905				
rs4749926	IL2RA	-0.607					
rs4752432	PLPP4		0.725				
rs4917817	PYROXD2	-0.506					
rs4934762	PCAT5	-0.560					
rs6482836	DOCK1	-0.709					
rs7070789	GPAM				-0.820		
rs7072255	ANTXRLP1		0.811				
rs7077721	SNRPD2P1	0.702					
rs7894809	PCGF5	0.501					
rs7896554	NACAP2	0.850		-0.953			
rs7897847	LGI1						0.929
rs7903853	FRMD4A		-1.185				
rs7920351	TCERG1L			-0.713			
rs881726	GFRA1						0.675
rs943213	DOCK1			-0.939			

Web Table 13: Analysis of the NHS T2D data using BSG-SS.

SNP	Gene		chol	act	gl	ceraf	alcohol
			2.045	-2.049	-2.204	-1.796	-4.436
rs1041168	PLPP4	0.638					
rs10765059	TCERG1L			0.709			
rs10786611	RF00019	0.773	0.556				
rs10829671	EBF3	-0.505					
rs10884466	RNA5SP326	-0.563		0.625			
rs10886442	GRK5		1.038				
rs10998780	ATP5MC1P7				0.704		
rs11017821	TCERG1L						0.665
rs11198590	CACUL1	-0.698			0.905	0.568	

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Web Table 13: Continued from the previous page.

SNP	Gene		chol	act	gl	ceraf	alcohol
rs11200996	CCSER2					0.508	
rs11259039	FRMD4A	1.174					
rs1219508	RPS15AP5	-0.787					
rs12265854	SLC16A12	0.681			-0.494		
rs12269237	RF00017					0.684	
rs12414552	TCERG1L	0.480					
rs12764378	ARID5B	-0.420					
rs12767723	SLC25A18P1	0.638				-0.559	
rs12775160	FOXI2	-0.762					0.893
rs1361709	PCDH15			-0.852			
rs1395465	RN7SL63P	0.292					
rs16916794	SLC39A12	-0.614	0.580	0.622			
rs16920092	PLXDC2						-0.692
rs17094114	GFRA1	-0.676					
rs17469499	KIAA1217					-0.527	
rs2472737	RET	0.629					
rs2577356	GFRA1					0.875	
rs2784767	PLAC9	-0.569	0.537				
rs2792708	GPAM	0.488					
rs2900814	SNRPD2P1	-0.460					
rs2926458	RNU6-463P	-0.680					
rs3763722	LARP4B		-1.251				1.186
rs4411238	PRKG1	0.619					
rs4747517	ITIH5		-1.257				
rs4752432	PLPP4		0.956				
rs4917817	PYROXD2	-0.626		0.630			
rs4922535	GDF10			-0.601		-0.649	
rs4934762	PCAT5	-0.640					
rs4934858	NRP1	0.281					
rs6482836	DOCK1	-0.773					
rs7070789	GPAM				-0.642		
rs7072255	ANTXRLP1		0.723				
rs7085788	RHOBTB1	-0.720					
rs7086058	RN7SKP143	-0.507					
rs716168	VTI1A		-0.570				
rs7894809	PCGF5	0.642					
rs7895870	RN7SKP167		-0.867				
rs7896554	NACAP2	1.097		-0.477			
rs7917422	HTR7						0.794
rs881726	GFRA1						0.933

Web Table 14: Analysis of the NHS T2D data using BL-SS.

SNP	Gene		chol	act	gl	ceraf	alcohol
			3.095	-2.406	-2.373	-1.716	-3.721
rs1041168	PLPP4	0.670					
rs10508670	KIAA1217		0.773				
rs10765059	TCERG1L			0.445			
rs10829671	EBF3	-0.717					
rs10884466	RNA5SP326	-0.528					
rs10998780	ATP5MC1P7				1.195		
rs11017821	TCERG1L						0.307
rs11198590	CACUL1				1.273		
rs11200996	CCSER2					0.509	
rs11202221	BMPR1A				0.954		
rs11259039	FRMD4A	1.020					
rs11594070	ATE1-AS1				-0.401		
rs1194657	THAP12P3				0.681		
rs12248205	CDH23				-0.938		
rs12256982	ZMIZ1				0.152		
rs12265854	SLC16A12	0.661			-0.830		
rs12269237	RF00017					0.864	
rs12412976	RPLP1P10			0.592	-0.590		
rs12414552	TCERG1L	0.549					
rs12414627	PNLIPRP1				-0.572		
rs12764378	ARID5B	-0.564					
rs12767723	SLC25A18P1	1.062					
rs12775160	FOXI2	-0.636					
rs1361709	PCDH15			-0.729			
rs1395465	RN7SL63P	0.562					
rs1573137	SORCS3				0.869		
rs16916794	SLC39A12	-0.430	0.862				
rs16920092	PLXDC2						-0.508
rs17094114	GFRA1	-0.734					
rs17469499	KIAA1217					-0.680	
rs2384105	SNRPEP8						-0.738
rs2420979	TACC2	-0.629					
rs2472737	RET	0.553					
rs2577356	GFRA1					0.739	
rs2784767	PLAC9	-0.593	0.576				
rs2792708	GPAM	0.568					
rs2900814	SNRPD2P1					-0.157	
rs2926458	RNU6-463P	-0.527					
rs3763722	LARP4B		-1.002				1.151
rs4411238	PRKG1	0.461					

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Web Table 14: Continued from the previous page.

SNP	Gene		chol	act	gl	ceraf	alcohol
rs4747009	LRRC20						1.016
rs4747517	ITIH5		-1.695				
rs4752432	PLPP4						0.787
rs4917817	PYROXD2	-0.637		0.751			
rs4934762	PCAT5	-0.771					
rs4934858	NRP1	0.496					
rs6482836	DOCK1	-0.899					
rs7069001	WDFY4		-0.942				
rs7070789	GPAM				-1.154		-0.771
rs7077718	DNMBP	-0.661					
rs7085788	RHOBTB1	-0.721					
rs7086058	RN7SKP143	-0.872					
rs716168	VTI1A		-0.662				
rs7894809	PCGF5	0.828					
rs7895870	RN7SKP167		-1.295				
rs7896554	NACAP2	0.989					
rs7917422	HTR7				0.663		1.306
rs7920351	TCERG1L				-1.059		
rs809836	LYZL1				1.109		
rs881726	GFRA1						0.922
rs915216	DUSP5		1.102				

Web Table 15: Analysis of the TCGA SKCM data using RBSG-SS.

Gene		clark	stage	age	gender
		0.834	0.228	-0.116	-0.183
AHNAKRS	0.107				
ANKRD28	0.134		0.138		
ASH2L		-0.297			
BTD		-0.312			
C1ORF140	-0.002	0.246	-0.083	-0.022	0.092
CD44					0.070
CHP1	0.107	0.045			
CXCL6	0.126	-0.120	-0.095		
DLG6	0.113	-0.015	0.067	0.185	-0.142
DOK5				-0.066	
ETNK2	0.152				
FILIP1	-0.030				
JADE1	-0.147				
JPH4		0.115			
KBF2	-0.032	0.182		0.034	-0.026

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Web Table 15: Continued from the previous page.

Gene		clark	stage	age	gender
LRRN2	-0.061				
MAGED4	-0.098		-0.020		
NHSL2	-0.088				
PITPNA	0.151	-0.051	-0.012	-0.033	0.008
SOX8	0.088		-0.212		
TMEM145					0.048
TMEM159	0.160	-0.121	-0.042		0.189
WBSCR27		0.070		0.126	

Web Table 16: Analysis of the TCGA SKCM data using RBL-SS.

Gene		clark	stage	age	gender
		0.926	-0.062	-0.011	0.388
AHNAKRS	0.084				
ANKRD28	0.191		0.207		
ASH2L		-0.258			
BAIAP2	0.043				
BTD		-0.309		-0.255	
C1ORF140		0.129			
C1ORF54					-0.102
CHP1	0.081				-0.111
CPXM1				0.005	
CSNK2A2	-0.003				
CYP1B1-AS1			0.104		
DAP	0.036			-0.116	
DLG6				0.242	
ETNK2	0.109				
FHL5		0.220			
FILIP1			-0.016		
GAMT				0.082	
IL11RA	-0.087				
IQCK					-0.090
JADE1	-0.161				
JPH4		0.159			
KDM6B			-0.142		
LRFN2		0.096			
MAGED4	-0.130				
MAPE					-0.191
MPD1	-0.078				
NHSL2	-0.144	-0.306			
PAX1	0.171		0.217		

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Web Table 16: Continued from the previous page.

Gene		clark	stage	age	gender
PBX2	0.141			0.130	
PITPNA	0.161			-0.056	
RNPEPL1			0.052		
SLC12A5					-0.081
SOX8	0.140		-0.091		
STPG1			0.184		
TMEM145					0.222
TMEM159	0.123				
TNFAIP1				0.283	
TP53TG1		0.102			-0.063
WBSCR27		0.090		0.126	

Web Table 17: Analysis of the TCGA SKCM data using BSG-SS.

Gene		clark	stage	age	gender
		0.487	0.163	0.048	0.087
AHNAKRS	0.120				
ANKRD28	0.138				
ARMC9	0.008				
ASH2L	0.019	-0.194		-0.107	
BTD		-0.303		-0.138	
C14ORF2		0.251			
C1ORF140		0.100	0.024		0.029
CD44					0.125
CHP1	0.123				
CPXM1	-0.047				
CXCL6	0.032				
DLG6		0.093		0.204	-0.061
DOK5			-0.052		
ETNK2	0.094				
FILIP1	-0.049				
GAMT		-0.004			
IL11RA	-0.045				
JADE1	-0.149				
JPH4		0.110			
KBF2	-0.077				
LRRN2	-0.073				
MAGED4	-0.122				
MAPE					-0.217
NHSL2	-0.026				
PBX2	0.133			0.155	

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Web Table 17: Continued from the previous page.

Gene		clark	stage	age	gender
PHP1B	-0.076				
PITPNA	0.150	0.077		0.038	-0.039
SOX8	0.103		-0.148		
STPG1			0.197		
TMEM145	0.015	-0.045			0.147
TMEM159	0.140				0.113
TNFRSF4		0.077			
TP53TG1		0.072			
WBSCR27		0.015		0.092	
ZFP62	-0.010				

Web Table 18: Analysis of the TCGA SKCM data using BL-SS.

Gene		clark	stage	age	gender
		0.545	0.308	0.080	0.047
AHNAKRS	0.102				
ANKRD28	0.180		0.134		
ASH2L				-0.185	
BTD		-0.386			
C14ORF2		0.126			
C1ORF140		0.199			
CELSR2			0.112		
CHP1	0.080				
CPXM1	-0.067				
CSNK2A2	-0.026				
CYP1B1-AS1			0.104		
DAP				-0.139	
DLG6	0.088			0.236	
ETNK2	0.206				-0.089
FHL5		0.076			
FILIP1			-0.062		
GAMT				0.058	
IL11RA	-0.056				
IQCK					-0.098
JADE1	-0.203				
JPH4		0.101			
KBF2	-0.089				
KDM6B			-0.173		
LRFN2		0.109			
LRRN2	-0.091				
MAGED4	-0.113				

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Web Table 18: Continued from the previous page.

Gene		clark	stage	age	gender
MAPE					-0.114
MPD1	-0.100				
NHSL2	-0.035				
PAX1			0.050		
PBX2	0.126			0.072	
PHP1B					-0.054
PIP4K2C			-0.101		
PITPNA	0.193				
PTP4A3			-0.138		
RNPEPL1			0.171		
SAA2	0.021			-0.058	
SLC12A5					-0.112
SOX8	0.132		-0.084		
TIE1	-0.093				
TMEM145					0.188
TMEM159	0.174				0.181
TP53TG1		0.156			-0.030
WBSCR27		0.048		0.105	

2.6 Implications of the markers identified by RBSG–SS

2.6.1 Nurses' Health Study (NHS) data

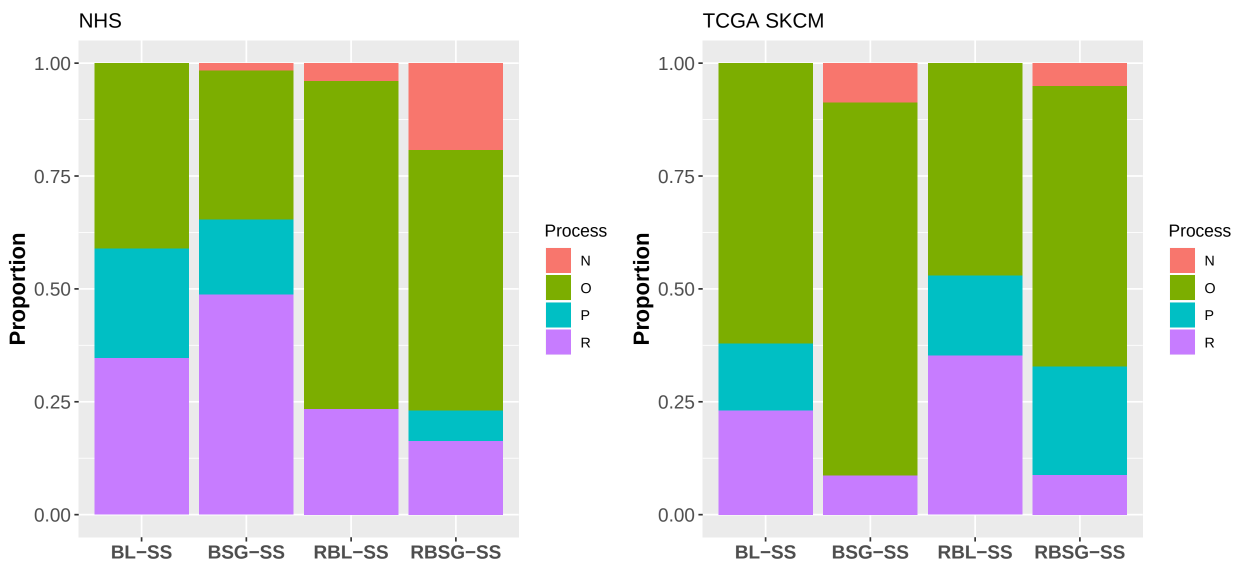
The proposed RBSG-SS identifies 22 main SNP effects and 45 G×E interactions. The detailed estimation results are provided in Web Table 11. We observe that the proposed method identifies the main and interaction effects of SNPs with important implications in obesity. For example, two important SNPs, rs6482836 and rs10741150, located within gene DOCK1 are identified. DOCK1 (Dedicator Of Cytokinesis 1) has been reported as a putative candidate for obesity–related to adiponectin and triceps skinfold by previous studies (Kim et al. (2019); Vaughan et al. (2015)). RBSG-SS identifies the main effect of rs6482836 and its interaction with the E factor act. Physical activity plays an important role in the prevention of overweight and obesity (Wareham et al. (2005)). This result suggests that individuals carrying this variant in DOCK1 may react differently than others to increasing physical activity in obesity prevention. RBSG-SS also identifies the interaction between rs10741150 and the E factor chol, suggesting that the effect of DOCK1 can be mediated by cholesterol level. Interestingly, a previous study has shown that the expression level of DOCK5, an important paralog of DOCK1, is increased in individuals exposed to a diet high in saturated fatty acids (El-Sayed Moustafa et al. (2012)). Our results provide more evidence of the importance of DOCK1 in obesity and obesity–related diseases. Another example is the SNP rs11196539, located within gene NRG3. NRG3 (Neuregulin 3) has been found to be associated with both the basal metabolic rate (BMR) and body mass index (BMI) (Lee et al. (2016)). RBSG-SS identifies its interaction with the E factors, gl and alcohol. Both glycemic load and alcohol intake are important dietary variables associated with obesity. The continued intake of high-glycemic load meals leads to an increased risk of obesity (Brand-Miller et al. (2002)). The increasing alcohol consumption is associated with a decline in body mass index in women (Nanchahal et al. (2000)), however, heavy drinking can increase risk of the metabolic syndrome (Baik and Shin (2008)). Our results suggest that further investigation of NRG3 may help explain the mechanism of the effects of glycemic load and alcohol intake on obesity. For the environment main effects, two E factors, chol and gl, have positive coefficients, and the other three, act, ceraf and alcohol, have negative coefficients, which are consistent with findings in the previous literature.

2.6.2 TCGA skin cutaneous melanoma data

The proposed approach RBSG-SS identifies 16 main SNP effects and 32 G$\times$E interactions. The detailed estimation results are provided in Web Table 15. One important gene identified is CXCL6 (C-X-C Motif Chemokine Ligand 6), a chemokine with neutrophil chemotactic and angiogenic activities. It has been reported that CXCL6 plays an important role in melanoma growth and metastasis (Verbeke et al. (2011)). RBSG-SS identifies its main effect and its interactions with E factors, stage and Clark level. This suggests that CXCL6 can have different effects at different stages of melanoma. Another important finding is the gene MAGED4, one of the members in the MAGE (Melanoma-associated antigen) family. MAGE family contains genes that are highly attractive targets for cancer immunotherapy (Zhang et al. (2014)). MAGED4 has been found to be a potential target for glioma immunotherapy (Sang et al. (2011)). RBSG-SS identifies the main effect of MAGED4 and its interaction with the E factor tumor stage, suggesting that MAGED4 may also play an important role in SKCM and its effect may change over different tumor stages. For the main effects of the E factors, Clark level and tumor stage have positive coefficients, and age and gender have negative coefficients, which match observations in the literature.

2.7 Biological similarity analysis

We examined the Gene Ontology (GO) biological processes which provide us with a deeper insight into the differences of the markers identified by different methods. We identified 77 unique genes using our proposed method along with three other methods for the NHS data. We conducted the GO enrichment analysis using the R package GOSim and found these genes involved in a total of 158 GO biological processes, the p-values of which are smaller than 0.1 in the GO enrichment analysis. Then we divided the 158 processes into four categories: positive regulation (P), negative regulation (N), regulation (R, without a well-defined "direction") and other (O). We computed the proportions of genes that involve in the four categories of processes for each of the four methods. Similarly, for the TCGA SKCM data, 109 genes were identified by our method along with three other alternative methods. GO enrichment analysis showed that they involve in 183 biological processes. The results for NHS and TCGA SKCM are provided in Web Figure 3, which shows an obvious difference between the proposed method and the three alternatives in both datasets.



Web Figure 3: Gene Ontology (GO) analysis: proportions of genes that have the four categories of processes with different approaches. Left: NHS data. Right: TCGA SKCM data.

3 Web Appendix C

3.1 Additional simulation results

For the 6 methods with spike–and–slab priors, we rerun Example 1–4 by reporting identification results for main and interaction effects separately. The mean square error (MSE) for regression coefficients corresponding to all effects, zero–effects and nonzero–effects have also been provided. The advantage of RBSG-SS over alternatives including RBL-SS has been clearly observed. Identification results for main effects and interaction effects separately show similar patterns as what have been observed for the total effects. By comparing RBSG-SS to RBL-SS, we generally observe smaller standard deviation associated with the point estimates, which indicate a more stable performance of RBSG-SS. For estimation accuracy, RBSG-SS has the lowest MSE in terms of total effects, zero-effects and non-zero effects under heavy-tailed error distributions (Error 2-5). For example, under Error 2 in Example 1 (Web Table 20), the MSE of RBSG-SS is 2.10(sd0.94) for total effects, 1.79(sd0.72) for non-zero effects and 0.32(sd0.43) for zero-effects. While the MSE of RBL-SS is 3.39(sd1.28) for total effects, 2.92(sd1.03) for non-zero effects and 0.47(sd0.51) for zero-effects. RBSG-SS has smaller MSE in all three categories. These results add strength to the superiority of RBSG-SS over the rest including RBL-SS.

Furthermore, in the 5th example, an additional data generating scenario has been considered. The gene expression data are generated based on the correlation structure extracted from the TCGA SKCM data in the case study. Specifically, 500 subjects are simulated with a multivariate normal distribution with marginal means zero and a correlation matrix computed from the first 100 genes from the SKCM data. The same conclusion on the advantage of RBSG–SS can be drawn based on the results in the Web Tables 39–43. We have made the same conclusions with respect to the advantage of RBSG-SS over the alternative methods.

In the above simulations, the total number of non-zero effects (main and interaction) is fixed at 25, but the number of the non-zero main effects and the number of the non-zero interaction effects can be different in each replicate. We conducted simulations at different fixed numbers of non-zero main effects, and found that all the conclusions still hold. As a demonstrating example, we show the results with the number of non-zero main effects fixed at 4 (the number of non-zero interaction effects is 21) under Example 1 setting in Web Tables 44–48.

3.1.1 Additional simulation results for Example 1

Web Table 19: Simulation results in Example 1 Error 1. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1 (N)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.91(0.29)	25.00(0.00)	24.68(0.57)	24.95(0.22)	25.00(0.00)	24.77(0.45)
	Main	4.29(1.44)	4.29(1.44)	4.26(1.45)	4.29(1.44)	4.29(1.44)	4.27(1.45)
	Int.	20.62(1.45)	20.71(1.44)	20.42(1.43)	20.66(1.46)	20.71(1.44)	20.50(1.47)
FP	Total	1.33(1.41)	29.78(2.03)	1.48(1.53)	0.77(0.84)	29.24(1.18)	0.52(0.73)
	Main	0.31(0.54)	4.84(1.51)	0.35(0.63)	0.16(0.37)	4.75(1.49)	0.13(0.34)
	Int.	1.02(1.19)	24.94(2.14)	1.13(1.30)	0.61(0.75)	24.49(1.59)	0.39(0.69)
MSE	Total	0.27(0.12)	0.52(0.14)	0.31(0.17)	0.19(0.08)	0.42(0.11)	0.21(0.10)
	Non-zero	0.22(0.08)	0.26(0.09)	0.25(0.14)	0.16(0.06)	0.21(0.08)	0.19(0.09)
	Zero	0.05(0.05)	0.25(0.10)	0.06(0.07)	0.03(0.03)	0.20(0.08)	0.02(0.03)
Pred. Error		0.84(0.03)	0.87(0.04)	0.85(0.03)	1.10(0.08)	1.16(0.08)	1.11(0.08)

Web Table 20: Simulation results in Example 1 Error 2. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	20.85(1.93)	24.90(0.44)	17.92(1.95)	19.35(2.06)	24.58(0.82)	14.42(2.09)
	Main	3.60(1.26)	4.25(1.27)	3.14(1.26)	3.39(1.28)	4.20(1.29)	2.51(1.27)
	Int.	17.25(2.06)	20.65(1.39)	14.78(2.07)	15.96(2.14)	20.38(1.42)	11.91(1.99)
FP	Total	1.67(1.39)	32.10(5.21)	1.87(1.80)	1.98(1.52)	31.16(5.25)	1.15(1.09)
	Main	0.37(0.65)	5.25(1.62)	0.28(0.59)	0.27(0.49)	5.09(1.46)	0.19(0.42)
	Int.	1.30(1.18)	26.85(4.40)	1.59(1.69)	1.71(1.44)	26.07(4.71)	0.96(0.98)
MSE	Total	2.10(0.94)	2.82(1.02)	3.39(1.28)	3.04(1.15)	3.77(1.13)	5.26(1.67)
	Non-zero	1.79(0.72)	1.33(0.50)	2.92(1.03)	2.55(0.93)	1.83(0.61)	4.71(1.41)
	Zero	0.32(0.34)	1.49(0.76)	0.47(0.51)	0.49(0.46)	1.94(0.86)	0.55(0.64)
Pred. Error		2.17(0.11)	2.21(0.13)	2.27(0.13)	9.33(1.07)	9.48(1.08)	10.35(1.22)

Web Table 21: Simulation results in Example 1 Error 3. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3 (Mix.L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	21.09(1.76)	24.92(0.39)	17.92(1.97)	19.14(2.20)	24.54(0.85)	14.32(1.96)
	Main	3.70(1.34)	4.25(1.42)	3.16(1.35)	3.22(1.39)	4.17(1.37)	2.48(1.23)
	Int.	17.39(2.04)	20.67(1.39)	14.76(2.09)	15.92(2.25)	20.37(1.59)	11.84(1.95)
FP	Total	1.49(1.15)	31.30(4.06)	1.53(1.45)	2.05(1.49)	31.02(4.59)	1.31(1.27)
	Main	0.23(0.47)	5.12(1.54)	0.32(0.55)	0.34(0.52)	5.09(1.64)	0.16(0.39)
	Int.	1.26(1.02)	26.18(3.71)	1.21(1.24)	1.71(1.32)	25.93(3.93)	1.15(1.12)
MSE	Total	2.19(0.84)	2.88(0.90)	3.61(1.32)	3.45(1.30)	4.22(1.30)	6.11(1.91)
	Non-zero	1.86(0.70)	1.36(0.45)	3.14(1.09)	2.84(1.03)	2.05(0.72)	5.30(1.44)
	Zero	0.33(0.36)	1.52(0.66)	0.47(0.55)	0.61(0.57)	2.17(0.93)	0.81(0.84)
Pred. Error		2.30(0.12)	2.34(0.12)	2.40(0.13)	10.86(1.14)	11.03(1.19)	11.98(1.36)

Web Table 22: Simulation results in Example 1 Error 4. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4 (t2)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	23.76(1.22)	24.98(0.20)	21.77(1.79)	18.05(4.54)	23.65(3.38)	14.48(4.02)
	Main	4.32(1.43)	4.48(1.47)	4.05(1.49)	3.30(1.73)	4.20(1.58)	2.63(1.57)
	Int.	19.44(1.93)	20.50(1.47)	17.72(2.26)	14.75(3.87)	19.45(3.05)	11.85(3.47)
FP	Total	0.59(0.81)	29.14(1.11)	0.55(0.86)	2.42(2.92)	33.35(10.93)	1.23(1.40)
	Main	0.12(0.33)	4.54(1.46)	0.14(0.35)	0.37(0.65)	5.30(2.25)	0.12(0.33)
	Int.	0.47(0.76)	24.60(1.81)	0.41(0.75)	2.05(2.57)	28.05(9.31)	1.11(1.32)
MSE	Total	0.53(0.27)	0.85(0.26)	0.94(0.49)	3.78(4.18)	4.75(5.94)	4.97(3.89)
	Non-zero	0.48(0.24)	0.45(0.16)	0.88(0.45)	2.80(2.32)	2.02(1.89)	4.24(2.73)
	Zero	0.04(0.08)	0.39(0.17)	0.05(0.10)	0.98(2.52)	2.73(4.72)	0.73(1.72)
Pred. Error		1.50(0.13)	1.51(0.13)	1.54(0.14)	12.86(14.25)	12.58(14.41)	13.43(14.31)

Web Table 23: Simulation results in Example 1 Error 5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5 (logNor)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.27(0.89)	24.96(0.28)	22.88(1.39)	20.44(2.69)	24.60(0.90)	16.87(2.99)
	Main	4.18(1.41)	4.30(1.40)	3.91(1.44)	3.53(1.46)	4.25(1.41)	2.91(1.36)
	Int.	20.09(1.64)	20.66(1.44)	18.97(1.68)	16.91(2.70)	20.35(1.45)	13.96(2.82)
FP	Total	0.36(0.58)	28.98(0.83)	0.27(0.62)	2.09(2.20)	34.32(10.62)	1.35(1.57)
	Main	0.06(0.24)	4.69(1.42)	0.05(0.22)	0.24(0.51)	5.57(2.29)	0.18(0.41)
	Int.	0.30(0.50)	24.29(1.53)	0.22(0.50)	1.85(2.10)	28.75(8.90)	1.17(1.45)
MSE	Total	0.26(0.14)	0.47(0.14)	0.43(0.23)	1.66(1.12)	2.46(2.00)	2.61(1.43)
	Non-zero	0.24(0.12)	0.26(0.09)	0.40(0.21)	1.29(0.75)	1.04(0.60)	2.26(1.18)
	Zero	0.02(0.04)	0.22(0.09)	0.02(0.06)	0.37(0.53)	1.41(1.60)	0.35(0.48)
Pred. Error		1.16(0.08)	1.19(0.08)	1.18(0.08)	5.18(1.53)	5.42(1.66)	5.54(1.56)

3.1.2 Additional simulation results for Example 2

Web Table 24: Simulation results in Example 2 Error 1. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1 (N)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.94(0.24)	25.00(0.00)	24.84(0.44)	24.98(0.14)	25.00(0.00)	24.90(0.39)
	Main	4.05(1.26)	4.05(1.26)	4.04(1.26)	4.05(1.26)	4.05(1.26)	4.05(1.26)
	Int.	20.89(1.25)	20.95(1.26)	20.80(1.31)	20.93(1.26)	20.95(1.26)	20.85(1.31)
FP	Total	1.69(1.40)	35.90(7.83)	1.93(1.69)	1.02(1.05)	30.32(3.58)	0.59(0.84)
	Main	0.30(0.48)	6.10(1.85)	0.34(0.62)	0.19(0.39)	5.17(1.48)	0.08(0.27)
	Int.	1.39(1.25)	29.80(6.60)	1.59(1.53)	0.83(1.02)	25.15(3.04)	0.51(0.77)
MSE	Total	0.78(0.47)	1.82(0.82)	0.83(0.46)	0.54(0.29)	1.17(0.51)	0.53(0.41)
	Non-zero	0.66(0.42)	1.14(0.62)	0.71(0.43)	0.47(0.25)	0.76(0.39)	0.49(0.39)
	Zero	0.12(0.13)	0.67(0.34)	0.13(0.13)	0.06(0.08)	0.40(0.21)	0.04(0.06)
Pred. Error		0.85(0.04)	0.88(0.04)	0.86(0.04)	1.09(0.08)	1.15(0.08)	1.10(0.08)

Web Table 25: Simulation results in Example 2 Error 2. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	21.64(2.15)	24.96(0.28)	18.54(2.06)	19.99(2.35)	24.78(0.69)	14.89(2.03)
	Main	3.62(1.42)	4.19(1.48)	3.12(1.30)	3.31(1.38)	4.14(1.44)	2.52(1.28)
	Int.	18.02(2.50)	20.77(1.45)	15.42(2.31)	16.68(2.65)	20.64(1.60)	12.37(2.18)
FP	Total	1.87(1.66)	36.24(8.81)	1.96(1.72)	2.29(1.58)	33.78(6.86)	1.36(1.30)
	Main	0.29(0.52)	6.01(2.06)	0.31(0.58)	0.41(0.59)	5.62(1.83)	0.17(0.40)
	Int.	1.58(1.51)	30.23(7.52)	1.65(1.49)	1.88(1.42)	28.16(5.92)	1.19(1.13)
MSE	Total	5.70(3.08)	8.93(4.69)	9.74(3.80)	8.55(4.41)	11.12(5.23)	14.53(4.80)
	Non-zero	5.07(2.79)	5.44(3.35)	8.80(3.43)	7.51(4.01)	6.80(3.83)	13.37(4.60)
	Zero	0.63(0.72)	3.48(1.86)	0.94(0.95)	1.03(1.00)	4.32(2.22)	1.16(1.17)
Pred. Error		2.24(0.13)	2.19(0.10)	2.37(0.17)	10.42(1.29)	9.30(0.99)	11.25(1.51)

Web Table 26: Simulation results in Example 2 Error 3. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3 (Mix.L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	21.53(1.93)	24.96(0.28)	17.99(2.21)	19.41(2.32)	24.68(0.74)	13.73(1.88)
	Main	3.74(1.46)	4.24(1.43)	3.19(1.38)	3.41(1.35)	4.16(1.41)	2.43(1.30)
	Int.	17.79(2.17)	20.72(1.44)	14.80(2.22)	16.00(2.35)	20.52(1.54)	11.30(1.76)
FP	Total	2.04(1.39)	36.48(8.03)	2.20(1.47)	2.31(1.60)	35.02(7.97)	1.32(1.12)
	Main	0.31(0.58)	6.00(1.93)	0.38(0.62)	0.34(0.64)	5.79(1.81)	0.10(0.30)
	Int.	1.73(1.33)	30.48(6.88)	1.82(1.32)	1.97(1.34)	29.23(6.96)	1.22(1.03)
MSE	Total	5.96(3.25)	8.95(4.83)	10.72(4.64)	9.94(5.07)	12.96(6.28)	17.34(6.66)
	Non-zero	5.26(2.95)	5.57(3.81)	9.59(4.13)	8.77(4.75)	7.88(4.67)	15.98(6.36)
	Zero	0.71(0.67)	3.39(1.56)	1.13(1.06)	1.16(0.91)	5.07(2.91)	1.36(1.37)
Pred. Error		2.38(0.15)	2.31(0.11)	2.52(0.17)	12.12(1.43)	10.65(0.94)	13.19(1.86)

Web Table 27: Simulation results in Example 2 Error 4. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4 (t2)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.05(0.98)	24.98(0.20)	21.64(2.13)	16.45(5.11)	23.59(2.50)	11.84(4.28)
	Main	3.89(1.54)	4.03(1.55)	3.44(1.46)	2.44(1.61)	3.71(1.55)	1.67(1.37)
	Int.	20.16(1.80)	20.95(1.56)	18.20(2.44)	14.01(4.56)	19.88(2.58)	10.16(3.61)
FP	Total	0.79(0.92)	29.58(2.08)	0.66(0.72)	2.56(2.70)	40.49(22.84)	1.41(1.94)
	Main	0.19(0.44)	5.06(1.58)	0.12(0.33)	0.23(0.47)	6.97(3.90)	0.08(0.31)
	Int.	0.61(0.76)	24.52(2.36)	0.54(0.69)	2.33(2.53)	33.53(19.29)	1.33(1.88)
MSE	Total	1.85(1.00)	3.25(1.28)	4.12(2.44)	16.16(13.79)	27.64(46.16)	22.18(13.15)
	Non-zero	1.71(0.94)	2.05(1.03)	3.86(2.30)	14.33(12.91)	15.48(24.09)	20.53(12.86)
	Zero	0.14(0.22)	1.19(0.53)	0.26(0.49)	1.83(2.21)	12.15(23.50)	1.65(2.19)
Pred. Error		1.84(0.17)	1.83(0.16)	1.91(0.18)	23.87(36.27)	21.28(36.44)	24.22(36.20)

Web Table 28: Simulation results in Example 2 Error 5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5 (logNor)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.14(0.94)	25.00(0.00)	21.80(1.80)	17.90(3.68)	24.42(1.12)	12.88(3.26)
	Main	3.94(1.33)	4.11(1.40)	3.62(1.31)	2.93(1.54)	4.02(1.42)	1.98(1.40)
	Int.	20.20(1.63)	20.89(1.40)	18.18(2.05)	14.97(3.25)	20.40(1.66)	10.90(2.79)
FP	Total	0.79(0.93)	29.85(2.27)	0.59(0.71)	2.62(2.23)	39.70(18.79)	1.80(1.76)
	Main	0.17(0.43)	5.03(1.43)	0.12(0.39)	0.31(0.60)	6.67(3.45)	0.24(0.48)
	Int.	0.62(0.80)	24.82(2.40)	0.46(0.61)	2.30(2.15)	33.03(15.70)	1.56(1.67)
MSE	Total	1.78(1.07)	3.02(1.00)	4.12(2.72)	13.07(9.63)	18.12(22.39)	20.20(11.05)
	Non-zero	1.63(0.98)	1.95(0.73)	3.91(2.60)	11.26(8.56)	10.29(13.69)	18.13(9.62)
	Zero	0.15(0.24)	1.06(0.48)	0.21(0.40)	1.81(2.33)	7.83(10.06)	2.07(2.72)
Pred. Error		1.79(0.13)	1.79(0.13)	1.86(0.14)	15.23(5.26)	12.60(4.01)	15.99(4.53)

3.1.3 Additional simulation results for Example 3

Web Table 29: Simulation results in Example 3 Error 1. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1 (N)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.68(0.55)	25.00(0.00)	24.16(0.97)	24.82(0.44)	25.00(0.00)	24.31(0.81)
	Main	4.22(1.47)	4.26(1.46)	4.09(1.44)	4.23(1.46)	4.26(1.46)	4.13(1.47)
	Int.	20.46(1.56)	20.74(1.46)	20.07(1.74)	20.59(1.54)	20.74(1.46)	20.18(1.68)
FP	Total	1.92(1.58)	34.10(5.81)	2.01(1.46)	1.18(1.29)	29.60(1.81)	0.74(0.79)
	Main	0.29(0.54)	5.59(1.88)	0.42(0.61)	0.18(0.41)	4.84(1.48)	0.14(0.38)
	Int.	1.63(1.47)	28.51(4.82)	1.59(1.26)	1.00(1.15)	24.76(2.16)	0.60(0.70)
MSE	Total	0.97(0.54)	2.10(0.59)	1.28(0.89)	0.67(0.42)	1.54(0.44)	0.89(0.67)
	Non-zero	0.77(0.47)	0.92(0.30)	1.07(0.79)	0.55(0.35)	0.73(0.23)	0.81(0.62)
	Zero	0.20(0.21)	1.18(0.45)	0.21(0.23)	0.12(0.16)	0.81(0.31)	0.08(0.13)
Pred. Error		0.85(0.04)	0.88(0.04)	0.86(0.04)	1.09(0.08)	1.16(0.09)	1.11(0.09)

Web Table 30: Simulation results in Example 3 Error 2. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	17.50(2.04)	24.49(1.02)	14.09(1.71)	15.59(2.00)	23.71(1.50)	11.24(1.79)
	Main	3.07(1.25)	4.08(1.26)	2.49(1.18)	2.68(1.21)	3.96(1.25)	2.01(0.98)
	Int.	14.43(2.11)	20.41(1.56)	11.60(1.83)	12.91(2.07)	19.75(1.82)	9.23(1.60)
FP	Total	2.47(1.61)	32.87(6.55)	2.24(1.66)	2.75(1.60)	30.41(6.65)	1.63(1.19)
	Main	0.38(0.53)	5.48(1.66)	0.32(0.58)	0.50(0.69)	5.06(1.66)	0.28(0.53)
	Int.	2.09(1.45)	27.39(5.61)	1.92(1.42)	2.25(1.44)	25.35(5.69)	1.35(1.03)
MSE	Total	8.66(2.88)	10.94(4.13)	12.65(3.00)	11.30(3.09)	13.76(4.39)	17.60(3.41)
	Non-zero	7.08(2.13)	5.14(2.03)	10.61(2.22)	9.13(2.56)	6.71(2.13)	15.17(3.02)
	Zero	1.58(1.43)	5.80(2.73)	2.04(1.77)	2.18(1.53)	7.05(3.19)	2.44(1.99)
Pred. Error		2.30(0.13)	2.15(0.09)	2.35(0.14)	10.65(1.24)	9.24(0.92)	11.13(1.51)

Web Table 31: Simulation results in Example 3 Error 3. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3 (Mix.L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	17.23(2.10)	24.45(0.91)	13.78(1.54)	14.90(2.24)	23.36(1.67)	10.55(1.80)
	Main	2.98(1.36)	4.14(1.35)	2.42(1.17)	2.63(1.24)	3.88(1.30)	1.77(1.04)
	Int.	14.25(1.98)	20.31(1.48)	11.36(1.64)	12.27(2.14)	19.48(1.86)	8.78(1.60)
FP	Total	2.28(1.42)	32.31(6.86)	1.86(1.34)	2.52(1.60)	29.98(6.20)	1.56(1.33)
	Main	0.38(0.58)	5.32(1.86)	0.29(0.54)	0.37(0.56)	5.01(1.69)	0.19(0.44)
	Int.	1.90(1.29)	26.99(5.70)	1.57(1.21)	2.15(1.47)	24.97(5.23)	1.37(1.20)
MSE	Total	8.89(2.96)	11.02(3.86)	13.27(3.08)	12.51(3.45)	15.92(5.55)	19.76(4.44)
	Non-zero	7.50(2.39)	5.15(1.87)	11.49(2.55)	10.25(3.00)	7.67(2.84)	16.86(3.63)
	Zero	1.39(1.23)	5.86(2.86)	1.78(1.76)	2.27(1.65)	8.25(3.73)	2.90(2.56)
Pred. Error		2.40(0.13)	2.26(0.11)	2.47(0.13)	11.99(1.35)	10.42(1.14)	12.38(1.36)

Web Table 32: Simulation results in Example 3 Error 4. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4 (t2)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	23.24(1.65)	24.90(0.44)	19.76(2.04)	16.47(4.17)	23.46(3.00)	12.26(3.37)
	Main	3.81(1.48)	4.07(1.44)	3.27(1.20)	2.61(1.36)	3.76(1.43)	2.03(1.17)
	Int.	19.43(2.07)	20.83(1.52)	16.49(2.16)	13.86(3.61)	19.70(3.04)	10.23(2.82)
FP	Total	1.08(0.98)	29.64(2.59)	0.84(1.01)	3.31(3.10)	36.54(18.56)	2.24(2.37)
	Main	0.20(0.40)	5.02(1.51)	0.18(0.44)	0.42(0.67)	6.24(3.50)	0.21(0.43)
	Int.	0.88(0.87)	24.62(2.58)	0.66(0.88)	2.89(2.89)	30.30(15.42)	2.03(2.30)
MSE	Total	2.10(1.43)	3.24(1.05)	4.81(2.06)	12.71(13.94)	18.51(24.89)	18.03(12.95)
	Non-zero	1.85(1.26)	1.57(0.61)	4.39(1.93)	8.99(5.53)	7.54(8.30)	14.43(6.30)
	Zero	0.25(0.31)	1.67(0.64)	0.42(0.57)	3.73(10.84)	10.97(17.95)	3.59(9.59)
Pred. Error		1.50(0.14)	1.52(0.14)	1.57(0.15)	14.65(24.37)	14.99(24.50)	15.27(24.36)

Web Table 33: Simulation results in Example 3 Error 5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5 (logNor)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.30(0.89)	25.00(0.00)	22.22(1.90)	18.80(3.10)	24.42(1.25)	14.10(2.72)
	Main	3.82(1.53)	3.92(1.55)	3.55(1.42)	3.02(1.48)	3.82(1.56)	2.32(1.36)
	Int.	20.48(1.78)	21.08(1.55)	18.67(2.28)	15.78(3.01)	20.60(1.82)	11.78(2.41)
FP	Total	0.69(1.12)	29.00(0.00)	0.46(0.80)	2.56(2.15)	34.44(8.82)	1.85(1.83)
	Main	0.20(0.53)	5.08(1.55)	0.09(0.32)	0.34(0.57)	5.99(2.08)	0.19(0.39)
	Int.	0.49(0.85)	23.92(1.55)	0.37(0.69)	2.22(2.06)	28.45(7.58)	1.66(1.74)
MSE	Total	1.06(0.82)	2.24(0.84)	2.53(1.85)	7.33(4.22)	10.30(7.76)	12.69(4.93)
	Non-zero	0.94(0.65)	1.09(0.46)	2.33(1.63)	5.92(3.16)	4.36(2.61)	10.86(3.83)
	Zero	0.12(0.25)	1.15(0.54)	0.20(0.49)	1.41(1.87)	5.94(5.73)	1.83(2.21)
Pred. Error		1.23(0.08)	1.26(0.09)	1.26(0.09)	5.83(1.51)	5.98(1.62)	6.35(1.56)

3.1.4 Additional simulation results for Example 4

Web Table 34: Simulation results in Example 4 Error 1. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1 (N)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	25.00(0.00)	25.00(0.00)	24.96(0.19)	25.00(0.00)	25.00(0.00)	24.99(0.11)
	Main	4.16(1.42)	4.16(1.42)	4.16(1.42)	4.16(1.42)	4.16(1.42)	4.16(1.42)
	Int.	20.84(1.42)	20.84(1.42)	20.80(1.43)	20.84(1.42)	20.84(1.42)	20.82(1.41)
FP	Total	1.09(1.30)	30.65(3.69)	1.51(1.36)	0.76(0.98)	29.38(1.46)	0.54(0.71)
	Main	0.26(0.57)	5.11(1.54)	0.35(0.66)	0.10(0.30)	4.90(1.40)	0.10(0.30)
	Int.	0.82(0.99)	25.54(3.40)	1.16(1.07)	0.66(0.91)	24.48(2.01)	0.44(0.67)
MSE	Total	0.58(0.40)	1.08(0.46)	0.67(0.45)	0.43(0.27)	0.92(0.45)	0.41(0.23)
	Non-zero	0.53(0.37)	0.74(0.42)	0.59(0.41)	0.40(0.25)	0.66(0.41)	0.39(0.23)
	Zero	0.05(0.07)	0.34(0.15)	0.08(0.09)	0.03(0.05)	0.26(0.11)	0.03(0.04)
Pred. Error		0.85(0.03)	0.88(0.03)	0.86(0.03)	1.10(0.06)	1.18(0.07)	1.10(0.06)

Web Table 35: Simulation results in Example 4 Error 2. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	21.55(2.40)	23.90(1.35)	17.79(2.60)	19.07(3.08)	22.74(1.68)	14.46(3.20)
	Main	3.96(1.47)	4.06(1.47)	3.92(1.46)	3.79(1.54)	3.92(1.44)	3.59(1.59)
	Int.	17.59(2.46)	19.84(1.98)	13.86(2.62)	15.29(2.72)	18.81(2.16)	10.88(2.84)
FP	Total	1.68(1.62)	30.93(6.04)	1.73(1.58)	1.76(1.62)	27.36(5.84)	1.20(1.26)
	Main	0.20(0.43)	5.08(1.93)	0.25(0.49)	0.23(0.48)	4.42(1.77)	0.12(0.37)
	Int.	1.48(1.65)	25.85(4.99)	1.48(1.50)	1.54(1.58)	22.94(5.05)	1.07(1.26)
MSE	Total	7.15(6.41)	7.82(4.97)	15.80(17.37)	10.99(7.83)	9.43(5.23)	22.00(15.15)
	Non-zero	6.68(6.35)	5.83(4.66)	15.16(16.80)	10.31(7.60)	7.18(5.14)	21.26(14.81)
	Zero	0.46(0.54)	1.99(0.84)	0.64(0.85)	0.68(0.72)	2.26(1.08)	0.74(0.99)
Pred. Error		2.24(0.11)	2.21(0.08)	2.36(0.13)	10.18(1.01)	9.61(0.76)	11.34(1.31)

Web Table 36: Simulation results in Example 4 Error 3. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3 (Mix.L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	20.43(2.93)	23.43(1.73)	16.52(2.85)	17.55(3.69)	21.94(2.50)	12.60(3.08)
	Main	3.80(1.31)	3.84(1.34)	3.64(1.28)	3.49(1.35)	3.69(1.33)	3.20(1.28)
	Int.	16.62(2.98)	19.59(2.05)	12.89(2.93)	14.06(3.49)	18.25(2.38)	9.40(2.91)
FP	Total	1.50(1.24)	30.50(6.25)	1.73(1.44)	2.16(1.66)	26.51(6.42)	1.61(1.42)
	Main	0.28(0.45)	5.15(1.69)	0.33(0.63)	0.33(0.57)	4.39(1.63)	0.14(0.41)
	Int.	1.23(1.18)	25.35(5.37)	1.40(1.30)	1.84(1.53)	22.12(5.50)	1.48(1.31)
MSE	Total	9.31(9.71)	9.36(9.05)	21.10(18.57)	16.29(12.24)	12.66(8.63)	30.32(19.91)
	Non-zero	8.87(9.60)	7.30(8.88)	20.46(18.40)	15.36(12.20)	10.07(8.49)	29.22(19.89)
	Zero	0.45(0.45)	2.06(0.98)	0.64(0.62)	0.94(0.79)	2.59(1.36)	1.09(0.98)
Pred. Error		2.36(0.12)	2.34(0.10)	2.49(0.13)	11.84(1.24)	11.09(0.89)	13.17(1.27)

Web Table 37: Simulation results in Example 4 Error 4. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4 (t2)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.66(0.80)	24.78(0.69)	23.58(1.39)	18.88(5.60)	22.33(3.61)	15.07(5.43)
	Main	4.23(1.32)	4.23(1.32)	4.22(1.31)	3.78(1.50)	4.01(1.37)	3.46(1.53)
	Int.	20.42(1.58)	20.55(1.57)	19.35(1.88)	15.10(4.99)	18.32(3.27)	11.61(4.74)
FP	Total	0.57(0.77)	29.10(2.53)	0.60(0.83)	3.39(3.86)	36.15(17.01)	3.04(3.49)
	Main	0.12(0.33)	4.75(1.43)	0.12(0.36)	0.59(1.03)	5.74(3.00)	0.40(0.71)
	Int.	0.44(0.67)	24.35(2.43)	0.47(0.68)	2.81(3.26)	30.41(14.33)	2.64(3.25)
MSE	Total	1.34(1.67)	2.54(1.71)	3.70(7.73)	16.10(19.16)	16.82(27.99)	26.44(23.32)
	Non-zero	1.28(1.62)	1.83(1.53)	3.58(7.66)	13.28(17.67)	8.92(10.09)	23.08(21.35)
	Zero	0.07(0.12)	0.72(0.66)	0.11(0.23)	2.82(5.46)	7.90(24.14)	3.36(5.97)
Pred. Error		1.54(0.09)	1.59(0.09)	1.58(0.11)	13.26(12.11)	13.79(12.53)	14.41(12.05)

Web Table 38: Simulation results in Example 4 Error 5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5 (logNor)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.21(1.16)	24.52(0.97)	21.89(2.26)	16.41(4.90)	21.71(2.96)	11.72(4.78)
	Main	4.49(1.41)	4.49(1.41)	4.49(1.41)	3.74(1.53)	4.16(1.40)	3.36(1.56)
	Int.	19.73(1.87)	20.04(1.64)	17.40(2.54)	12.68(4.28)	17.55(2.80)	8.36(3.86)
FP	Total	0.79(0.99)	29.10(3.63)	0.70(1.10)	2.67(3.07)	31.46(15.83)	2.09(2.90)
	Main	0.09(0.28)	4.45(1.58)	0.06(0.24)	0.23(0.48)	4.70(2.74)	0.15(0.36)
	Int.	0.70(0.88)	24.65(3.20)	0.64(1.08)	2.45(3.02)	26.76(13.48)	1.94(2.85)
MSE	Total	1.98(2.06)	3.38(2.51)	8.98(22.54)	21.33(28.59)	16.20(16.24)	30.97(23.93)
	Non-zero	1.85(2.00)	2.46(2.38)	8.76(22.26)	18.10(22.71)	11.56(12.76)	27.47(19.10)
	Zero	0.13(0.18)	0.91(0.51)	0.22(0.44)	3.23(8.46)	4.64(8.04)	3.50(10.39)
Pred. Error		1.77(0.10)	1.82(0.10)	1.84(0.12)	13.02(2.89)	13.33(3.71)	14.82(3.43)

3.1.5 Additional simulation results for Example 5

Web Table 39: Simulation results in Example 5 Error 1. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1 (N)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.90(0.30)	25.00(0.00)	24.59(0.67)	24.93(0.26)	25.00(0.00)	24.73(0.51)
	Main	4.24(1.42)	4.24(1.42)	4.18(1.40)	4.23(1.42)	4.24(1.42)	4.22(1.42)
	Int.	20.66(1.49)	20.76(1.42)	20.41(1.53)	20.70(1.46)	20.76(1.42)	20.51(1.55)
FP	Total	1.14(1.15)	30.14(2.51)	1.46(1.37)	0.64(0.76)	29.54(1.73)	0.53(0.80)
	Main	0.19(0.49)	4.95(1.51)	0.19(0.44)	0.10(0.30)	4.85(1.42)	0.09(0.38)
	Int.	0.95(1.03)	25.19(2.46)	1.27(1.17)	0.54(0.70)	24.69(2.14)	0.44(0.67)
MSE	Total	0.28(0.12)	0.62(0.18)	0.34(0.18)	0.20(0.09)	0.50(0.15)	0.23(0.14)
	Non-zero	0.23(0.09)	0.31(0.11)	0.28(0.15)	0.18(0.07)	0.26(0.10)	0.21(0.13)
	Zero	0.05(0.06)	0.31(0.13)	0.06(0.07)	0.02(0.03)	0.24(0.09)	0.02(0.03)
Pred. Error		0.85(0.04)	0.87(0.04)	0.86(0.04)	1.09(0.08)	1.16(0.09)	1.10(0.09)

Web Table 40: Simulation results in Example 5 Error 2. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	20.67(2.13)	24.78(0.63)	17.18(2.29)	18.91(2.54)	24.21(1.13)	14.43(2.27)
	Main	3.70(1.24)	4.27(1.18)	3.05(1.24)	3.33(1.26)	4.11(1.17)	2.52(1.26)
	Int.	16.97(2.17)	20.51(1.28)	14.13(2.13)	15.58(2.23)	20.10(1.40)	11.91(1.96)
FP	Total	1.71(1.49)	31.20(4.21)	1.82(1.53)	2.02(1.50)	29.85(4.26)	1.34(1.11)
	Main	0.25(0.44)	5.06(1.43)	0.34(0.61)	0.34(0.61)	4.90(1.43)	0.17(0.40)
	Int.	1.46(1.41)	26.14(3.58)	1.48(1.33)	1.68(1.33)	24.95(3.55)	1.17(1.00)
MSE	Total	2.35(1.02)	3.00(0.99)	3.97(1.31)	3.37(1.19)	3.91(1.20)	5.69(1.61)
	Non-zero	1.93(0.73)	1.41(0.48)	3.35(0.96)	2.74(0.88)	1.93(0.57)	4.90(1.22)
	Zero	0.42(0.48)	1.59(0.74)	0.62(0.65)	0.63(0.54)	1.98(0.85)	0.79(0.78)
Pred. Error		2.18(0.09)	2.20(0.10)	2.29(0.11)	9.47(0.85)	9.44(0.87)	10.34(1.03)

Web Table 41: Simulation results in Example 5 Error 3. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3 (Mix.L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	20.43(2.18)	24.68(0.74)	16.82(1.98)	18.24(2.42)	24.22(1.14)	13.47(1.94)
	Main	3.24(1.49)	4.04(1.44)	2.70(1.42)	2.85(1.48)	3.93(1.46)	2.09(1.39)
	Int.	17.19(2.35)	20.64(1.68)	14.12(2.17)	15.39(2.47)	20.29(1.72)	11.38(1.94)
FP	Total	1.55(1.53)	30.64(4.44)	1.57(1.41)	2.06(1.35)	30.08(4.95)	1.36(1.19)
	Main	0.30(0.66)	5.18(1.65)	0.28(0.62)	0.36(0.61)	5.12(1.55)	0.18(0.44)
	Int.	1.25(1.26)	25.46(3.96)	1.29(1.29)	1.70(1.28)	24.96(4.57)	1.18(1.11)
MSE	Total	2.50(1.01)	3.27(1.27)	4.23(1.15)	4.11(1.51)	4.93(1.79)	6.90(1.91)
	Non-zero	2.11(0.81)	1.53(0.55)	3.67(0.95)	3.38(1.20)	2.38(0.91)	5.96(1.37)
	Zero	0.39(0.44)	1.75(0.93)	0.56(0.62)	0.73(0.57)	2.55(1.29)	0.94(0.99)
Pred. Error		2.29(0.11)	2.32(0.11)	2.41(0.12)	10.92(1.12)	10.90(1.08)	12.02(1.21)

Web Table 42: Simulation results in Example 5 Error 4. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4 (t2)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.04(1.00)	25.00(0.00)	22.08(1.59)	17.78(4.92)	23.62(2.63)	13.81(4.92)
	Main	4.16(1.61)	4.24(1.63)	3.80(1.62)	3.10(1.72)	3.96(1.55)	2.34(1.60)
	Int.	19.88(1.85)	20.76(1.63)	18.28(2.08)	14.68(4.37)	19.66(2.79)	11.47(4.22)
FP	Total	0.52(0.71)	29.25(1.20)	0.44(0.75)	2.61(3.56)	34.77(13.98)	1.67(2.61)
	Main	0.07(0.26)	4.80(1.62)	0.08(0.31)	0.29(0.63)	5.77(2.71)	0.15(0.39)
	Int.	0.44(0.66)	24.44(1.99)	0.36(0.65)	2.32(3.35)	29.00(11.85)	1.52(2.52)
MSE	Total	0.56(0.29)	1.12(0.35)	1.11(0.54)	6.10(10.00)	8.29(14.54)	7.67(9.47)
	Non-zero	0.50(0.25)	0.54(0.17)	1.03(0.48)	3.94(3.48)	2.77(2.72)	5.94(4.00)
	Zero	0.05(0.10)	0.59(0.26)	0.08(0.16)	2.16(7.76)	5.52(12.19)	1.73(7.24)
Pred. Error		1.56(0.13)	1.60(0.13)	1.61(0.14)	13.45(14.31)	13.72(14.38)	14.53(14.53)

Web Table 43: Simulation results in Example 5 Error 5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5 (logNor)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.09(0.89)	24.98(0.20)	22.10(1.68)	18.77(3.21)	24.13(1.48)	14.65(3.13)
	Main	4.10(1.46)	4.23(1.48)	3.77(1.46)	3.24(1.42)	4.05(1.42)	2.42(1.33)
	Int.	19.99(1.57)	20.75(1.49)	18.33(1.90)	15.53(2.88)	20.08(1.89)	12.23(2.78)
FP	Total	0.46(0.66)	29.08(0.94)	0.40(0.65)	2.81(2.28)	35.21(8.91)	1.63(1.57)
	Main	0.11(0.35)	4.78(1.47)	0.11(0.31)	0.40(0.59)	5.84(2.10)	0.14(0.40)
	Int.	0.35(0.58)	24.30(1.71)	0.29(0.54)	2.41(2.16)	29.37(7.48)	1.49(1.55)
MSE	Total	0.54(0.27)	0.97(0.36)	1.07(0.61)	3.99(2.83)	6.01(5.57)	6.08(3.45)
	Non-zero	0.49(0.21)	0.50(0.19)	1.00(0.56)	2.99(1.79)	2.29(1.64)	5.04(2.27)
	Zero	0.05(0.11)	0.47(0.23)	0.07(0.13)	1.00(1.44)	3.73(4.29)	1.04(1.92)
Pred. Error		1.51(0.11)	1.54(0.11)	1.55(0.11)	9.14(2.89)	9.51(3.16)	9.94(3.00)

3.1.6 Additional simulation results for fixed number of main effects

Web Table 44: Simulation results in Example 1 Error 1 with fixed number of main effects. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1 (N)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.92(0.27)	25.00(0.00)	24.75(0.46)	24.99(0.10)	25.00(0.00)	24.75(0.44)
	Main	4.00(0.00)	4.00(0.00)	3.99(0.10)	4.00(0.00)	4.00(0.00)	4.00(0.00)
	Int.	20.92(0.27)	21.00(0.00)	20.76(0.45)	20.99(0.10)	21.00(0.00)	20.75(0.44)
FP	Total	1.26(1.11)	29.84(2.09)	1.46(1.38)	0.71(0.80)	29.24(1.46)	0.54(0.63)
	Main	0.14(0.35)	5.14(0.35)	0.18(0.46)	0.06(0.24)	5.04(0.24)	0.05(0.22)
	Int.	1.12(1.07)	24.70(1.74)	1.28(1.22)	0.65(0.77)	24.20(1.21)	0.49(0.63)
MSE	Total	0.25(0.10)	0.51(0.14)	0.29(0.14)	0.18(0.06)	0.41(0.10)	0.21(0.10)
	Non-zero	0.21(0.08)	0.26(0.08)	0.24(0.11)	0.16(0.05)	0.21(0.06)	0.19(0.10)
	Zero	0.04(0.05)	0.25(0.11)	0.05(0.05)	0.02(0.02)	0.20(0.08)	0.02(0.02)
Pred. Error		0.85(0.04)	0.87(0.03)	0.86(0.04)	1.09(0.07)	1.16(0.08)	1.10(0.09)

Web Table 45: Simulation results in Example 1 Error 2 with fixed number of main effects. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	20.68(2.01)	24.86(0.51)	17.46(2.15)	18.89(2.22)	24.43(1.05)	14.20(2.00)
	Main	3.41(0.77)	3.98(0.14)	2.89(0.86)	3.10(0.77)	3.90(0.30)	2.29(0.91)
	Int.	17.27(1.84)	20.88(0.46)	14.57(1.79)	15.79(2.07)	20.53(0.92)	11.91(1.80)
FP	Total	1.43(1.16)	31.42(4.48)	1.57(1.35)	1.88(1.53)	30.35(4.91)	1.08(1.19)
	Main	0.23(0.49)	5.40(0.75)	0.28(0.53)	0.28(0.51)	5.23(0.85)	0.17(0.38)
	Int.	1.20(0.99)	26.02(3.74)	1.29(1.17)	1.60(1.39)	25.12(4.10)	0.91(1.08)
MSE	Total	2.09(0.81)	2.66(0.91)	3.45(1.23)	3.12(1.07)	3.59(1.24)	5.22(1.57)
	Non-zero	1.84(0.72)	1.30(0.51)	3.04(1.05)	2.65(0.86)	1.83(0.64)	4.68(1.34)
	Zero	0.25(0.25)	1.36(0.69)	0.41(0.46)	0.47(0.48)	1.76(0.88)	0.54(0.66)
Pred. Error		2.19(0.10)	2.21(0.10)	2.30(0.11)	9.60(0.85)	9.64(0.88)	10.52(1.05)

Web Table 46: Simulation results in Example 1 Error 3 with fixed number of main effects. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3 (Mix.L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	21.34(1.96)	24.86(0.51)	17.96(2.12)	19.33(2.40)	24.38(0.96)	14.34(2.26)
	Main	3.42(0.68)	3.96(0.20)	2.89(0.83)	3.06(0.74)	3.89(0.31)	2.25(0.97)
	Int.	17.92(1.67)	20.90(0.39)	15.07(1.87)	16.27(2.08)	20.49(0.83)	12.09(1.94)
FP	Total	1.56(1.34)	31.96(5.24)	1.66(1.56)	2.25(1.46)	30.76(5.22)	1.24(1.22)
	Main	0.25(0.48)	5.51(0.86)	0.27(0.57)	0.40(0.62)	5.30(0.88)	0.17(0.40)
	Int.	1.31(1.24)	26.45(4.39)	1.39(1.34)	1.85(1.34)	25.46(4.39)	1.07(1.14)
MSE	Total	2.06(0.87)	3.03(1.03)	3.48(1.29)	3.44(1.26)	4.32(1.26)	6.10(1.88)
	Non-zero	1.75(0.74)	1.44(0.50)	3.03(1.06)	2.81(1.04)	2.14(0.67)	5.39(1.55)
	Zero	0.31(0.31)	1.59(0.80)	0.45(0.52)	0.63(0.53)	2.17(1.00)	0.71(0.86)
Pred. Error		2.30(0.12)	2.35(0.12)	2.40(0.12)	10.87(1.18)	11.08(1.17)	12.00(1.33)

Web Table 47: Simulation results in Example 1 Error 4 with fixed number of main effects. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4 (t2)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	23.61(1.50)	24.96(0.28)	21.69(1.91)	18.17(5.02)	23.33(4.08)	14.14(4.77)
	Main	3.83(0.43)	3.99(0.10)	3.51(0.70)	2.79(1.09)	3.68(0.76)	2.12(1.17)
	Int.	19.78(1.35)	20.97(0.22)	18.18(1.71)	15.38(4.15)	19.65(3.42)	12.02(3.91)
FP	Total	0.69(0.80)	29.16(1.32)	0.46(0.69)	3.25(3.45)	36.19(13.55)	1.91(2.41)
	Main	0.15(0.39)	5.03(0.22)	0.12(0.38)	0.43(0.62)	6.24(2.30)	0.19(0.46)
	Int.	0.54(0.73)	24.13(1.12)	0.34(0.61)	2.82(3.38)	29.95(11.28)	1.72(2.33)
MSE	Total	0.53(0.28)	0.87(0.30)	0.90(0.42)	5.52(11.85)	11.81(36.01)	6.65(10.01)
	Non-zero	0.48(0.26)	0.44(0.15)	0.84(0.39)	3.31(4.34)	3.03(5.32)	4.86(4.52)
	Zero	0.05(0.08)	0.43(0.19)	0.06(0.11)	2.21(8.93)	8.79(31.71)	1.78(6.74)
Pred. Error		1.47(0.13)	1.50(0.13)	1.51(0.14)	12.15(16.59)	12.63(16.73)	12.80(16.50)

Web Table 48: Simulation results in Example 1 Error 5 with fixed number of main effects. $(n, q, k, p) = (500,\ 3,\ 5,\ 100)$. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5 (logNor)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.17(0.87)	24.94(0.34)	22.74(1.45)	19.96(2.69)	24.45(1.22)	16.39(3.03)
	Main	3.89(0.31)	3.98(0.14)	3.69(0.58)	3.28(0.78)	3.89(0.37)	2.63(0.95)
	Int.	20.28(0.83)	20.96(0.24)	19.05(1.31)	16.68(2.41)	20.56(0.97)	13.76(2.66)
FP	Total	0.37(0.60)	28.94(0.92)	0.36(0.56)	2.26(2.95)	35.73(13.62)	1.61(2.69)
	Main	0.11(0.35)	5.00(0.14)	0.10(0.33)	0.29(0.56)	6.14(2.24)	0.14(0.40)
	Int.	0.26(0.50)	23.94(0.81)	0.26(0.48)	1.97(2.96)	29.59(11.40)	1.47(2.68)
MSE	Total	0.27(0.13)	0.50(0.15)	0.45(0.21)	1.94(1.73)	2.84(2.69)	2.93(2.02)
	Non-zero	0.25(0.12)	0.27(0.10)	0.42(0.20)	1.44(0.91)	1.14(0.63)	2.43(1.40)
	Zero	0.02(0.04)	0.23(0.08)	0.03(0.05)	0.50(1.14)	1.71(2.22)	0.50(1.04)
Pred. Error		1.17(0.08)	1.19(0.08)	1.19(0.09)	5.52(1.90)	5.83(2.11)	5.93(2.05)

3.2 Simulation results for bayesQR

Web Table 49: Simulation results for comparing with bayesQR. (n, q, k, p) = (500, 3, 5, 50). The quantile of bayesQR is set to 0.5. mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 50 replicates under the setting of Example 1.

Error 2 (L)		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS	bayesQR
TP	Total	24.23(1.01)	25.00(0.00)	22.77(1.50)	23.40(1.52)	25.00(0.00)	19.40(1.67)	17.83(2.07)
	Main	4.07(1.20)	4.17(1.21)	3.80(1.24)	3.77(1.43)	4.17(1.21)	3.20(1.35)	3.07(1.51)
	Int.	20.17(1.42)	20.83(1.21)	18.97(1.85)	19.63(1.54)	20.83(1.21)	16.20(1.54)	14.77(1.92)
FP	Total	2.67(1.54)	30.60(3.12)	1.60(1.22)	3.70(1.74)	30.00(2.27)	1.27(1.05)	2.00(1.34)
	Main	0.57(0.68)	5.10(1.32)	0.23(0.43)	0.70(0.88)	5.00(1.31)	0.27(0.58)	0.37(0.49)
	Int.	2.10(1.27)	25.50(2.85)	1.37(1.22)	3.00(1.66)	25.00(2.10)	1.00(0.87)	1.63(1.13)
MSE	Total	1.53(0.68)	2.55(0.79)	2.16(0.97)	2.66(1.07)	3.64(1.02)	4.58(1.42)	5.46(1.99)
	Non-zero	1.22(0.56)	1.31(0.47)	1.84(0.83)	2.04(0.93)	1.91(0.70)	4.08(1.32)	5.24(1.93)
	Zero	0.32(0.24)	1.24(0.50)	0.32(0.34)	0.62(0.38)	1.73(0.68)	0.50(0.47)	0.22(0.28)
Pred. Error		2.14(0.11)	2.18(0.10)	2.18(0.13)	9.17(0.83)	9.40(0.83)	9.84(0.92)	2.45(0.16)

3.3 Estimation results for data analysis (inclusion probability)

Web Table 50: Analysis of the NHS T2D data using RBSG-SS (inclusion probability).

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs10741150	DOCK1		0.784				
rs10765059	TCERG1L	0.606					0.648
rs10786611	RF00019	0.924	0.604		0.669		
rs10884466	RNA5SP326	0.827		0.780			
rs10885423	NRG3				0.597		
rs10886442	GRK5		0.787				
rs11196539	NRG3				0.631		0.690
rs11198590	CACUL1	0.795				0.650	0.669
rs11259039	FRMD4A	0.976					
rs1194657	THAP12P3				0.668		
rs1219508	RPS15AP5	0.948					
rs12265854	SLC16A12	0.668					
rs12414552	TCERG1L	0.822		0.578	0.625		0.653
rs12767723	SLC25A18P1	0.980				0.768	
rs12772559	TACR2				0.571	0.530	
rs12774333	LRMDA	0.616					
rs12775160	FOXI2	0.878	0.573				0.708
rs16916794	SLC39A12	0.905	0.768	0.615			
rs16920092	PLXDC2						0.616
rs17094114	GFRA1	0.725					
rs2492664	OR6L1P	0.715			0.621		
rs2784767	PLAC9	0.682					
rs2814322	GRID1				0.667		
rs3740063	ABCC2				0.583		
rs3763722	LARP4B	0.634	0.759				0.793
rs4411238	PRKG1	0.680					
rs4578341	CHST15		0.610			0.579	
rs4747517	ITIH5		0.747			0.545	
rs4749926	IL2RA	0.736	0.541				
rs4917817	PYROXD2	0.879		0.627			
rs4918904	XRCC6P1					0.549	
rs6482836	DOCK1	0.892		0.564			
rs7070789	GPAM				0.896		0.696
rs7072255	ANTXRLP1		0.623				
rs7077721	SNRPD2P1	0.847		0.595			
rs7896554	NACAP2	0.912		0.791	0.641		
rs7897847	LGI1						0.596
rs870753	CFAP58				0.622		
rs881726	GFRA1						0.567

∗ Genes that SNPs belong to or are the closest to.

Web Table 51: Analysis of the NHS T2D data using RBL-SS (inclusion probability).

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs1041168	PLPP4	0.638					
rs10741150	DOCK1		0.690				
rs10786611	RF00019	0.895					
rs10794069	ADAM12	0.621					
rs10824802	MBL2	0.520					
rs10884466	RNA5SP326	0.767		0.591			
rs10885423	NRG3				0.572		
rs10886047	MIR3663HG						0.515
rs10886442	GRK5		0.749				
rs10998780	ATP5MC1P7				0.523		
rs11003665	RNA5SP318		0.520				
rs11013740	KIAA1217						0.547
rs11196539	NRG3						0.672
rs11198590	CACUL1	0.625					
rs11202221	BMPR1A				0.560		
rs11259039	FRMD4A	0.964					
rs11595123	AKR1E2			0.603			
rs11813505	KIAA1217					0.527	
rs1194657	THAP12P3				0.664		
rs1219508	RPS15AP5	0.920					
rs12265854	SLC16A12	0.693					
rs12269237	RF00017					0.534	
rs12414552	TCERG1L	0.709					
rs12414627	PNLIPRP1				0.554		
rs12767723	SLC25A18P1	0.971					
rs12772559	TACR2				0.519		
rs12774333	LRMDA	0.649					
rs12775160	FOXI2	0.828					
rs1573137	SORCS3				0.533		
rs16916794	SLC39A12	0.796	0.669				
rs16920092	PLXDC2						0.615
rs17094114	GFRA1	0.803					
rs2291314	PLPP4	0.536					
rs2420979	TACC2					0.551	
rs2492664	OR6L1P	0.674			0.518		
rs2664339	RNU6-543P	0.510					
rs2666236	IATPR					0.541	
rs2784767	PLAC9	0.705	0.53				
rs2814322	GRID1				0.659		
rs2842129	DYNC1I2P1	0.522					
rs2900814	SNRPD2P1	0.527					

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Web Table 51: Continued from the previous page.

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs3740063	ABCC2				0.579		
rs3763722	LARP4B						0.676
rs4411238	PRKG1	0.685					
rs4578341	CHST15		0.567			0.512	
rs4747009	LRRC20						0.566
rs4747517	ITIH5		0.621				
rs4749926	IL2RA	0.755					
rs4752432	PLPP4		0.526				
rs4917817	PYROXD2	0.859					
rs4934762	PCAT5	0.591					
rs6482836	DOCK1	0.876					
rs7070789	GPAM				0.875		
rs7072255	ANTXRLP1		0.655				
rs7077721	SNRPD2P1	0.758					
rs7894809	PCGF5	0.667					
rs7896554	NACAP2	0.837		0.625			
rs7897847	LGI1						0.575
rs7903853	FRMD4A		0.530				
rs7920351	TCERG1L			0.536			
rs881726	GFRA1						0.577
rs943213	DOCK1			0.541			

∗ Genes that SNPs belong to or are the closest to.

Web Table 52: Analysis of the NHS T2D data using BSG-SS.

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs1041168	PLPP4	0.777					
rs10765059	TCERG1L			0.569			
rs10786611	RF00019	0.594	0.532				
rs10829671	EBF3	0.674					
rs10884466	RNA5SP326	0.872		0.580			
rs10886442	GRK5		0.555				
rs10998780	ATP5MC1P7				0.617		
rs11017821	TCERG1L						0.633
rs11198590	CACUL1	0.584			0.549	0.528	
rs11200996	CCSER2					0.605	
rs11259039	FRMD4A	0.860					
rs1219508	RPS15AP5	0.673					
rs12265854	SLC16A12	0.757			0.671		
rs12269237	RF00017					0.587	
rs12414552	TCERG1L	0.551					

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Web Table 52: Continued from the previous page.

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs12764378	ARID5B	0.634					
rs12767723	SLC25A18P1	0.893				0.518	
rs12775160	FOXI2	0.728					0.541
rs1361709	PCDH15			0.570			
rs1395465	RN7SL63P	0.587					
rs16916794	SLC39A12	0.758	0.672	0.503			
rs16920092	PLXDC2						0.582
rs17094114	GFRA1	0.683					
rs17469499	KIAA1217					0.565	
rs2472737	RET	0.628					
rs2577356	GFRA1					0.561	
rs2784767	PLAC9	0.651	0.590				
rs2792708	GPAM	0.648					
rs2900814	SNRPD2P1	0.536					
rs2926458	RNU6-463P	0.618					
rs3763722	LARP4B		0.582				0.606
rs4411238	PRKG1	0.749					
rs4747517	ITIH5		0.838				
rs4752432	PLPP4		0.503				
rs4917817	PYROXD2	0.741		0.540			
rs4922535	GDF10			0.530		0.512	
rs4934762	PCAT5	0.589					
rs4934858	NRP1	0.585					
rs6482836	DOCK1	0.801					
rs7070789	GPAM				0.747		
rs7072255	ANTXRLP1		0.603				
rs7085788	RHOBTB1	0.706					
rs7086058	RN7SKP143	0.565					
rs716168	VTI1A		0.558				
rs7894809	PCGF5	0.599					
rs7895870	RN7SKP167		0.571				
rs7896554	NACAP2	0.946		0.517			
rs7917422	HTR7						0.684
rs881726	GFRA1						0.578

∗ Genes that SNPs belong to or are the closest to.

Web Table 53: Analysis of the NHS T2D data using BL-SS (inclusion probability).

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs1041168	PLPP4	0.894					
rs10508670	KIAA1217		0.553				
rs10765059	TCERG1L			0.623			
rs10829671	EBF3	0.805					
rs10884466	RNA5SP326	0.847					
rs10998780	ATP5MC1P7				0.523		
rs11017821	TCERG1L						0.615
rs11198590	CACUL1				0.588		
rs11200996	CCSER2					0.717	
rs11202221	BMPR1A				0.673		
rs11259039	FRMD4A	0.965					
rs11594070	ATE1-AS1				0.581		
rs1194657	THAP12P3				0.602		
rs12248205	CDH23				0.625		
rs12256982	ZMIZ1				0.625		
rs12265854	SLC16A12	0.688			0.68		
rs12269237	RF00017					0.672	
rs12412976	RPLP1P10			0.516	0.571		
rs12414552	TCERG1L	0.667					
rs12414627	PNLIPRP1				0.721		
rs12764378	ARID5B	0.665					
rs12767723	SLC25A18P1	0.919					
rs12775160	FOXI2	0.784					
rs1361709	PCDH15			0.539			
rs1395465	RN7SL63P	0.525					
rs1573137	SORCS3				0.583		
rs16916794	SLC39A12	0.52	0.809				
rs16920092	PLXDC2						0.518
rs17094114	GFRA1	0.662					
rs17469499	KIAA1217					0.525	
rs2384105	SNRPEP8						0.581
rs2420979	TACC2	0.511					
rs2472737	RET	0.566					
rs2577356	GFRA1					0.558	
rs2784767	PLAC9	0.62	0.644				
rs2792708	GPAM	0.864					
rs2900814	SNRPD2P1					0.525	
rs2926458	RNU6-463P	0.587					
rs3763722	LARP4B		0.605				0.874
rs4411238	PRKG1	0.517					
rs4747009	LRRC20						0.511

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Web Table 53: Continued from the previous page.

SNP	Gene*		chol	act	gl	ceraf	alcohol
rs4747517	ITIH5						0.511
rs4752432	PLPP4						0.799
rs4917817	PYROXD2	0.791		0.513			
rs4934762	PCAT5	0.642					
rs4934858	NRP1	0.588					
rs6482836	DOCK1	0.855					
rs7069001	WDFY4		0.577				
rs7070789	GPAM				0.959		0.537
rs7077718	DNMBP	0.501					
rs7085788	RHOBTB1	0.752					
rs7086058	RN7SKP143	0.549					
rs716168	VTI1A		0.553				
rs7894809	PCGF5	0.58					
rs7895870	RN7SKP167		0.795				
rs7896554	NACAP2	0.988					
rs7917422	HTR7				0.631		0.921
rs7920351	TCERG1L				0.515		
rs809836	LYZL1				0.765		
rs881726	GFRA1						0.518
rs915216	DUSP5		0.591				

∗ Genes that SNPs belong to or are the closest to.

Web Table 54: Analysis of the TCGA SKCM data using RBSG-SS (inclusion probability).

Gene		clark	stage	age	gender
AHNAKRS	0.602				
ANKRD28	0.608		0.585		
ASH2L		0.608			
BTD		0.684			
C1ORF140	0.567	0.809	0.657	0.580	0.698
CD44					0.508
CHP1	0.717	0.595			
CXCL6	0.692	0.618	0.568		
DLG6	0.740	0.700	0.667	0.981	0.769
DOK5				0.577	
ETNK2	0.745				
FILIP1	0.626				
JADE1	0.683				
JPH4		0.617			
KBF2	0.794	0.588		0.555	0.545
LRRN2	0.570				
MAGED4	0.727		0.587		
NHSL2	0.633				
PITPNA	0.887	0.616	0.616	0.623	0.628
SOX8	0.640		0.759		
TMEM145					0.621
TMEM159	0.831	0.589	0.584		0.617
WBSCR27		0.642		0.698	

Web Table 55: Analysis of the TCGA SKCM data using RBL-SS (inclusion probability).

Gene		clark	stage	age	gender
AHNAKRS	0.511				
ANKRD28	0.753		0.623		
ASH2L		0.513			
BAIAP2	0.515				
BTD		0.718		0.577	
C1ORF140		0.718			
C1ORF54					0.512
CHP1	0.590				0.520
CPXM1				0.516	
CSNK2A2	0.529				
CYP1B1-AS1			0.519		
DAP	0.517			0.528	
DLG6				0.930	
ETNK2	0.769				

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Web Table 55: Continued from the previous page.

Gene		clark	stage	age	gender
FHL5		0.531			
FILIP1			0.561		
GAMT				0.565	
IL11RA	0.536				
IQCK					0.508
JADE1	0.908				
JPH4		0.587			
KDM6B			0.535		
LRFN2		0.553			
MAGED4	0.654				
MAPE					0.574
MPD1	0.631				
NHSL2	0.581	0.535			
PAX1	0.597		0.599		
PBX2	0.769			0.526	
PITPNA	0.874			0.521	
RNPEPL1			0.564		
SLC12A5					0.518
SOX8	0.774		0.531		
STPG1			0.507		
TMEM145					0.894
TMEM159	0.675				
TNFAIP1				0.515	
TP53TG1		0.580			0.667
WBSCR27		0.593		0.553	

Web Table 56: Analysis of the TCGA SKCM data using BSG-SS (inclusion probability).

Gene		clark	stage	age	gender
AHNAKRS	0.605				
ANKRD28	0.571				
ARMC9	0.571				
ASH2L	0.532	0.533		0.543	
BTD		0.747		0.537	
C14ORF2		0.539			
C1ORF140		0.807	0.585		0.578
CD44					0.527
CHP1	0.601				
CPXM1	0.579				
CXCL6	0.555				
DLG6		0.567		0.913	0.561

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Web Table 56: Continued from the previous page.

Gene		clark	stage	age	gender
DOK5			0.538		
ETNK2	0.689				
FILIP1	0.644				
GAMT		0.546			
IL11RA	0.536				
JADE1	0.709				
JPH4		0.769			
KBF2	0.838				
LRRN2	0.610				
MAGED4	0.678				
MAPE					0.541
NHSL2	0.702				
PBX2	0.537			0.525	
PHP1B	0.560				
PITPNA	0.973	0.565		0.560	0.563
SOX8	0.671		0.696		
STPG1			0.542		
TMEM145	0.623	0.524			0.690
TMEM159	0.830				0.559
TNFRSF4		0.527			
TP53TG1		0.543			
WBSCR27		0.603		0.679	
ZFP62	0.538				

Web Table 57: Analysis of the TCGA SKCM data using BL-SS (inclusion probability).

Gene		clark	stage	age	gender
AHNAKRS	0.554				
ANKRD28	0.854		0.584		
ASH2L				0.551	
BTD				0.551	
C14ORF2		0.542			
C1ORF140		0.724			
CELSR2			0.550		
CHP1	0.562				
CPXM1	0.552				
CSNK2A2	0.560				
CYP1B1-AS1			0.562		
DAP				0.553	
DLG6	0.557			0.984	
ETNK2	0.844				0.556

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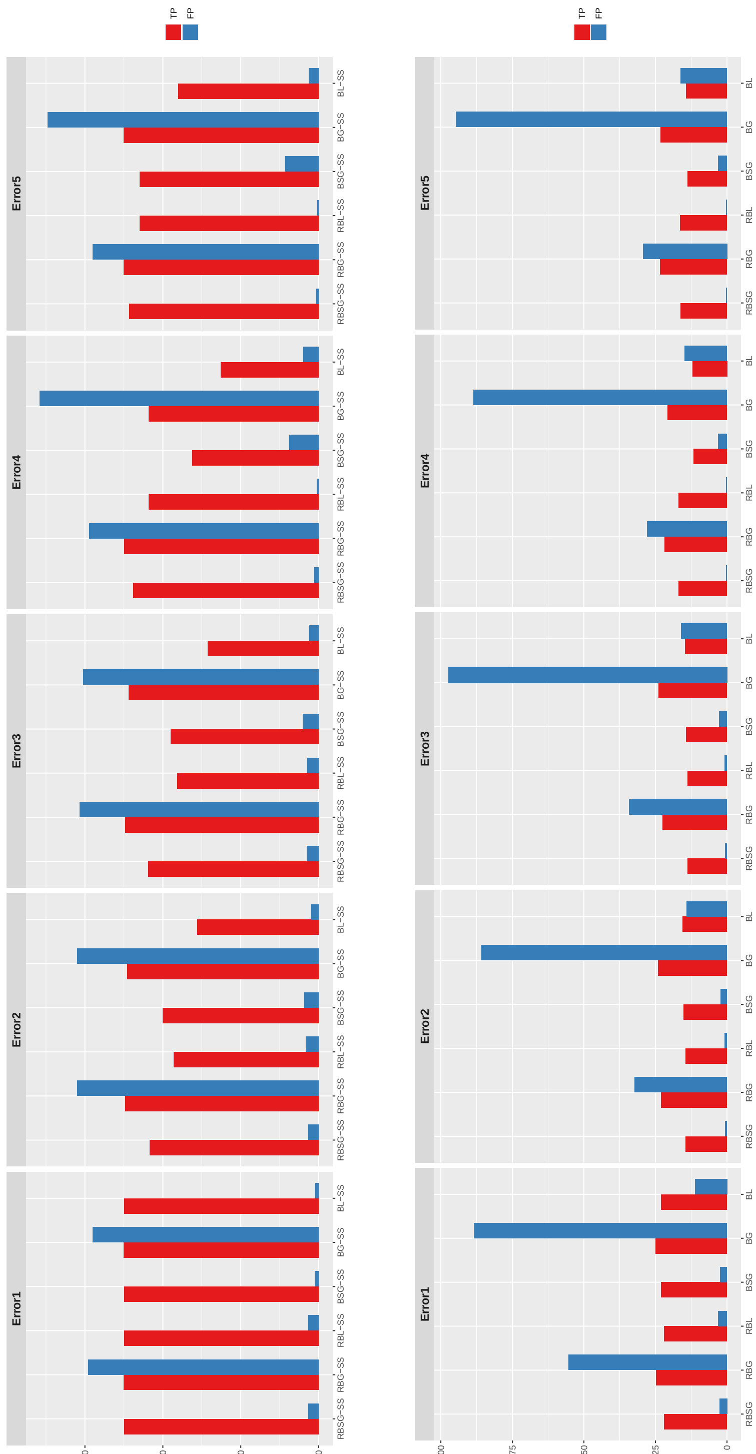
Web Table 57: Continued from the previous page.

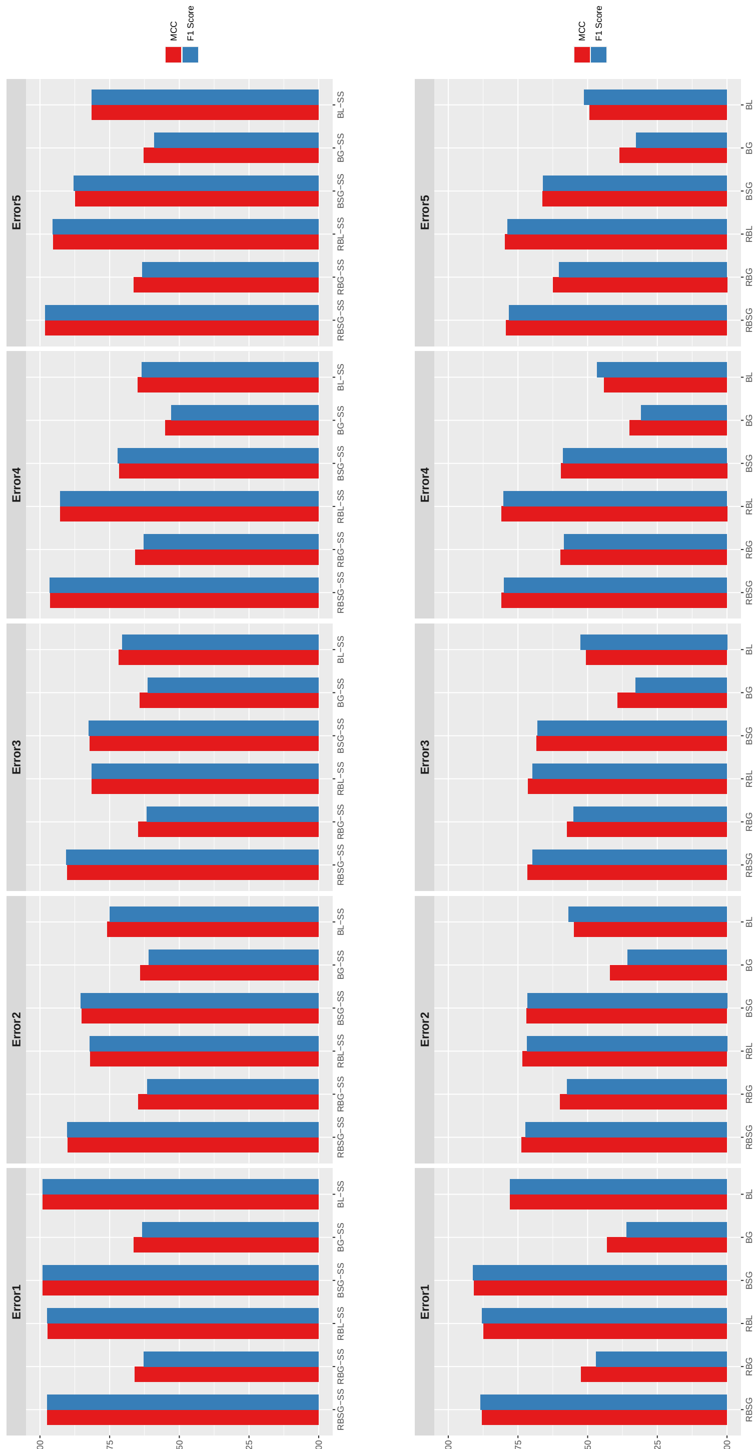
Gene		clark	stage	age	gender
FHL5		0.538			
FILIP1			0.576		
GAMT				0.581	
IL11RA	0.574				
IQCK					0.551
JADE1	0.933				
JPH4		0.638			
KBF2	0.536				
KDM6B			0.548		
LRFN2		0.570			
LRRN2	0.568				
MAGED4	0.618				
MAPE					0.595
MPD1	0.645				
NHSL2	0.555				
PAX1			0.556		
PBX2	0.708			0.557	
PHP1B					0.561
PIP4K2C			0.552		
PITPNA	0.990				
PTP4A3			0.548		
RNPEPL1			0.555		
SAA2	0.567			0.586	
SLC12A5					0.577
SOX8	0.873		0.560		
TIE1	0.543				
TMEM145					0.908
TMEM159	0.856				0.557
TP53TG1		0.577			0.575
WBSCR27		0.555		0.632	

4 Web Appendix D

4.1 The graphical representation for identification performance



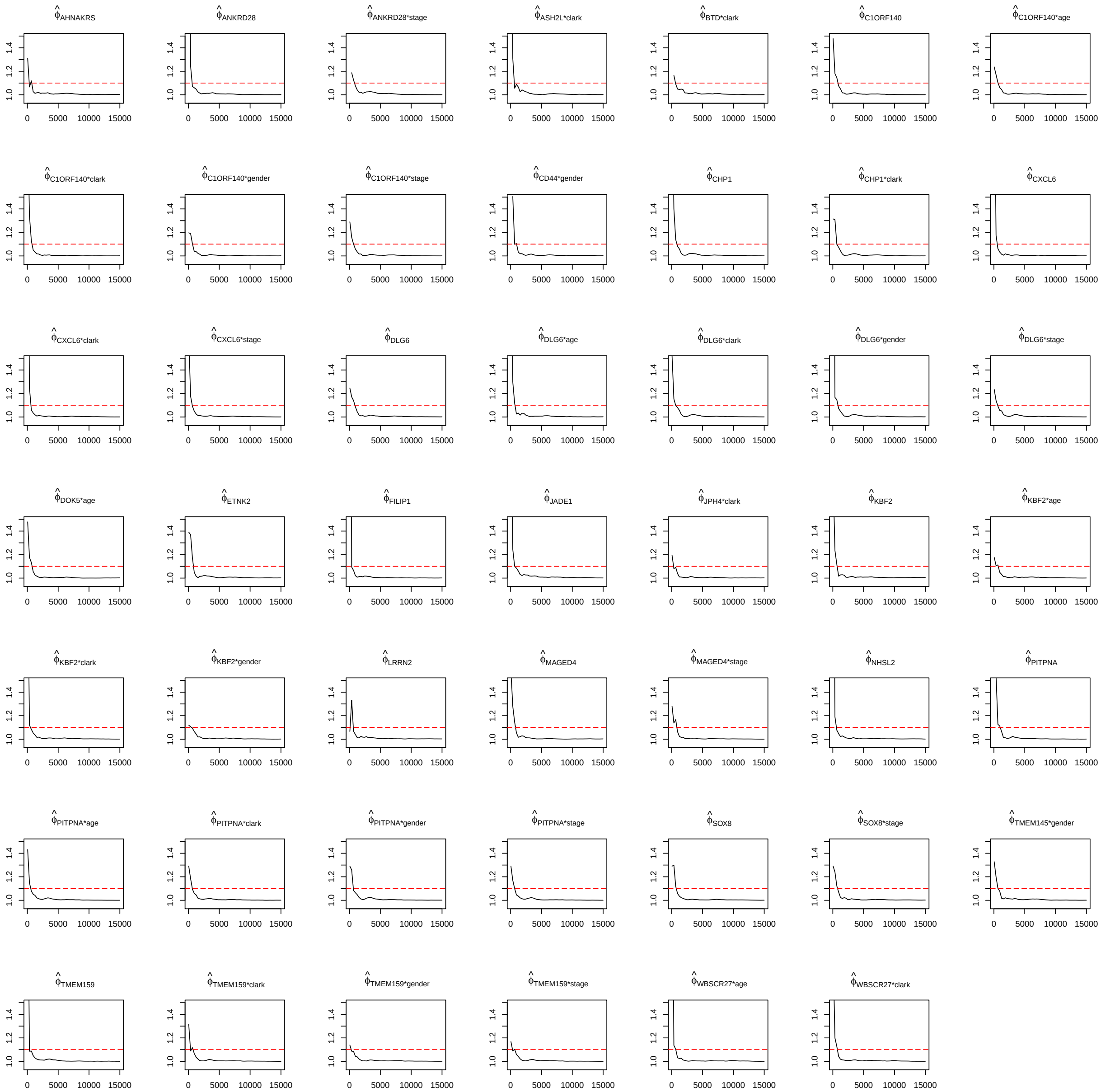
Web Figure 4: TP and FP for Table 1 (left) and Table 2 (right).



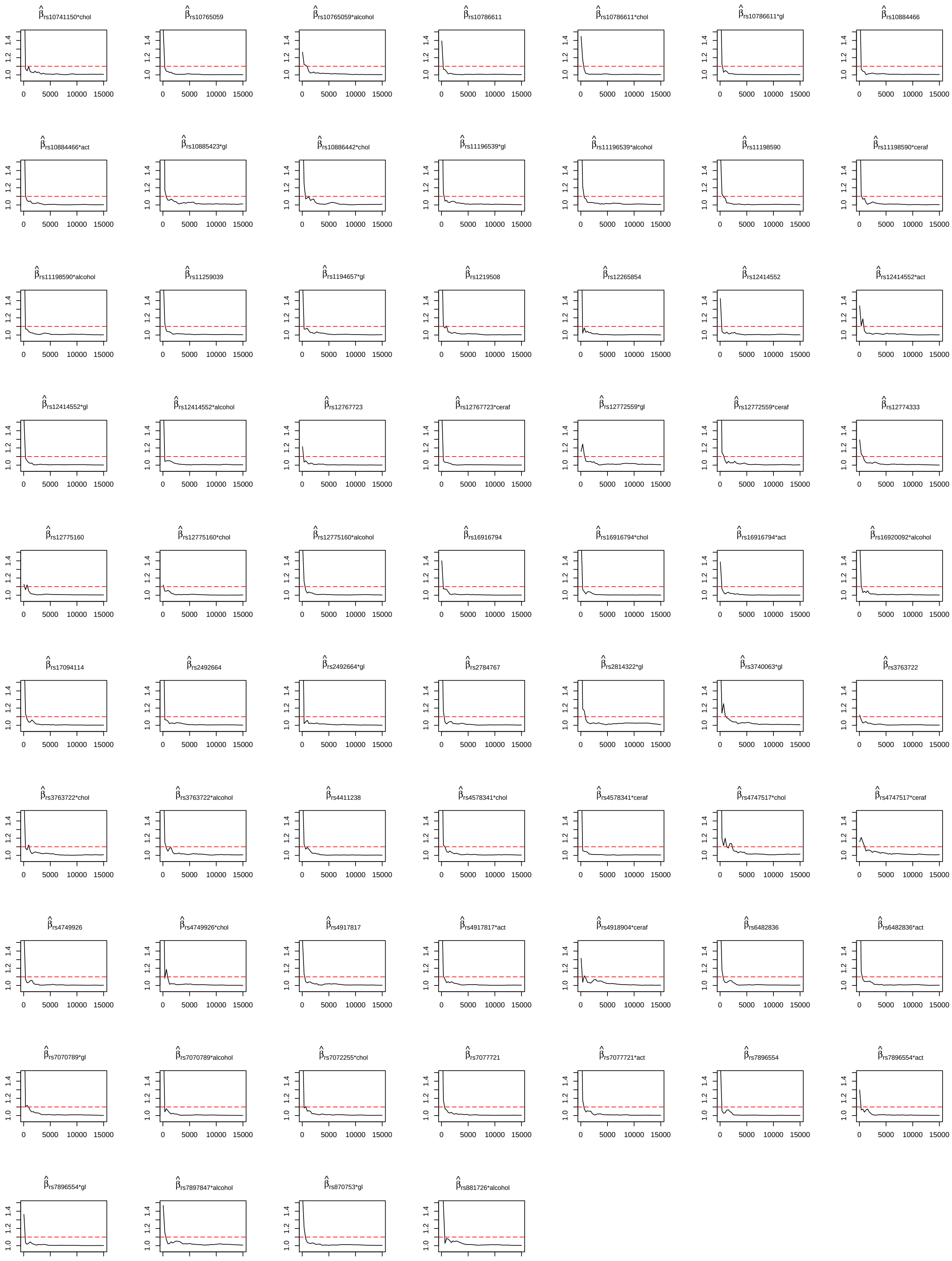
Web Figure 5: MCC and F1 scores for Table 1 (left) and Table 2 (right).

4.2 Convergence of MCMC chains in case studies

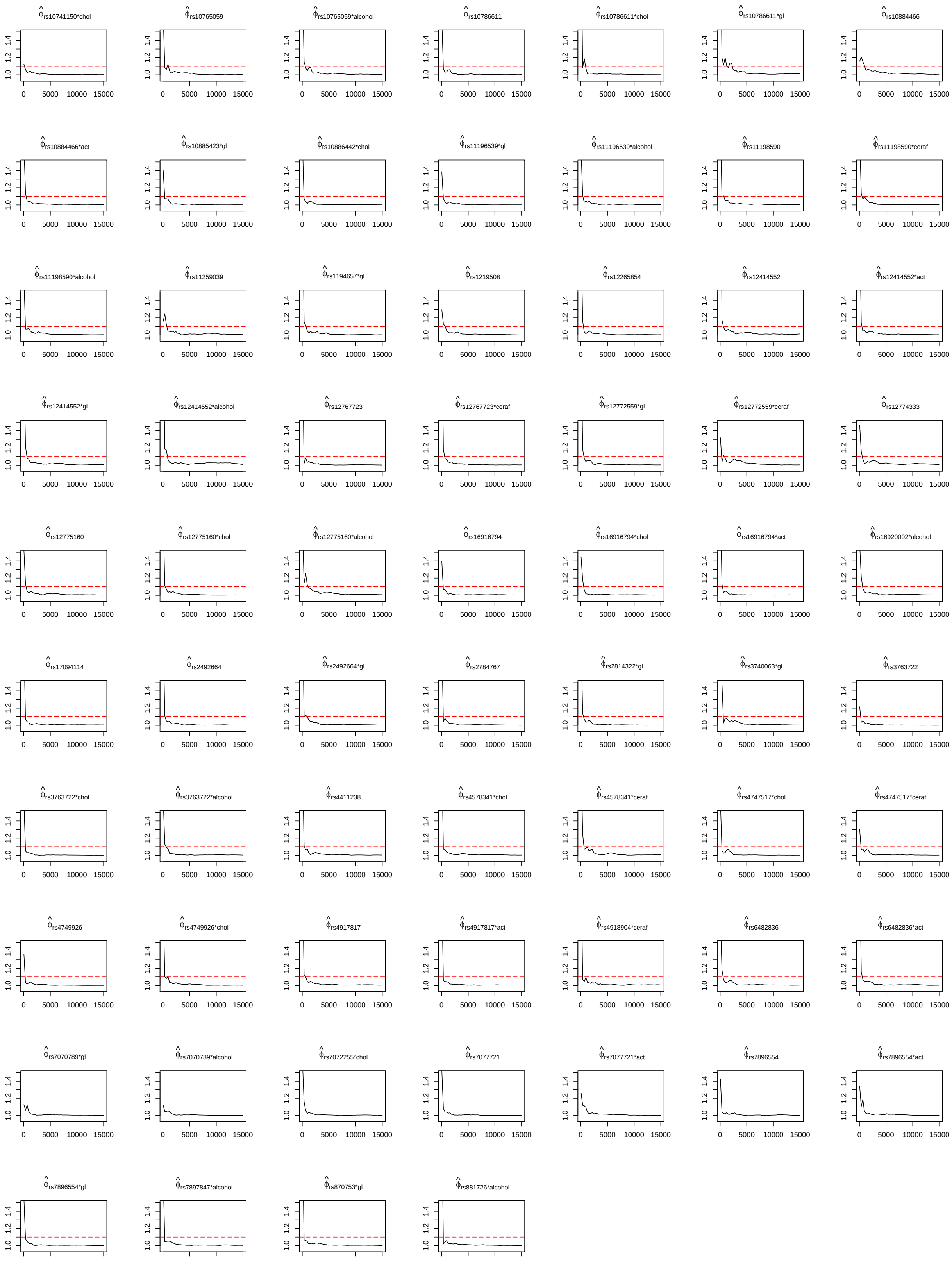
Web Figure 6: Potential scale reduction factor (PSRF) against iterations for effects $(\widehat{\beta})$ identified by RBSG-SS in TCGA SKCM data. Black line: the PSRF. Red line: the threshold of 1.1.



Web Figure 7: Potential scale reduction factor (PSRF) against iterations for indicators ($\widehat{\phi}$) corresponding to effects identified by RBSG-SS in TCGA SKCM data. Black line: the PSRF. Red line: the threshold of 1.1.



Web Figure 8: PSRF against iterations for effects $(\widehat{\beta})$ identified by RBSG-SS in NHS data. Black line: the PSRF. Red line: the threshold of 1.1.



Web Figure 9: PSRF against iterations for indicators ($\widehat{\phi}$) corresponding to effects identified by RBSG-SS in NHS data. Black line: the PSRF. Red line: the threshold of 1.1.

4.3 Comparison between Bayesian and frequentist methods

Additional simulations are conducted to compare the performance of the proposed method with existing frequentist methods. Three frequentist methods, Quantile Lasso (QL), quantile group Lasso (QGL) and sparse group Lasso (SGL) are evaluated using R packages rqPen (Sherwood and Maidman (2020)) and SGL (Simon et al. (2019)). For QL and QGL, the prediction error is defined as MAD. For SGL, the prediction error is defined as MSE. The results for Example 1 are given in Web Table 58 – 62. Under all error distributions, RBSG-SS shows better performance in both identification and prediction than the frequentist methods. Specifically, RBSG-SS has much lower FPs than the frequentist methods in identification. For prediction, RBSG-SS has lower PMADs compared to the two robust frequentist methods, QL and QGL. The same patterns have been observed for Examples 2, 3, and 4.

Web Table 58: Simulation results in Example 1 (Error 1) with frequentist methods. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS	QL	QGL	SGL
TP	Total	24.92(0.27)	25.00(0.00)	24.71(0.57)	24.94(0.24)	25.00(0.00)	24.70(0.59)	24.97(0.17)	25.00(0.00)	24.59(0.62)
	Main	4.19(1.37)	4.20(1.37)	4.19(1.37)	4.19(1.37)	4.20(1.37)	4.16(1.43)	4.20(1.37)	4.20(1.37)	4.19(1.38)
	Int.	20.73(1.41)	20.80(1.37)	20.52(1.45)	20.75(1.41)	20.80(1.37)	20.54(1.49)	20.77(1.38)	20.80(1.37)	20.40(1.41)
FP	Total	1.24(1.27)	30.44(2.84)	1.50(1.45)	0.60(0.97)	29.42(1.76)	0.64(0.79)	83.84(29.63)	62.06(16.98)	7.63(6.02)
	Main	0.24(0.45)	5.04(1.50)	0.33(0.53)	0.06(0.24)	4.87(1.41)	0.11(0.31)	14.98(6.40)	9.98(3.89)	1.05(1.21)
	Int.	1.00(1.14)	25.40(2.59)	1.17(1.35)	0.54(0.89)	24.55(1.97)	0.53(0.72)	68.86(24.31)	52.08(14.53)	6.58(5.21)
MSE	Total	0.26(0.12)	0.50(0.15)	0.30(0.16)	0.20(0.09)	0.41(0.11)	0.24(0.16)	0.55(0.16)	0.43(0.14)	1.03(0.36)
	Non-zero	0.21(0.08)	0.25(0.07)	0.25(0.13)	0.17(0.07)	0.21(0.07)	0.21(0.15)	0.37(0.12)	0.23(0.10)	1.01(0.36)
	Zero	0.05(0.06)	0.25(0.10)	0.05(0.06)	0.02(0.04)	0.19(0.08)	0.02(0.03)	0.18(0.10)	0.20(0.08)	0.02(0.02)
Pred. Error		0.84(0.03)	0.87(0.03)	0.86(0.04)	1.09(0.08)	1.16(0.09)	1.11(0.09)	0.92(0.04)	0.87(0.03)	1.82(0.34)

Web Table 59: Simulation results in Example 1 (Error 2) with frequentist methods. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS	QL	QGL	SGL
TP	Total	20.45(2.21)	24.68(0.84)	16.73(2.51)	18.38(2.71)	24.04(1.58)	13.06(2.31)	23.24(1.49)	24.71(0.84)	22.95(1.49)
	Main	3.35(1.33)	4.30(1.41)	2.89(1.36)	3.19(1.38)	4.19(1.40)	2.24(1.34)	3.88(1.43)	4.28(1.41)	4.09(1.39)
	Int.	17.10(2.55)	20.38(1.63)	13.84(2.43)	15.19(2.56)	19.85(1.87)	10.82(2.32)	19.36(1.87)	20.43(1.63)	18.86(1.93)
FP	Total	1.27(1.12)	30.40(4.44)	1.53(1.33)	1.63(1.52)	30.02(4.84)	0.75(0.90)	79.09(23.82)	69.04(18.11)	65.13(17.33)
	Main	0.20(0.43)	4.88(1.60)	0.25(0.48)	0.28(0.51)	4.82(1.59)	0.05(0.26)	13.84(5.04)	11.43(4.10)	14.45(5.08)
	Int.	1.07(0.95)	25.52(3.95)	1.28(1.11)	1.35(1.30)	25.20(4.26)	0.70(0.86)	65.25(19.98)	57.61(15.04)	50.68(13.54)
MSE	Total	2.23(0.98)	2.66(0.93)	3.60(1.32)	3.23(1.14)	3.86(1.16)	5.34(1.60)	2.35(0.62)	2.01(0.58)	2.38(0.51)
	Non-zero	1.95(0.81)	1.34(0.54)	3.19(1.07)	2.77(0.90)	1.94(0.68)	4.92(1.27)	1.63(0.53)	0.95(0.38)	1.92(0.47)
	Zero	0.28(0.34)	1.32(0.63)	0.41(0.48)	0.46(0.50)	1.91(0.79)	0.42(0.62)	0.72(0.34)	1.05(0.39)	0.46(0.18)
Pred. Error		2.20(0.11)	2.22(0.11)	2.29(0.11)	9.44(0.93)	9.57(1.00)	10.50(1.06)	2.29(0.12)	2.21(0.10)	9.79(0.96)

Web Table 60: Simulation results in Example 1 (Error 3) with frequentist methods. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS	QL	QGL	SGL
TP	Total	21.07(2.01)	24.62(0.84)	17.15(2.28)	18.17(2.78)	24.12(1.34)	13.34(2.76)	23.64(1.08)	24.85(0.56)	22.65(1.45)
	Main	3.45(1.46)	3.95(1.45)	2.81(1.38)	2.93(1.43)	3.83(1.40)	2.02(1.26)	3.76(1.48)	3.99(1.51)	3.81(1.44)
	Int.	17.62(1.98)	20.67(1.56)	14.34(2.22)	15.24(2.45)	20.29(1.79)	11.32(2.38)	19.88(1.66)	20.86(1.50)	18.84(1.78)
FP	Total	1.25(1.10)	29.98(3.67)	1.33(1.24)	1.29(1.31)	29.70(4.85)	0.85(0.97)	76.92(25.32)	65.91(21.31)	62.39(18.26)
	Main	0.28(0.51)	5.15(1.57)	0.26(0.52)	0.22(0.44)	5.14(1.74)	0.11(0.35)	13.45(5.43)	11.21(4.37)	14.14(5.08)
	Int.	0.97(0.98)	24.83(3.35)	1.07(1.04)	1.07(1.18)	24.56(4.00)	0.74(0.82)	63.47(21.16)	54.70(17.67)	48.25(14.26)
MSE	Total	2.13(1.03)	2.80(1.05)	3.72(1.71)	3.52(1.77)	4.22(1.50)	5.84(2.09)	2.38(0.64)	2.00(0.62)	2.63(0.59)
	Non-zero	1.83(0.78)	1.42(0.58)	3.27(1.25)	3.04(1.27)	2.05(0.79)	5.27(1.55)	1.60(0.45)	0.93(0.34)	2.15(0.56)
	Zero	0.30(0.41)	1.38(0.67)	0.45(0.73)	0.49(0.75)	2.17(1.14)	0.57(0.88)	0.78(0.40)	1.08(0.45)	0.48(0.20)
Pred. Error		2.29(0.12)	2.33(0.12)	2.41(0.14)	11.06(1.34)	11.10(1.23)	12.14(1.39)	2.42(0.12)	2.31(0.11)	11.43(1.27)

Web Table 61: Simulation results in Example 1 (Error 4) with frequentist methods. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS	QL	QGL	SGL
TP	Total	23.86(1.10)	24.96(0.28)	21.70(1.89)	17.38(4.51)	23.50(2.58)	13.39(4.43)	24.72(0.51)	24.99(0.10)	22.31(2.18)
	Main	4.17(1.41)	4.33(1.43)	3.85(1.40)	2.94(1.50)	4.11(1.41)	2.19(1.45)	4.28(1.44)	4.34(1.42)	4.02(1.43)
	Int.	19.69(1.68)	20.63(1.48)	17.85(1.99)	14.44(3.67)	19.39(2.44)	11.20(3.59)	20.44(1.40)	20.65(1.45)	18.29(2.24)
FP	Total	0.59(0.75)	29.16(1.32)	0.39(0.74)	3.44(4.17)	37.28(17.45)	1.88(2.19)	82.71(25.88)	64.00(20.32)	57.80(18.83)
	Main	0.14(0.38)	4.69(1.48)	0.11(0.35)	0.44(0.76)	6.02(3.16)	0.17(0.45)	14.78(5.79)	10.66(4.00)	13.00(5.57)
	Int.	0.45(0.66)	24.47(1.70)	0.28(0.60)	3.000(3.89)	31.26(14.63)	1.71(2.04)	67.93(21.39)	53.34(17.31)	44.80(14.85)
MSE	Total	0.46(0.23)	0.85(0.24)	0.88(0.50)	4.31(4.24)	5.78(6.98)	5.45(3.95)	0.92(0.28)	0.68(0.20)	2.31(1.14)
	Non-zero	0.42(0.21)	0.44(0.16)	0.83(0.47)	2.90(2.24)	2.14(2.08)	4.34(2.59)	0.63(0.24)	0.35(0.14)	1.79(0.81)
	Zero	0.04(0.07)	0.42(0.14)	0.04(0.09)	1.41(2.63)	3.64(5.46)	1.10(2.07)	0.29(0.13)	0.33(0.11)	0.51(0.46)
Pred. Error		1.47(0.13)	1.50(0.12)	1.51(0.13)	13.33(12.38)	13.55(12.58)	13.80(12.21)	1.58(0.13)	1.49(0.12)	12.81(12.26)

Web Table 62: Simulation results in Example 1 (Error 5) with frequentist methods. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS	QL	QGL	SGL
TP	Total	24.05(1.04)	24.96(0.28)	22.33(1.59)	19.83(3.21)	24.54(1.10)	16.14(3.54)	24.87(0.34)	25.00(0.00)	23.20(1.44)
	Main	3.99(1.37)	4.10(1.35)	3.79(1.41)	3.39(1.43)	4.06(1.37)	2.85(1.46)	4.08(1.35)	4.10(1.36)	3.93(1.36)
	Int.	20.06(1.63)	20.86(1.39)	18.54(1.98)	16.43(3.13)	20.48(1.69)	13.29(3.24)	20.79(1.34)	20.89(1.36)	19.27(1.76)
FP	Total	0.31(0.74)	29.10(1.19)	0.20(0.49)	1.64(2.24)	33.16(9.41)	1.07(1.93)	78.74(22.82)	60.26(14.99)	53.46(22.10)
	Main	0.03(0.17)	4.91(1.39)	0.05(0.22)	0.21(0.44)	5.56(2.13)	0.11(0.32)	13.56(5.11)	9.96(3.11)	11.66(5.56)
	Int.	0.28(0.67)	24.19(1.60)	0.15(0.44)	1.42(1.99)	27.61(7.91)	0.96(1.82)	65.18(19.11)	50.30(12.99)	41.80(17.68)
MSE	Total	0.27(0.14)	0.51(0.16)	0.47(0.26)	1.67(0.97)	2.40(1.43)	2.49(1.22)	0.57(0.18)	0.42(0.13)	1.48(0.47)
	Non-zero	0.26(0.13)	0.27(0.09)	0.46(0.26)	1.38(0.80)	1.04(0.55)	2.25(1.13)	0.40(0.14)	0.23(0.09)	1.24(0.38)
	Zero	0.01(0.04)	0.24(0.10)	0.01(0.04)	0.30(0.46)	1.36(1.09)	0.24(0.41)	0.17(0.08)	0.20(0.08)	0.24(0.16)
Pred. Error		1.17(0.08)	1.20(0.08)	1.19(0.08)	5.49(1.73)	5.67(1.74)	5.90(1.77)	1.25(0.09)	1.9(0.08)	5.82(1.71)

4.4 Additional simulation with both positive and negative effects

Web Table 63: Simulation results in Example 1 (Error 1) with both positive and negative effects. Non-zero effects are randomly selected to have negative signs with a probability of 0.5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 1		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.95(0.22)	25.00(0.00)	24.78(0.45)	24.95(0.22)	25.00(0.00)	24.80(0.44)
	Main	4.30(1.34)	4.30(1.34)	4.27(1.36)	4.30(1.34)	4.30(1.34)	4.30(1.34)
	Int.	20.65(1.36)	20.70(1.34)	20.52(1.41)	20.65(1.36)	20.70(1.34)	20.50(1.51)
FP	Total	1.30(1.25)	31.10(3.46)	1.60(1.50)	0.60(0.92)	29.70(2.24)	0.52(0.95)
	Main	0.23(0.53)	5.05(1.49)	0.33(0.57)	0.17(0.49)	4.82(1.35)	0.10(0.44)
	Int.	1.07(0.99)	26.05(3.12)	1.267(1.26)	0.433(0.65)	24.88(2.44)	0.42(0.74)
MSE	Total	0.25(0.10)	0.52(0.16)	0.28(0.14)	0.17(0.07)	0.39(0.12)	0.19(0.11)
	Non-zero	0.20(0.06)	0.25(0.07)	0.22(0.11)	0.15(0.06)	0.20(0.07)	0.17(0.09)
	Zero	0.05(0.05)	0.27(0.12)	0.06(0.06)	0.02(0.03)	0.19(0.08)	0.02(0.03)
Pred. Error		0.84(0.04)	0.87(0.04)	0.85(0.04)	1.07(0.08)	1.14(0.09)	1.08(0.08)

Web Table 64: Simulation results in Example 1 (Error 2) with both positive and negative effects. Non-zero effects are randomly selected to have negative signs with a probability of 0.5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 2		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	20.79(2.09)	24.86(0.51)	17.73(2.44)	18.91(2.42)	24.42(1.00)	14.06(1.98)
	Main	3.43(1.60)	4.18(1.60)	2.94(1.38)	3.12(1.45)	4.10(1.59)	2.24(1.31)
	Int.	17.36(2.21)	20.68(1.57)	14.79(2.38)	15.79(2.47)	20.32(1.63)	11.82(1.94)
FP	Total	1.57(1.23)	32.26(4.92)	1.64(1.37)	1.95(1.35)	30.66(4.59)	1.28(1.19)
	Main	0.30(0.50)	5.34(1.78)	0.29(0.52)	0.36(0.56)	5.08(1.78)	0.15(0.36)
	Int.	1.27(1.11)	26.92(4.41)	1.35(1.23)	1.59(1.17)	25.58(4.02)	1.13(1.12)
MSE	Total	2.06(0.93)	2.70(0.88)	3.26(1.28)	3.06(1.09)	3.59(1.12)	5.40(1.59)
	Non-zero	1.77(0.78)	1.28(0.45)	2.79(1.01)	2.55(0.93)	1.81(0.69)	4.67(1.21)
	Zero	0.29(0.31)	1.42(0.67)	0.47(0.48)	0.51(0.42)	1.79(0.79)	0.72(0.78)
Pred. Error		2.18(0.12)	2.22(0.12)	2.27(0.13)	9.53(1.01)	9.57(1.06)	10.43(1.12)

Web Table 65: Simulation results in Example 1 (Error 3) with both positive and negative effects. Non-zero effects are randomly selected to have negative signs with a probability of 0.5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 3		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	21.22(2.03)	24.90(0.44)	17.70(2.27)	18.27(2.82)	24.28(1.21)	13.18(2.59)
	Main	3.83(1.32)	4.53(1.25)	3.25(1.28)	3.30(1.25)	4.33(1.31)	2.33(1.47)
	Int.	17.38(2.24)	20.37(1.39)	14.45(2.30)	14.97(2.76)	19.95(1.59)	10.85(2.26)
FP	Total	1.33(1.34)	30.70(3.45)	1.18(1.20)	1.63(1.34)	29.82(4.36)	0.90(0.99)
	Main	0.20(0.48)	4.73(1.52)	0.13(0.43)	0.18(0.39)	4.68(1.36)	0.07(0.25)
	Int.	1.13(1.21)	25.97(2.84)	1.05(1.08)	1.45(1.36)	25.13(4.06)	0.83(0.96)
MSE	Total	2.02(0.90)	2.88(0.97)	3.43(1.23)	3.60(1.44)	4.15(1.21)	6.06(1.75)
	Non-zero	1.72(0.72)	1.37(0.52)	3.04(0.97)	3.06(1.21)	2.01(0.70)	5.38(1.37)
	Zero	0.30(0.36)	1.51(0.64)	0.39(0.61)	0.54(0.52)	2.14(0.84)	0.68(0.93)
Pred. Error		2.27(0.10)	2.31(0.09)	2.37(0.11)	10.75(1.07)	10.86(0.98)	11.84(1.32)

Web Table 66: Simulation results in Example 1 (Error 4) with both positive and negative effects. Non-zero effects are randomly selected to have negative signs with a probability of 0.5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 4		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	23.80(1.13)	24.97(0.26)	21.27(2.06)	17.70(5.37)	23.52(3.57)	13.28(4.82)
	Main	3.60(1.43)	4.17(1.378)	3.25(1.58)	2.72(1.81)	3.52(1.76)	2.03(1.74)
	Int.	20.20(1.88)	20.7931(1.47)	18.02(2.30)	14.98(4.46)	20.00(3.31)	11.25(3.82)
FP	Total	0.52(0.79)	29.10(0.78)	0.33(0.57)	3.20(3.63)	37.68(12.08)	2.08(2.04)
	Main	0.08(0.28)	5.18(1.61)	0.07(0.25)	0.30(0.67)	6.68(2.53)	0.15(0.36)
	Int.	0.43(0.67)	23.92(1.80)	0.27(0.55)	2.90(3.27)	31.00(10.26)	1.93(1.97)
MSE	Total	0.54(0.41)	0.86(0.30)	1.01(0.62)	4.71(7.84)	6.51(10.33)	5.68(6.10)
	Non-zero	0.49(0.39)	0.46(0.20)	0.96(0.59)	2.92(2.73)	2.17(2.58)	4.35(2.57)
	Zero	0.05(0.09)	0.40(0.17)	0.05(0.10)	1.78(5.59)	4.34(7.94)	1.33(4.09)
Pred. Error		1.47(0.10)	1.50(0.10)	1.53(0.10)	12.74(15.64)	14.85(29.01)	12.63(10.31)

Web Table 67: Simulation results in Example 1 (Error 5) with both positive and negative effects. Non-zero effects are randomly selected to have negative signs with a probability of 0.5. (n, q, k, p) = (500, 3, 5, 100). mean(sd) of true positives (TP), false positives (FP)and prediction errors (Pred) based on 100 replicates.

Error 5		RBSG-SS	RBG-SS	RBL-SS	BSG-SS	BG-SS	BL-SS
TP	Total	24.21(0.90)	25.00(0.00)	22.61(1.55)	20.36(2.59)	24.60(0.98)	16.69(3.00)
	Main	3.89(1.09)	4.04(1.10)	3.64(1.12)	3.24(1.16)	3.92(1.10)	2.58(1.22)
	Int.	20.32(1.46)	20.96(1.10)	18.98(1.79)	17.12(2.41)	20.68(1.35)	14.11(2.61)
FP	Total	0.31(0.59)	29.00(0.00)	0.23(0.48)	2.23(2.21)	33.60(8.20)	1.30(1.47)
	Main	0.09(0.28)	4.96(1.10)	0.06(0.24)	0.29(0.62)	5.78(1.69)	0.11(0.32)
	Int.	0.22(0.50)	24.04(1.10)	0.16(0.40)	1.94(1.91)	27.82(6.98)	1.19(1.40)
MSE	Total	0.29(0.15)	0.50(0.15)	0.46(0.26)	1.65(1.66)	2.31(2.60)	2.36(1.39)
	Non-zero	0.26(0.14)	0.26(0.09)	0.44(0.23)	1.20(0.71)	0.90(0.52)	2.02(1.11)
	Zero	0.03(0.05)	0.24(0.09)	0.02(0.06)	0.45(1.13)	1.42(2.19)	0.33(0.46)
Pred. Error		1.18(0.09)	1.21(0.09)	1.21(0.10)	5.57(2.54)	5.73(2.72)	5.87(2.54)

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