Bayesian iterative screening in ultra-high dimensional linear regressions

Run Wang*, Somak Dutta* and Vivekananda Roy*

Abstract. Variable selection in ultra-high dimensional linear regression is often preceded by a screening step to significantly reduce the dimension. Here we develop a Bayesian variable screening method (BITS) guided by the posterior model probabilities. BITS can successfully integrate prior knowledge, if any, on effect sizes, and the number of true variables. BITS iteratively includes potential variables with the highest posterior probability accounting for the already selected variables. It is implemented by a fast Cholesky update algorithm and is shown to have the screening consistency property. BITS is built based on a model with Gaussian errors, yet, the screening consistency is proved to hold under more general tail conditions. The notion of posterior screening consistency allows the resulting model to provide a good starting point for further Bayesian variable selection methods. A new screening consistent stopping rule based on posterior probability is developed. Simulation studies and real data examples are used to demonstrate scalability and fine screening performance.

Keywords: Forward regression, Large $p$ small $n$, Screening consistency, Spike and slab, Sure independent screening, Variable selection.

1. Introduction

These days, in diverse disciplines, data sets with hundreds of thousands of variables are commonly arising although only a very few of these variables are believed to be relevant for the response. Thus variable selection in linear regression has been a major topic of research over the last two decades in both frequentist and Bayesian statistics. A common approach to variable selection as well as coefficient estimation is by penalizing a loss function. These shrinkage methods include, but are not limited to, the ridge regression (Hoerl and Kennard, 1970), the popular Lasso (Tibshirani, 1996), the bridge regression (Huang et al., 2008), the SCAD (Fan and Li, 2001), the elastic net (Zou and Hastie, 2005), the Dantzig selector (Candes and Tao, 2007; Mazumder and Radchenko, 2017) and the adaptive Lasso (Zou, 2006).

Several Bayes and empirical Bayes penalized regression methods have been developed in the literature. See, for example, Park and Casella (2008), Kyung et al. (2010), and Roy and Chakraborty (2017). Another approach to Bayesian variable selection is using auxiliary indicator variables (1 indicating presence

*Department of Statistics, Iowa State University, USA

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and 0 indicating absence of the corresponding covariate in the model) to obtain a ‘spike and slab’ prior on the regression coefficients (see e.g. Mitchell and Beauchamp, 1988; George and McCulloch, 1993; Yuan and Lin, 2005; Ishwaran and Rao, 2005; Liang et al., 2008; Johnson and Rossell, 2012; Ročková and George, 2014; Narisetty and He, 2014; Castillo et al., 2015; Roy et al., 2018; Shin et al., 2018; Li et al., 2023b; Barbieri et al., 2021). Here the ‘spike’ corresponds to the probability mass concentrated at zero or around zero for the variables vulnerable to deletion and the ‘slab’ specifies prior uncertainty for coefficients of other variables. We will discuss one such model in details in Section 2.1. Analysis using such models determines (selects) the most promising variables by summarizing the posterior density of the indicator variables and/or the regression coefficients.

In the ultra-high dimensional settings where the number of variables (p) is much larger than the sample size (n), previously mentioned variable selection methods may not work and the computational cost for large-scale optimization or Markov chain Monte Carlo (MCMC) exploration (in the Bayesian methods) becomes too high to afford. This is why, in practice, a computationally inexpensive screening is performed before conducting a refined model selection analysis. Motivated by these, Fan and Lv (2008) proposed the sure independence screening (SIS) method where marginal Pearson correlations between the response and the variables are used to screen out unimportant variables, and thus rapidly reduce the dimension to a manageable size. The SIS method has been extended to generalized linear models (Fan and Song, 2010) and additive models (Fan et al., 2011) among others. Various other correlation measures as for example general correlation (Hall and Miller, 2009), distance correlation (Li et al., 2012b), rank correlation (Li et al., 2012a), tilted correlation (Cho and Fryzlewicz, 2012; Lin and Pang, 2014) and quantile partial correlation (Ma et al., 2017) have also been proposed to rank and screen variables. Chang et al. (2013) discussed a marginal likelihood ratio test, Mai and Zou (2013) used Kolmogorov-Smirnov statistic, Xu and Chen (2014) suggested maximum likelihood estimate to remove unimportant variables, respectively. He et al. (2013) discussed a nonparametric screening method, Zhou et al. (2019) used a divergence based screening method and Mukhopadhyay and Dunson (2020) proposed the randomized independence screening. Wang (2009) studied the popular forward regression (FR) method (see also Hao and Zhang, 2014) and Wang and Leng (2016) proposed the high dimensional ordinary least squares projection (HOLP) for screening variables in ultra-high dimensional settings. However, currently, there is no available screening method based on a Bayesian model that allows the incorporation of prior information on the variables. On
the other hand, in biological GWAS studies, such as the one considered in the paper, scientists often have prior knowledge on whether a trait is complex or simple. Scientists believe that complex traits result from variations within multiple genes while simple traits result from variations within a few genes with strong influence Kaler et al. (2020). Such knowledge are used to elicit the prior on model size and effect size. In addition, prior knowledge on linkage disequilibrium can help choosing the shrinkage parameter. In this paper we develop a Bayesian screening method allowing the use of such prior information.

In order to develop a Bayesian screening method, we consider a hierarchical model with zero inflated mixture priors which are special cases of the spike and slab priors. As mentioned earlier, variants of these hierarchical models have previously been used for variable selection and MCMC algorithms are generally used to approximate posterior probabilities. On the other hand, the sequential screening method proposed here called \textit{Bayesian iterative screening} (BITS) does not involve any MCMC sampling. Under the hierarchical model considered here, the marginal posterior probability mass function (pmf) of the latent indicator vector is analytically available up to a normalizing constant. BITS uses this pmf to iteratively include variables that have maximum posterior inclusion probability conditional on the already selected variables. The computation of the posterior probabilities is done by a one-step delayed Cholesky update. Wang and Leng (2016) mention that there are two important aspects of a successful screening method: computational efficiency and screening consistency property under flexible conditions. Even though BITS allows incorporation of prior information, it is computationally competitive with the frequentist screening methods like HOLP. The hierarchical model on which BITS is based assumes Gaussian errors. But we show that BITS has screening consistency even under the more general $q$-exponential tail condition on the errors. Also, we do not assume that the marginal correlations for the important variables are bounded away from zero—an assumption that is often violated in practice but used for showing screening consistency of SIS. Finally, we introduce the notion of posterior screening consistency and discuss its usefulness in Bayesian high dimensional data analysis.

BITS although is similar in spirit to the popular, classical variable screening method, namely forward regression (FR) (Wang, 2009) there are important differences between the two. By introducing the notion of ridge partial correlations, we show that unlike FR, BITS takes into account ridge partial variances to include potential variables. Also, by varying the ridge penalty, BITS can include groups of correlated important variables whereas FR selects only a candidate from each group which is not desirable for a screening method. For deciding
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the screened model size Wang (2009) considers the extended BIC (EBIC) criterion developed by Chen and Chen (2008). In addition to the use of EBIC and the liberal choice of having a model as large as the sample size, we construct a new stopping rule based on the posterior probability (PP). Furthermore, we prove that the PP stopping rule is screening consistent again under the general $q$-exponential tail condition on the errors. Through examples we demonstrate how the PP criterion can lead to informative screening by specifying suitable prior hyperparameter values.

The rest of the paper is organized as follows. We describe the hierarchical model and BITS in Section 2. We establish screening consistency properties of BITS in Section 2.3 as well as discuss the notion of posterior screening consistency. In Section 2.4 we emphasize the contrast between the proposed method and FR. In Section 2.5 we describe different possible stopping rules for BITS and establish screening consistency of the proposed PP stopping rule. Section 2.6 contains derivations of BITS for some other priors. Section 3 lays out the fast statistical computation algorithm for BITS. Section 4 contains results from extensive simulation examples. In particular, these examples are used to study the posterior mass coverage of BITS and to compare BITS with other frequentist screening methods. A real data set from a genomewide association studies with more than half a million markers is analyzed in Section 5. Some concluding remarks are given in Section 6. A supplement document containing the proofs of the theoretical results and some further simulation results is provided with sections referenced here with the prefix ‘S’. The methodology proposed here is implemented as a function named \texttt{bits} in an accompanying \texttt{R} package \texttt{bravo} (Li et al., 2023a).

2. A Bayesian iterative screening method

2.1 A hierarchical Gaussian regression model

Let the vector $y = (y_1, \ldots, y_n)$ denote the $n \times 1$ vector of responses and the $n \times p$ matrix $X = (X_1, \ldots, X_p)$ denote the matrix of covariate values with vector of regression coefficients $\beta = (\beta_1, \ldots, \beta_p)$. The Bayesian variable selection model we consider here assumes latent indicator vector $\gamma = (\gamma_1, \ldots, \gamma_p)^T \in \{0,1\}^p$, such that $X_j$ is included in the linear regression model if and only if $\gamma_j = 1$. Let $X_\gamma$ be the $n \times |\gamma|$ sub-matrix of $X$ that consists of columns of $X$ corresponding to model $\gamma$, $\beta_\gamma$ be the vector that contains the regression coefficients for model $\gamma$, and $|\gamma| = \sum_{i=1}^p \gamma_i$ be the model size. Without loss
of generality, each column of $X$ is assumed standardized. We then assume the Bayesian Gaussian hierarchical model

$$y | \beta_0, \beta, \gamma, \sigma^2 \sim N_n(1_n \beta_0 + X_\gamma \beta_\gamma, \sigma^2 I_n),$$

(2.1a)

$$(\sigma^2, \beta_0) \sim f(\beta_0, \sigma^2) \propto 1/\sigma^2,$$

(2.1b)

$$\beta_j | \gamma, \sigma^2 \sim \text{ind } N(0, \frac{\gamma_j}{\lambda} \sigma^2) \text{ for } j = 1, \ldots, p,$$

(2.1c)

$$\gamma | w \sim f(\gamma | w) = w^{\gamma}|(1 - w)^{|\gamma|}. \quad (2.1d)$$

In this hierarchical setup a popular non-informative prior is set for $(\beta_0, \sigma^2)$ in (2.1b) and a conjugate independent normal prior is used on $\beta$ given $\gamma$ in (2.1c) with $\lambda > 0$ controlling the precision of the prior independently from the scales of measurements. Note that under this prior, if a covariate is not included in the model, the prior on the corresponding regression coefficient degenerates at zero. In (2.1d) an independent Bernoulli prior is set for $\gamma$, where $w \in (0, 1)$ reflects the prior inclusion probability of each predictor. We assume $\lambda$ and $w$ are known non-random functions of $n$ and $p$.

Our Bayesian screening method hinges on the fact that given $\gamma$, it is possible to integrate out other variables analytically. Indeed, integrating out $(\beta_\gamma, \beta_0, \sigma^2)$ we derive the following marginal distribution of $y$ given $\gamma$,

$$f(y | \gamma) = \int_{R_+} \int_R \int_{R^{|\gamma|}} f(y | \gamma, \sigma^2, \beta_0, \beta_\gamma) f(\beta_\gamma | \gamma, \sigma^2, \beta_0) f(\sigma^2, \beta_0) \, d\beta_\gamma d\beta_0 d\sigma^2$$

$$= c_n |\gamma|^{n/2} |X_\gamma^T X_\gamma + \lambda I|^{-1/2} \left[ \tilde{y}^T \tilde{y} - \tilde{\beta}_\gamma^T (X_\gamma^T X_\gamma + \lambda I) \tilde{\beta}_\gamma \right]^{-n-1}(2.2)$$

where, $c_n = \Gamma((n - 1)/2)/\pi^{(n-1)/2}$ is a constant depending only on the sample size $n$, $\tilde{y} = y - \bar{y} 1_n$, and $\tilde{\beta}_\gamma = (X_\gamma^T X_\gamma + \lambda I)^{-1} X_\gamma^T \tilde{y}$. The hierarchical Gaussian regression model (2.1) and its variants have been used extensively and exclusively for variable selection. In particular, several works have established strong model selection consistency results (Narisetty and He, 2014) under the ultra-high dimensional setup that is considered here. In practice, however, these methods are mostly used after reducing the number of covariates using frequentist screening methods that are not driven by the same Bayesian hierarchical model. In the next section we describe a novel Bayesian screening method based on the hierarchical model (2.1).

### 2.2 The BITS algorithm

We now describe our proposed screening method. This method uses the posterior pmf of $\gamma$, $f(\gamma | y)$ which is available up to a normalizing constant. Indeed, if
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If $w$ is assumed fixed, then

$$
\log f(\gamma|y) = \text{const} + \frac{|\gamma|}{2} \log \lambda - \frac{1}{2} \log |X_\gamma^T X_\gamma + \lambda I| - \frac{n-1}{2} \log [\tilde{y}^T \tilde{y} - \tilde{y}^T X_\gamma (X_\gamma^T X_\gamma + \lambda I)^{-1} X_\gamma^T \tilde{y}] + |\gamma| \log \frac{w}{1-w}. \quad (2.3)
$$

Let $e_i$ be the $i$th $p$ dimensional canonical basis vector, that is, the $i$th element of $e_i$ is one, and all other elements are zero. In the first step, we select the variable $i_1$ such that $i_1 = \arg\max_{j \in \{1, \ldots, p\}} \log P(\gamma = e_j|y)$. Thus we select the unit vector $e_j$ with highest posterior probability. In the next step, we select the variable $i_2$ with $i_2 = \arg\max_{j \neq i_1} \log P(\gamma = e_{i_1} + e_j|y)$. Note that for $j \neq i_1$,

$$
P(\gamma_j = 1|\gamma_{i_1} = 1, \gamma_k = 0, k \neq i_1; y) = \left(1 + \frac{P(\gamma = e_{i_1}|y)}{P(\gamma = e_{i_1} + e_j|y)}\right)^{-1}. \quad (2.4)
$$

So, $P(\gamma_j = 1|\gamma_{i_1} = 1, \gamma_k = 0, k \neq i_1; y)$ and $P(\gamma = e_{i_1} + e_j|y)$ are maximized at the same $j \neq i_1$. Thus, in the second step, we choose the variable which has maximum posterior inclusion probability given that $i_1$ (the variable selected in the first step) is included in the model. An efficient computational method for calculating $P(\gamma = e_{i_1} + e_j|y)$ using a fast Cholesky update is given in Section 3. One problem with marginal correlation based screening methods like SIS (Fan and Lv, 2008) is that unimportant variables that are correlated with important variables may get selected. This is not likely to happen in our proposed screening procedure as the only variables that have high (conditional) posterior inclusion probabilities after taking into account the selected variables survive the screening. Let $\gamma^{(m)} = \sum_{k=1}^m e_{i_k}$ be the $\gamma$ vector at the $m$th step. Below we describe the $(m + 1)$st iteration of the BITS.

**Iteration $m + 1$ of the screening algorithm:**

Given $\gamma^{(m)}$, let

$$
i_{m+1} = \arg\max_{j \notin \gamma^{(m)}} \log P(\gamma = \gamma^{(m)} + e_j|y). \quad (2.5)
$$

Set $\gamma^{(m+1)} = \gamma^{(m)} + e_{i_{m+1}}$. 

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Using the same argument as (2.4), the \(i_{m+1}\)st variable has the highest posterior probability of being included given that \(i_1, i_2, \ldots, i_m\) have already been included in the model. BITS although is not guaranteed to produce the posterior mode, or any other standard summary measures of the posterior distribution \(f(\gamma | y)\), in the next section we show that it enjoys screening consistency.

**Remark 1.** Since, \(P(\gamma = e_j | y) \propto [1 - r_j^2/(1 + \lambda/n)]^{-(n-1)/2}\), with \(r_j = X_j^\top \tilde{y}\), the first step of the BITS algorithm selects the variable with largest marginal correlation as in Fan and Lv’s (2008) SIS algorithm.

**Remark 2.** Under the Bernoulli prior (2.1d) on \(\gamma\) the selection path \(i_1, i_2, i_3, \ldots\) does not depend on the hyperparameter \(w\) because the prior is only a function of \(|\gamma|\). However, as we shall see later in this section, \(w\) has an effect on some stopping rules and the screening consistency.

### 2.3 Screening consistency of BITS

Ideally, as the sample size increases we would like all the important variables to be included in \(\gamma^{(m)}\) after a reasonable number of \(m(< n)\) steps. The notion of frequentist screening consistency (Fan and Lv, 2008; Wang, 2009) states that if \(E(y) = X_t \beta_t\), for some subset \(t \subset \{1, \ldots, p\}\) then \(P(t \in \gamma^{(m)}\) for some \(m \leq n)\) should converge to 1 as \(n \to \infty\), under some regularity conditions. In order to state the assumptions and the results more rigorously, we use the following notations. Abusing notation, we interchangeably use a model \(\gamma\) either as a \(p\)-dimensional binary vector or as a set of indices of non-zero entries of the binary vector. For models \(\gamma\) and \(s\), \(\gamma^c\) denotes the complement of the model \(\gamma\). For \(1 \leq i \leq p\), we say \(i \in \gamma\) if \(\gamma_i = 1\) and \(i \notin \gamma\) if \(\gamma_i = 0\). For two positive real sequences \(\{a_n\}\) and \(\{b_n\}\), \(a_n \sim b_n\) means \(a_n/b_n \to c\) for some constant \(c > 0\); \(a_n \geq b_n\) (or \(b_n \leq a_n\)) means \(b_n = O(a_n)\); \(a_n \gtrsim b_n\) (or \(b_n \lessapprox a_n\)) means \(b_n = o(a_n)\). Again, abusing notations, for two real numbers \(a\) and \(b\), \(a \vee b\) and \(a \wedge b\) denote \(\max(a, b)\) and \(\min(a, b)\), respectively. Finally, let \(\beta_+ = \min_{i \in t} |\beta_i|\). We first consider the orthogonal design case in Section 2.3 and then more general design matrices and misspecified errors in Section 2.3.

### Orthogonal design with Gaussian errors

The following theorem shows that under a Gaussianity assumption and some mild conditions on the effects sizes, BITS include all and only the important variables in the first \(|t|\) steps.
Theorem 1. Suppose $X^\top X = nI_p, y = \beta_0 1_n + X_t\beta_t + \sigma \epsilon$ where $\epsilon \sim \mathcal{N}(0, I_n)$, $|t| = O(n^a)$, for some $a < 1$, and $n\beta_1^2 > \log n$. Then for any $\lambda > 0$, $P(\gamma^{(1)}) = t) \to 1$ as $n \to \infty$.

Such a strong conclusion holds for the orthogonal design because the variables are uncorrelated and hence the marginal correlations are asymptotically ordered by the magnitudes of the regression coefficients (Fan and Lv, 2008). Furthermore, the orthogonality restricts $p$ to be at most $n$. Thus, it is unrealistic to expect the same conclusion to hold in general situations. In particular, note that the first variable included is the one with the highest absolute marginal correlation with the response (Remark 1). There are ample examples of realistic designs (Fan and Lv, 2008; Wang et al., 2021) where an unimportant variable has the highest absolute marginal correlation with the response.

Screening consistency in more general cases

Although BITS is developed under the Gaussianity assumption on $y$ for computational tractability, we would like to establish screening consistency even under more general tail conditions. As we shall see, the tail behavior of the error distribution plays a crucial role in proving screening consistency. To that end, we consider the family of distributions with $q$-exponential tail condition (Wang and Leng, 2016) given below.

Definition 1 ($q$-exponential tail condition). A zero-mean distribution $F$ is said to have $q$-exponential tail, if there exists a function $q : [0, \infty) \to \mathbb{R}$ such that

for any $N \geq 1$, $\eta_1, \ldots, \eta_N \iid \sim F$, $\ell \in \mathcal{R}^N$ with $||\ell|| = 1$, and $\zeta > 0$ we have $P(\ell^\top \eta) > \zeta) \leq \exp\{1 - q(\zeta)\}$ where $\eta = (\eta_1, \ldots, \eta_N)$.

This tail condition is assumed by Wang and Leng (2016) in establishing screening consistency of their HOLP screening method. In particular, as shown in Vershynin (2012), for standard normal distribution, $q(\zeta) = \zeta^2 / 2$, when $F$ is sub-Gaussian $q(\zeta) = c_F \zeta^2$ for some constant $c_F > 0$ depending on $F$, and when $F$ is sub-exponential distribution $q(\zeta) = c'_F \zeta$ for some constant $c'_F > 0$ depending on $F$. Finally, when only first $2k$ moments of $F$ are finite, $q(\zeta) - 2k \log(\zeta) = O(1)$.

We assume the following set of conditions:

C1 $y = \beta_0 1_n + X_t\beta_t + \sigma \epsilon$ where $t$ is the true model, $\epsilon = (\epsilon_1, \ldots, \epsilon_n), \epsilon_i \iid F_0$ which has $q$-exponential tail with unit variance.
C2 \( |\log \lambda| = O(\log n) \).

C3 There exist \( K_n \) and \( 0 < \delta < 1/\sigma \) such that \((K_n + 1)|t| \leq n\),

\[
\frac{|t|\|\beta_t\|^2 \log n}{\tau_+^2 \beta_+^4} < K_n \leq n \log n \min \left\{ \frac{\tau_+}{\lambda}, \frac{1}{|\log(1/w - 1)|} \right\}
\]

\[
q(s_n \delta) - K_n |t| \log p - \log |t| \to \infty
\]

where \( s_n = \sqrt{n} \tau_+ \beta_+^2 / (\|\beta_t\| \sqrt{|t|}) \) and \( \tau_+ \) is the smallest nonzero eigenvalue of \( X_n^\top X_n / n \) with \( |\gamma| \leq (K_n + 1)|t| \).

Although our assumption on \( p \) is related only to the tail behavior of the error distribution, it is evident that under sub-Gaussian or sub-exponential tailed \( F_0 \), BITS is screening consistent in the ultra-high dimensional setting. For example, suppose \( \|\beta_t\| = O(1), \tau_+ \sim n^{-h_1}, \beta_+ \sim n^{-h_2}, \log p \sim n^{h_3}, |t| \sim n^{h_4}, w = n^{-h_5} \), for some \( h_i > 0, i = 1, \ldots, 5 \), and \( K_n = n^{2h_1 + 4h_2 + h_4} (\log n)^2 \). Note that, these values of \( \beta_+ \) and \( |t| \) are as in Wang and Leng (2016). Also, suppose \( \lambda = n^{h_6} \) for some constant \( h_6 \). When \( F_0 \) is sub-Gaussian, simple calculations show that a sufficient condition for (C1)–(C3) is that \( 4h_1 + 8h_2 + h_3 + 3h_4 + h_6 < 1 \) if \( h_1 + h_6 < 0 \) and \( 4h_1 + 8h_2 + h_3 + 3h_4 < 1 \) if \( h_1 + h_6 < 0 \). If \( F_0 \) is subexponential, a sufficient condition is \( 6h_1 + 12h_2 + 2h_3 + 5h_4 + h_6 < 1 \) if \( h_1 + h_6 < 0 \) and \( 6h_1 + 12h_2 + 2h_3 + 5h_4 < 1 \) if \( h_1 + h_6 < 0 \), which is slightly more stringent than the sub-Gaussian case. Furthermore, under any of these sufficient conditions, \( K_n |t| < |n / \log n| \) which is typically the screened model size of SIS (Fan et al., 2009). Note that, C2 assumes quite a weak condition on the prior shrinkage parameter \( \lambda \), allowing us to run BITS for different choices of \( \lambda \), and unifying these results to produce the screened model. Condition C3 lays out the explicit scaling law of \( w \) against \(|t| \) for screening consistency of BITS and the PP stopping rule. We now present the screening consistency result.

**Theorem 2.** Under conditions (C1)–(C3), there exists \( c > 0 \) such that for all sufficiently large \( n \),

\[
P(\gamma(K_n|t|) \geq t) \geq 1 - \exp(1 - q(s_n \delta) + K_n |t| \log p + \log |t|) - P(\|\tilde{y}\|^2 > n u_n),
\]

where \( u_n = \tau_+^2 \beta_+^4 K_n / (c |t| \|\beta_t\|^2 \log n) \).

Note that, the limit of \( (\|\tilde{y}\|^2 - \beta_t^\top X_t^\top X_t \beta_t) / n \) is bounded above by \( \sigma^2 \) almost everywhere. Thus, if \( \beta_t^\top X_t^\top X_t \beta_t / n < u_n \), it is easy to see from C3 that \( P(\gamma(K_n|t|) \geq t) \to 1 \). That is, with overwhelmingly large probability, the true model is included in at most \( K_n |t| \) many steps. Note that, the condition
\( \beta_t^\top X_t^\top X_t \beta_t/n \prec u_n \) is weaker than the condition \( \text{var}(y) = O(1) \) assumed in Wang and Leng (2016). However, when higher order moments of \( \epsilon_1 \) exist, further lower bounds to \( P(\gamma^{(K_n|t)} \supseteq t) \) can be obtained as described in the following corollary.

**Corollary 1.** Suppose conditions (C1)–(C3) holds. If further, \( \beta_t^\top X_t^\top X_t \beta_t/n \prec u_n \land n \) and \( E(\epsilon_1^4) < \infty \) then with \( \kappa = \text{Var}(\epsilon_1^2) \), \( v_n = u_n - \beta_t^\top X_t^\top X_t \beta_t/n - 1 \) and a constant \( c_1 > 0 \), for all sufficiently large \( n \),

\[
P(\|\tilde{y}\|^2 > nu_n) < \frac{\sigma^2 \sqrt{\kappa}}{\sqrt{2n\pi v_n}} \exp \left( -\frac{nv_n^2}{2\sigma^4\kappa} \right) + \frac{4\sigma^4 \beta_t^\top X_t^\top X_t \beta_t}{n^2}.
\]

**Posterior screening consistency**

The screening consistency considered in Sections 2.3 and 2.3 are in the frequentist sense and therefore are not guaranteed to be fidelitous to the posterior inference. In this section we discuss the concept of posterior screening consistency (see also Song and Liang, 2015, Theorem 3). We start with the following definition.

**Definition 2.** A sequence of models \( \{\gamma^{[n]}\} \), with \(|\gamma^{[n]}| \leq n \) is said to be posterior screening consistent if

\[
P(\gamma \in \mathcal{P}_t(\gamma^{[n]})|y) \equiv \sum_{t \subseteq \gamma \subseteq \gamma^{[n]}} f(\gamma|y) \to 1 \tag{2.6}
\]

in probability as \( n \to \infty \), where \( \mathcal{P}_t(\gamma^{[n]}) \) is the set of all sub-models of \( \gamma^{[n]} \) containing \( t \).

In other words, with probability tending to 1, the posterior mass of \( \gamma \) is entirely supported on \( 2^{(|\gamma^{[n]}| - |t|)} \) models which are sub-models of \( \gamma^{[n]} \). Considering that there are originally \( 2^p \) possible models, this can be a great reduction in the search space for models with high posterior probabilities. Typically Bayesian variable selection algorithms search for the posterior mode and other high-posterior probability models. Many competitive algorithms are available to search for the best model including, but surely not limited to, the stochastic shotgun algorithm (Hans et al., 2007), simplified stochastic shotgun algorithm (Shin et al., 2018), shotgun with embedded screening (Li et al., 2023b), Gibbs sampling (Narisetty and He, 2014), Metropolis-Hastings algorithm (Zhou and Guan, 2019) and mixed integer optimization (Bertsimas et al., 2016). Since the size \( (2^p) \) of the model space grows exponentially with the number of variables,
due to computational cost and convergence issues of these iterative algorithms, when dealing with high dimensional data sets, generally a screening step is performed before applying a Bayesian variable selection algorithm. For example, Narisetty and He (2014), in their real data example, use SIS to reduce the number of variables from 22,575 to 400 before applying their variable selection algorithm. One important aspect of posterior screening consistency is that the best model (in terms of posterior probability) for variable selection can be searched among a much smaller number of models instead of among the humongous number \((2^p)\) of all possible models. Thus a posterior screening consistent model can serve as an excellent starting point for implementing further Bayesian variable selection methods.

In the above we have described important practical consequences of using posterior screening consistent algorithms. We now discuss conditions guaranteeing such consistency. In the context of ultra-high dimensional Bayesian variable selection, under different hierarchical model setups, recently several articles have established strong (posterior) selection consistency, that is, \(f(t|y) \to 1\) in probability as \(n \to \infty\) (see e.g. Narisetty and He, 2014; Yang et al., 2016; Shin et al., 2018; Li et al., 2023b). Thus under strong selection consistency, posterior probability of the true model goes to one as \(n \to \infty\). Now, for given \(\delta > 0\), denoting the events \(\{t \subseteq \gamma^{[n]}\}\) and \(\{f(t|y) > 1 - \delta\}\) by \(A_n\) and \(B_{n,\delta}\) respectively, we have \(P(\sum_{t \subseteq \gamma \subseteq \gamma^{[n]}} f(\gamma|y) > 1 - \delta) \geq P(A_n \cap B_{n,\delta}) \geq P(A_n) + P(B_{n,\delta}) - 1\). Thus, if a sequence of models \(\{\gamma^{[n]}\}\) is screening consistent and strong selection consistency holds, that is, if \(P(A_n) \to 1\) and \(P(B_{n,\delta}) \to 1\) as \(n \to \infty\) then \(\{\gamma^{[n]}\}\) is posterior screening consistent. Yang et al. (2016) and Li et al. (2023b) derive conditions for strong selection consistency for the model (2.1). So, by Theorem 2 we have posterior screening consistency results for BITS.

### 2.4 Comparison with frequentist screening methods

In this Section we compare BITS with two frequentist screening methods, namely Wang’s (2009) FR and Wang and Leng’s (2016) HOLP.

#### Contrast with the forward regression method

BITS although is similar in spirit to the forward selection, the step-wise regression method, there are significant differences between BITS and the FR method of Wang (2009). Firstly, under the conditions of Wang (2009), BITS is screening consistent:
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**Lemma 1.** Under the conditions of Wang (2009), that is, with $\beta_+ \geq \nu_\beta n^{-\xi_{\min}}$, $\log p \leq \nu n^\xi, |t| \leq \nu n^{\xi_0}, \|\beta_i\| \leq C_\beta$ for some finite constant $C_\beta$, $\tau_+ \geq \tau_{\min}$ for some finite constant $\tau_{\min}$, and $\xi + 6\xi_0 + 12\xi_{\min} < 1$, $\epsilon_i \sim N(0, 1)$, then $C_{3}$ holds with $K_n = n^{\xi_0 + 4\xi_{\min}} (\log n)^2$.

A proof of Lemma 1 is given in Section S3.1 of the supplement. We indeed prove that the lemma holds under a weaker condition of $\xi + 3\xi_0 + 8\xi_{\min} < 1$. In order to show the contrasts between BITS and FR, we introduce the notion of ridge partial correlations.

**Definition 3.** For any $\gamma$ and $i \notin \gamma$, the ridge partial correlation between $y$ and $X_i$ given $X_\gamma$ with ridge penalty $\lambda$ is given by

$$R_{i,\gamma,\lambda} \equiv R_{iy,\gamma,\lambda} = -v_{iy,\gamma,\lambda}/\{v_{i,\gamma,\lambda} \times v_{y,\gamma,\lambda}\}^{1/2}$$

where $v_{i,\gamma,\lambda} = n^{-1} X_i^\top X_i + n^{-1} \lambda - n^{-2} X_i^\top X_\gamma \left(n^{-1} X_\gamma^\top X_\gamma + \lambda/nI\right)^{-1} X_\gamma^\top X_i$ is the ridge (sample) partial variance of $X_i$ given $X_\gamma$, $v_{iy,\gamma,\lambda} = n^{-1} y^\top X_i - n^{-2} y^\top X_\gamma \left(n^{-1} X_\gamma^\top X_\gamma + \lambda/nI\right)^{-1} X_\gamma^\top y$, and

$$v_{y,\gamma,\lambda} = n^{-1} y^\top y - n^{-2} y^\top X_\gamma \left(n^{-1} X_\gamma^\top X_\gamma + \lambda/nI\right)^{-1} X_\gamma^\top y.$$

**Remark 3.** When $|\gamma| < n$ and $\lambda = 0$, $R_{i,\gamma,0}$ is exactly the (sample) partial correlation between $y$ and $X_i$ after eliminating the effects of $X_j, j \in \gamma$, and the ridge partial sample variances $v_{i,\gamma,0}$’s are exactly the (sample) partial variances of $X_i$’s given $X_j, j \in \gamma$.

In fact, BITS can be reformulated using these ridge sample partial correlations and ridge sample partial variances. To that end, we first show how the log-marginal posterior probability increments depend on the ridge partial correlations and partial variances.

**Lemma 2.** For the model (2.1), for any $\gamma$, and $i \notin \gamma$,

$$\frac{f(\gamma + e_i|y)}{f(\gamma|y)} = \frac{w(n\lambda)^{1/2}}{(1 - w)v_{i,\gamma,\lambda}^{1/2} (1 - R_{i,\gamma,\lambda}^2)^{(n-1)/2}}.$$
correlations $|R_{i-\gamma,0}|, (i \notin \gamma)$. In particular, BITS also takes into consideration the (sample) partial variances of each $X_i$ given the already included variables. Thus, between two candidates which have the same partial correlations with the response given already included variables, the one with smaller conditional variance is preferred. However, if the partial correlations with the response are different then because of the presence of the the multiplier $(n - 1)$, the effect of the conditional variance is practically insignificant. Furthermore, by shrinking the effects using the ridge penalty, BITS can include groups of important variables that are highly correlated among themselves in contrast to FR which would only select a candidate variable from the group. Finally, note that during screening it could be useful to be liberal and include more than $n$ variables. This however, is not possible by FR because all models of size bigger than $n - 1$ have zero residual sum of squares. BITS, on the other hand, allows to have a screened model of size bigger than $n$. In different simulation examples in section 4, we demonstrate that BITS performs much better than FR.

**Contrast with the HOLP**

For fixed, $\gamma, \sigma^2$, the mode of the posterior density of $\beta_{\gamma}$ under the prior (2.1c) is $\tilde{\beta}_\gamma$ mentioned in Section 2.1. The ridge regression estimate of $\beta$ corresponding to the ridge penalty $\lambda$ is $\hat{\beta}(\lambda) = (X^\top X + \lambda I)^{-1} X^\top \tilde{y}$. Thus, for given $\gamma$, $\tilde{\beta}_\gamma$ is the same as the ridge regression estimate. Wang and Leng (2016) showed that the HOLP estimator can be obtained as $\lim_{\lambda \to 0} \hat{\beta}(\lambda)$. The posterior probability $f(\gamma|y)$ given in (2.3) that steers the BITS algorithm involves $\tilde{\beta}_\gamma$. While BITS sequentially selects the variables based on (2.3), in their numerical examples Wang and Leng (2016) use either the variables with $n$ largest (absolute) HOLP estimates or the EBIC method (Chen and Chen, 2008) to implement the HOLP method. In the next Section, we provide a posterior probability based consistent stopping rule for BITS.

**2.5 Stopping criteria**

Note that BITS provide a sequence of predictor indices $i_1, i_2, \ldots$. A practical question is when to stop the algorithm. Theorem 2 suggests that the first $K_n|t|$ indices contain the true model with overwhelming probability. However, there is nothing to stop us from being liberal and include the first $n$ indices $i_1, i_2, \ldots, i_n$.

The aforementioned rule is not affected by the prior inclusion probability $w$. We now propose a new stopping rule, called the posterior probability (PP)
Bayesian iterative screening criterion that depends on \( w \). As we expect the important variables to be included early, the BITS algorithm is expected to provide a sequence of nested models \( \{\gamma^{(i)}\} \) with increasing posterior probabilities until all the important variables are included. Thus we may stop BITS when the first drop occurs in these posterior probabilities, that is, we stop at iteration

\[
T = \arg \min_{m < K_n|t|} \{ f(\gamma^{(m+1)} | y) < f(\gamma^{(m)} | y) \}.
\]

Since \( K_n|t| < n \), the PP criterion never selects more than \( n \) variables. Also, the PP rule, just like the BITS method, is not searching for the mode of the posterior pmf \( f(\gamma | y) \). Note that BITS does not prune variables. On the other hand, finding a local mode would require considering forward, backward, swap, and potentially other moves (Li et al., 2023b). Under the orthogonal design described in Section 2.3, we saw that with probability tending to one, BITS include all and only the important variables in the first \(|t|\) steps. In addition, we will now prove that the PP criterion stops right after \(|t|\) steps.

**Theorem 3.** If the conditions for Theorem 1 hold and in addition, that \( \|\beta_t\| = O(1) \) and that there exists \( 1/2 < c < 1 \) such that \( w = c'n^{-c} \) for some \( c' > 0 \). Then \( P(T = |t|) \rightarrow 1 \) as \( n \rightarrow \infty \).

However, in general, as we have seen in Section 2.3, BITS may include unimportant variables before it includes all the important variables. Thus it is unrealistic to require that the conclusions of the previous theorem holds in the more general case. However, the following theorem guarantees that \( \gamma^{(T)} \) is screening consistent.

**Theorem 4.** Under conditions (C1)–(C3), there exists a positive constant \( c^* \) such that for all sufficiently large \( n \),

\[
P(\gamma^{(T)} \supseteq t) \geq 1 - \exp(1 - q(s_n \delta) + K_n|t| \log p + \log |t|) - P(\|\tilde{y}\|^2 > nu_n^*),
\]

where \( u_n^* = \tau_+^2 \beta_t^4 K_n / (c^* |t| \|\beta_t\|^2 \log n) \).

Recall that \( \tilde{y} \) is the mean-centered \( y \), that is, \( \tilde{y} = y - \tilde{y}_1n \). Also, following the discussions right after Theorem 2 and Corollary 1, an upper bound to the last term \( P(\|\tilde{y}\|^2 > nu_n^*) \) can be obtained. This results in lower bounds to \( P(\gamma^{(T)} \supseteq t) \) and in particular, establishing \( P(\gamma^{(T)} \supseteq t) \rightarrow 1 \).

Alternatively, Wang (2009) and Wang and Leng (2016) also promote the use of EBIC (Chen and Chen, 2008). Under this stopping rule, the screening is stopped at the smallest EBIC, that is, at \( \arg \min_{1 \leq m \leq n-1} \text{EBIC}(m) \) where for
$1 \leq k < n$, EBIC($k$) = $\log \hat{\sigma}^2_{(k)} + k(\log n + 2 \log p)/n$, and $n\hat{\sigma}^2_{(k)}$ is the ordinary least squares residual sum of squares from regression of $y$ on the first $k$ screened variables. Evidently, due to its ultra-high dimensional penalty, EBIC is expected to be very conservative and yield small screened models. Compared to the PP rule, the EBIC rule is computationally expensive as it requires a model of size $n - 1$. On the other hand, a similar variant of the PP criterion can be to choose the model according to the largest drop in the posterior probability among the first $K_n|t|$ steps, that is, the model size is $\arg\max_{1 \leq m \leq K_n|t|} (f(\gamma(m)|y) - f(\gamma(m+1)|y))$.

### 2.6 BITS for other priors

A popular alternative to the independent normal prior in (2.1c) is the Zellner’s $g$-prior (Zellner, 1986) for $\beta$, indexed by a hyperparameter $g$ under the assumption that all $n \times n$ submatrices of $X$ are non-singular. That is, we also consider the hierarchical model (2.1) where the prior in (2.1c) is replaced with $\beta|\gamma, \sigma^2 \sim N|\gamma|0, g\sigma^2(X_\gamma^\top X_\gamma)^{-1}$, whence the marginal density $\tilde{f}(y|\gamma)$ becomes

$$\tilde{f}(y|\gamma) = c_n (g + 1)^{-|\gamma|/2} \left[ \tilde{y}^\top \tilde{y} \right. - \left. \frac{g}{g + 1} \tilde{y}^\top X_\gamma (X_\gamma^\top X_\gamma)^{-1} X_\gamma^\top \tilde{y} \right]^{-(n-1)/2}.$$  

It is evident that the Zellner’s $g$-prior provides the same screening path as FR because for fixed $|\gamma|$ the posterior pmf $\tilde{f}(\gamma|y)$ under Zellner’s prior is a monotonic decreasing function of the regression sum of squares $\tilde{y}^\top X_\gamma (X_\gamma^\top X_\gamma)^{-1} X_\gamma^\top \tilde{y}$. Also, the Zellner’s $g$-prior does not allow to have screened models of size more than $n$.

Similarly, BITS can easily accommodate beta-binomial prior distribution on $\gamma: p(|\gamma|a, b) = \mathcal{B}(|\gamma| + a, p - |\gamma| + b)/\mathcal{B}(a, b)$, where $\mathcal{B}$ is the beta function, and $a, b > 0$. Since the beta-binomial prior also depend on $\gamma$ only via $|\gamma|$, it does not have any effect on the screening path of BITS for a given $\lambda$.

Recently, Kojima and Komaki (2016) have proposed a class of discrete determinantal point process priors on the model space that discourages simultaneous selection of collinear predictors. The founding member of this class of priors is given by $f_d(\gamma) = |dX_\gamma^\top X_\gamma| / |dX^\top X + I_p|$, where $d > 0$ controls the prior expectation of the model size. A value of $d > 1$ promotes larger models, while $d \leq 1$ promotes smaller models. Although Kojima and Komaki (2016) have studied the prior when $p < n$, it can be also used when $p > n$. In particular, $f_d(\gamma)$ puts zero prior probability on all models of size greater than $n$. Notice that this prior is not a function of $|\gamma|$ and hence $d$ will have an effect on the BITS screening path.
3. Fast statistical computation

In this section we describe how BITS is implemented in practice. One major challenge in BITS is the computation of posterior probabilities of models $\gamma^{(m)} + e_j$ for all $j \notin \gamma^{(m)}$ in the $(m+1)$st iteration. We show how these can be computed in minimal computational complexity using a one-step delayed Cholesky updates.

Before delving into the algorithm, let us define the notation $\odot$ and $\oslash$ as the element-wise multiplication and division between two vectors. Also when adding or subtracting a scalar to or from each entry of a vector we use the traditional ‘+’ and ‘−’ operators. The original covariates may have unbalanced scales and the scaled covariate matrix $X$ is often a dense matrix. Let $Z$ be the $n \times p$ matrix of the original covariates. We denote by $r$ the vector $X^\top \tilde{y}$ which can be simply computed as $D^{-1/2}Z^\top \tilde{y}$ without having to store $X$. Also for greater numerical stability, we scale the vector $\tilde{y}$ so that $\|\tilde{y}\|^2 = n$, although the algorithm is described without this assumption.

In the first iteration, $i_1 = \arg \max_i r_i$ and thus $\gamma^{(1)} = \{i_1\}$. Let $R_1 \equiv b_1 = \sqrt{n + \lambda}$, denote the Cholesky factor of $X_{\gamma^{(1)}}^\top X_{\gamma^{(1)}} + \lambda I$. Also let $v_1 = r_{i_1}/b_1$ and let

$$\pi_1 = \frac{1}{2} \log \lambda - \log \det R_1 - \frac{1}{2} (n-1) \log \{\|\tilde{y}\|^2 - v_1^2\} + \log(1-w)$$

denote $\log f(\gamma^{(1)}|y)$ up to an additive constant. Under the PP stopping rule, we stop if $\pi_1 < -(n-1) \log(\|\tilde{y}\|^2)/2$, the right side being $\log f(\phi|y)$ up to the same additive constant.

Next, we also add the second index before going into a loop. To that end, let

$$S_1 = D^{-1/2}Z^\top (Z_{i_1} - \bar{Z}_{i_1} 1_n)/D_{i_1}^{1/2}, \quad \zeta_1 = S_1 \odot S_1$$

and $\omega_1 = \sqrt{n + \lambda - \zeta_1}$ where the square root is computed element-wise. Let $u_1 = (r - v_1 S_1) \oslash \omega_1$. Then,

$$i_2 = \arg \max_{i \neq i_1} \left[ - \log \det R_1 - \log \omega_{1,i} - \frac{1}{2} (n-1) \log \{\|\tilde{y}\|^2 - v_1^2 - u_{1,i}^2\} \right].$$

Set $\gamma^{(2)} = \gamma^{(1)} \cup \{i_2\}$, $b_2 = \omega_{1,i_2}$, $v_2 = (v_1, u_{1,i_2})$, and compute $\log f(\gamma^{(2)}|y)$ up to an additive constant as

$$\pi_2 = -\frac{1}{2} 2 \log \lambda - \log \det R_1 - \log b_2 - \frac{1}{2} (n-1) \log \{\|\tilde{y}\|^2 - \|v_2\|^2\} + 2 \log(1-w).$$

Under the PP stopping rule, we stop if $\pi_2 < \pi_1$.

For $k \geq 3$, until stopping we
- Compute $\alpha_{k-1} = R_{k-2}^{-\top} D_{\gamma(k-2)}^{-1/2} \left( Z_{i_{k-1}} - \bar{Z}_{i_{k-1}} 1_n \right) / D_{i_{k-1}}^{1/2}$, where $Z_{(k-2)} = [Z_{i_1}, Z_{i_2}, \cdots, Z_{i_{k-2}}]$. The order of the columns is important because the Cholesky factor is computed according the screening path.

- The Cholesky factor of $X_{\gamma(k-1)}^\top X_{\gamma(k-1)} + \lambda I_{k-1}$, up to an ordering of the columns, is given by
  $$R_{k-1} = \begin{pmatrix} R_{k-2} & \alpha_{k-1} \\ 0 & b_{k-1} \end{pmatrix}$$

- Update $\log \det R_{k-1} = \log \det R_{k-2} + \log b_{k-1}$.

- Set $\eta_{k-1} = b_{k-1}^{-1} D_{\gamma(k-2)}^{-1/2} Z_{(k-2)}^\top (X_{i_{k-1}} - X_{\gamma(k-2)} D_{\gamma(k-2)}^{-1/2} R_{k-2}^{-1/2} \alpha_{k-1})$.

- Update $\zeta_{k-1} = \zeta_{k-2} + \eta_{k-1} \odot \eta_{k-1}$ and set $\omega_{k-1} = \sqrt{n + \lambda - \zeta_{k-1}}$.

- Update $u_{k-1} = (u_{k-2} \odot \omega - u_{k-2,i_{k-1}} \eta_{k-1}) \odot \omega_{k-1}$.

- Set $\gamma^{(k)} = \gamma^{(k-1)} \cup \{ i_k \}$, $b_k = \omega_{k-1,i_k}$, $v_k = (v_{k-1}, u_{k-1,i_k})$, where
  $$i_k = \arg \max_{i \notin \gamma^{(k-1)}} \left\{ -\log \omega_{k-1,i} - \frac{1}{2} (n-1) \log \left\{ \| \tilde{y} \|^2 - \| v_{k-1} \|^2 - u_{k-1,i} \right\} \right\}$$

- Compute $\log f(\gamma^{(k)} | y)$ up to an additive constant as
  $$\pi_k = -\frac{k}{2} \log \lambda - \log \det R_{k-1} - \log b_{k} - \frac{n-1}{2} \log \left\{ \| \tilde{y} \|^2 - \| v_{k} \|^2 \right\} + k \log \frac{w}{1-w}.$$ 

As before, under the PP stopping criterion, we stop at the $k$th iteration and return $\gamma^{(k-1)}$ if $\pi_k < \pi_{k-1}$.

Overall, the computational complexity in the $k$th iteration is $O(k^2 + kn + np)$. Assuming the worse case scenario when the number of iterations is $O(n)$, the total computational cost is $O(n^3 + n^2 p)$. If $Z$ is sparse, then this reduces to $O(n^3 + n\|Z\|_0)$ where $\|Z\|_0$ is the number of non-zero entries in $Z$. This is same as the computational complexity of HOLP as it computes $\hat{\beta}_{HOLP} = X^\top (XX^\top)^{-1} y$, where computing $XX^\top$ incurs a cost of $O(n^2 p)$ and computing $(XX^\top)^{-1} y$ incurs a cost of $O(n^3)$. Also the computational complexity of robust rank correlation screening (Li et al., 2012a) is $O(n^2 p)$. In contrast, the computational complexities of iterated sure independence screening (Fan and Lv, 2008) and tilting procedures (Cho and Fryzlewicz, 2012; Lin and Pang, 2014) are much higher. Furthermore, the memory requirement of BPTS, in addition to storing the original matrix $Z$, is $O(n^2)$, mainly for storing the Cholesky
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factors $R_k's$. This is same as the memory requirement of HOLP even if the matrix $X$ is not explicitly stored. The complexity of the FR method as implemented in the github repository ‘screening’\footnote{https://github.com/wwrechard/screening} by Wang and Leng (2016) in the $k$th iteration is $O([k^3 + k^2n]p)$ although a faster implementation of FR can be achieved by the delayed Cholesky update proposed here.

4. Simulation studies

In this section, we study how much posterior mass is covered by BITS under different choices of $\lambda$ and stopping criteria. We consider our numerical study in the context of eight simulation models described below. For these examples E.1–E.8, the rows of $X$ are generated from multivariate normal distributions with mean zero and different covariance matrices. In all settings except E.7, the true model is taken to be $t = \{1, 2, \ldots, 9\}$. For $i \in t$ $\beta_i$’s $\sim \mathcal{N}(0, \sigma^2/\lambda_0)$ where $\sigma^2 = \lambda_0 = 1$; $\beta_i = 0$ for $i \neq t$.

E.1 Independent predictors (Ind.) Here the covariance matrix is $I_p$.

E.2 Compound symmetry (CS) In this example, the covariance matrix is $\rho_{ij}I_p$. The value of $\rho$ is set to be equal to 0.5.

E.3 Autoregressive correlation The auto regression, correlation structure among covariates is appropriate when there is an ordering (say, based on time) in covariates, and variables further apart are less correlated. We use the AR(1) structure where the $(i, j)$th entry of the covariance matrix is $\rho^{i-j}$. We set $\rho = 0.5$.

E.4 Factor models (Fac.) This example is from Meinshausen and B"uhlmann (2006) and Wang and Leng (2016). Fix $k = 10$. Let $F$ be a $p \times k$ matrix whose entries are iid $\mathcal{N}(0, 1)$. The covariance matrix is $FF^\top + I_p$.

E.5 Group structure (Grp.) This special correlation structure arises when variables are grouped together in the sense that the variables from the same group are highly correlated. This example is similar to example 4 of Zou and Hastie (2005) where 9 true variables are assigned to 3 groups. We generate the predictors as $X_m = z_1 + \zeta_1,m, X_3+m = z_2 + \zeta_2,m, X_6+m = z_3 + \zeta_3,m$ where $z_i \sim \mathcal{N}(0, I_n), \zeta_{i,m} \sim \mathcal{N}(0, 0.01I_n)$ and $z_i$’s and $\zeta_{i,m}$’s are independent for $1 \leq i \leq 3$ and for $m = 1, 2, 3$.\footnotemark
E.6 **Extreme correlation (Ext.)** We modify Wang’s (2009) challenging Example 4 to make it more complex. Simulate $Z_i \sim \mathcal{N}_n(0, I)$, $i = 1, \ldots, p$, and $W_i \sim \mathcal{N}_n(0, I)$, $i = 1, \ldots, 9$. Set $X_i = (Z_i + W_i)/\sqrt{2}$, $i = 1, \ldots, 9$ and $X_i = (Z_i + \sum_{i=1}^{9} W_i)/2$ for $i = 10, \ldots, p$. The marginal correlation between the response and any unimportant variable is $(2.5/\sqrt{3})$ times larger in magnitude than the same between the response and the true predictors.

E.7 **Sparse factor models (Sp.Fac.)** This example is a sparse version of E.4. Let $f_{ij}$ denotes the $(i, j)$th entry of $F$. Here, for each fixed $1 \leq j \leq 5$, $f_{ij} \sim \mathcal{N}(0, 1)$ if $5(j - 1) + 1 \leq i \leq 5j$, and $f_{ij} = 0$ otherwise. Also, $\Sigma = FF^\top + 0.01I_p$ and $\beta_j \sim \mathcal{N}(0, 1)$ for $1 \leq j \leq 25$ and $0$ for $j > 25$.

E.8 **Spurious correlation models (Spur.)** Here, the unimportant variables are highly correlated with the mean function. Specifically, $X_1, X_2, \ldots, X_9 \sim \mathcal{N}_n(0, I)$, $\mu = \sum_{i=1}^{9} \beta_i X_i$, and $X_i \sim \mathcal{N}_n(\mu, 0.25I)$ for $i \geq 9$.

For each of these cases, we generate data using $(n, p) = (50, 100), (75, 200), (100, 2000), (150, 2000), (200, 10000)$. We then run BITS with three different values of $\lambda$: a large value $\lambda = p/n$ (BITS1), a moderate value $\lambda = n \log n/p$ (BITS2) and a small value $\lambda = n/p$ (BITS3). In addition, BITS1, BITS2, BITS3 are run with two different stopping rules: top $n$ variables (denoted by ‘(n)’), and the PP criterion (denoted by ‘(PP)’) using $w = |t|/p$ where $|t|$ is the true model size. We also consider the union of the models from the three BITS settings (UBITS) for each stopping rule.

Next, for each screened model, we use SVEN (Li et al., 2023b) implemented in the package ‘bravo’ (Li et al., 2023a) to find the models with significant posterior probabilities under the data generating $\lambda_0$. We also use SVEN without screening to find models with significantly high posterior probabilities. This allows us to approximate the posterior mass covered by submodels of the screened models. We compute the three metrics: true positive rate (TPR) is the percentage of true variables included in the screened model, posterior mass coverage (PMC) is an approximation to the total mass of the submodels of the screened model, and the size of the screened model. We repeat the process 100 times for each setting. We report the mean TPRs, mean PMCs, and median model sizes. For comparison, also compute the TPRs of the three popular screening methods: HOLP (Wang and Leng, 2016), SIS (Fan and Lv, 2008), and forward regression (Wang, 2009), each with two stopping rules: models of size $n$ ($n - 2$ for FR) and using EBIC. For brevity, we report here two settings: $(n, p) = (50, 100)$.
and (200, 10000) in Tables 1 and 2; remaining cases are reported in Section S4 of the supplementary document.

From the results, we see that the optimal value of the tuning parameter depends on the correlation structure of the covariate matrix. A large value of $\lambda$ (BITS1) works well in most of the settings, but a small value of $\lambda$ (BITS3) works better for the factor model setting, and a moderate value of $\lambda$ (BITS2) works better in the sparse factor model setting. The PP stopping criteria have substantially worse TPR than models of size $n$. However, it misses variables with small coefficients, losing only a bit of PMC while giving substantially small screened models. The union of the models from BITS always performs better than the individual BITS algorithms. Thus, UBITS should provide a good hedging against the unknown correlation among the covariates.

Very interestingly, note that the union models have smaller sizes than the sums of the sizes of the three BITS models but have substantially larger posterior mass coverage than the individual BITS. This suggests that the three BITS models overlap substantially, but each picks up some important variables not picked up by others. In order to understand this better, we focus on the compound symmetry setting with $n = 50$ and $p = 100$ where the contrast is most stark. In Table 3, we bin the coefficients and report how often they are picked up to be among the top 50 variables by each of the three BITS settings. We see that small effect sizes are picked up more often by BITS3 with small shrinkage, whereas larger effect sizes are picked up slightly more often by BITS1, followed by BITS2 with larger shrinkage than BITS1. These findings also confirm that UBITS provides good hedging against unknown effect sizes.

BITS also appears to perform as well as or better than the frequentist screening methods. Generally, one of the three BITS settings closely matches or beats the best frequentist method in all but the spurious correlation setting. HOLP has better asymptotic TPR than the other methods under the spurious correlation structure. However, UBITS still captures substantial posterior mass because there are different models with high posterior probabilities.

5. Real data example

We compare the screening methods using a real data set from (Cook et al., 2012) on a genomewide association study for maize starch, protein and oil contents. The original field trial at Clayton, NC in 2006 consisted of more than 5,000 inbred lines and check varieties primarily coming from a diverse panel
Table 1: Simulation results for \( n = 50, p = 100 \).

| Method  | Ind. | CS   | AR   | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|---------|------|------|------|------|------|------|---------|------|
| BITS1(n) | 84.0 | 80.8 | 87.3 | 84.2 | 92.1 | 77.6 | 83.1 | 11.6 |
| BITS1(PP) | 71.9 | 64.3 | 67.3 | 58.4 | 70.2 | 74.9 | 50.4 | 7.8  |
| BITS2(n) | 84.1 | 80.3 | 87.2 | 84.0 | 92.4 | 77.4 | 83.5 | 11.7 |
| BITS2(PP) | 72.0 | 64.2 | 67.1 | 58.3 | 70.3 | 75.0 | 50.4 | 7.8  |
| BITS3(n) | 83.9 | 80.3 | 86.6 | 87.2 | 93.7 | 77.0 | 79.8 | 9.6  |
| BITS3(PP) | 72.4 | 62.9 | 64.8 | 59.7 | 52.3 | 73.9 | 49.3 | 5.0  |
| UBITS(n) | 89.8 | 86.3 | 92.8 | 90.6 | 96.0 | 79.7 | 89.6 | 14.0 |
| UBITS(PP) | 74.0 | 68.3 | 70.0 | 67.6 | 73.2 | 76.7 | 57.2 | 9.7  |
| HOLP(n) | 79.2 | 79.6 | 80.2 | 78.6 | 83.8 | 80.9 | 71.6 | 10.3 |
| HOLP(eBIC) | 34.6 | 27.1 | 34.2 | 47.3 | 31.8 | 40.0 | 15.0 | 0.3  |
| SIS(n) | 77.4 | 61.9 | 80.6 | 60.6 | 90.1 | 60.0 | 71.4 | 0.0  |
| SIS(eBIC) | 30.0 | 14.2 | 25.3 | 14.8 | 28.8 | 29.7 | 7.6  | 0.0  |
| FR(n-2) | 82.8 | 76.9 | 79.0 | 85.9 | 58.9 | 87.2 | 65.2 | 45.9 |
| FR(eBIC) | 50.2 | 36.2 | 41.4 | 47.1 | 24.6 | 47.6 | 16.9 | 0.0  |

Mean posterior mass coverages

| Method  | Ind. | CS   | AR   | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|---------|------|------|------|------|------|------|---------|------|
| BITS1(n) | 68.8 | 68.0 | 69.4 | 55.8 | 75.6 | 66.5 | 54.7 | 63.9 |
| BITS1(PP) | 62.3 | 59.0 | 62.3 | 47.2 | 64.4 | 57.4 | 38.8 | 47.5 |
| BITS2(n) | 68.7 | 67.5 | 69.1 | 56.6 | 75.3 | 65.9 | 57.0 | 63.8 |
| BITS2(PP) | 62.1 | 58.7 | 62.4 | 49.3 | 64.6 | 56.8 | 39.8 | 47.4 |
| BITS3(n) | 68.2 | 66.6 | 67.7 | 59.9 | 73.5 | 64.1 | 54.6 | 60.0 |
| BITS3(PP) | 61.6 | 57.9 | 61.1 | 51.9 | 63.1 | 55.4 | 39.0 | 45.1 |
| UBITS(n) | 91.1 | 94.4 | 91.2 | 88.1 | 97.8 | 90.3 | 97.6 | 99.0 |
| UBITS(PP) | 85.3 | 86.1 | 85.4 | 80.2 | 90.0 | 81.4 | 84.1 | 86.1 |

Median model sizes

| Method  | Ind. | CS   | AR   | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|---------|------|------|------|------|------|------|---------|------|
| BITS1(PP) | 14.0 | 15.0 | 12.0 | 12.0 | 15.0 | 10.0 | 17.5 | 22.0 |
| BITS2(PP) | 14.0 | 15.0 | 12.0 | 12.0 | 15.0 | 10.5 | 17.0 | 21.5 |
| BITS3(PP) | 14.5 | 15.5 | 11.5 | 11.0 | 10.0 | 9.5  | 19.0 | 19.0 |
| UBITS(n) | 67.0 | 65.0 | 66.0 | 62.0 | 66.0 | 60.0 | 65.0 | 58.0 |
| UBITS(PP) | 17.0 | 21.0 | 15.0 | 16.0 | 17.0 | 15.0 | 22.5 | 27.0 |
| HOLP(eBIC) | 3.0 | 2.0 | 3.0 | 5.0 | 3.0 | 3.5 | 2.5 | 1.0 |
| SIS(eBIC) | 2.0 | 1.0 | 2.0 | 2.0 | 1.0 | 2.0 | 1.0 | 1.0 |
| FR(eBIC) | 5.0 | 3.0 | 4.0 | 8.0 | 2.0 | 5.0 | 4.0 | 1.0 |
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Table 2: Simulation results for \( n = 200, p = 10,000 \).

| Method         | Ind. | CS  | AR  | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|----------------|------|-----|-----|------|------|------|---------|-------|
| Mean true positive rates |
| BITS1(n)       | 73.0 | 69.6| 83.3| 61.7 | 84.0 | 68.9 | 9.0     |
| BITS1(PP)      | 73.0 | 69.6| 81.8| 61.7 | 84.0 | 65.5 | 9.0     |
| BITS2(n)       | 76.4 | 71.6| 84.9| 80.1 | 91.0 | 83.7 | 85.4    |
| BITS2(PP)      | 76.2 | 70.9| 74.0| 77.7 | 49.0 | 83.3 | 75.5    |
| BITS3(n)       | 76.6 | 71.3| 82.4| 79.3 | 91.3 | 83.7 | 86.2    |
| BITS3(PP)      | 76.2 | 70.8| 74.0| 75.2 | 38.6 | 83.3 | 75.6    |
| UBITS(n)       | 78.2 | 74.3| 90.6| 80.4 | 92.0 | 87.1 | 89.3    |
| UBITS(PP)      | 78.1 | 74.0| 86.4| 80.6 | 89.7 | 86.9 | 83.1    |
| HOLP(n)        | 61.6 | 64.1| 72.6| 56.8 | 83.0 | 87.3 | 52.8    |
| HOLP(eBIC)     | 45.9 | 42.6| 41.4| 37.1 | 43.7 | 69.4 | 21.0    |
| SIS(n)         | 61.4 | 45.1| 72.8| 14.4 | 82.8 | 54.0 | 53.0    |
| SIS(eBIC)      | 45.8 | 22.9| 41.6| 2.4  | 43.9 | 46.9 | 20.7    |
| FR(n-2)        | 76.7 | 71.0| 74.0| 79.9 | 33.9 | 84.2 | 75.6    |
| FR(eBIC)       | 67.9 | 63.4| 65.4| 68.4 | 27.8 | 70.8 | 67.2    |
| Mean posterior mass coverages |
| BITS1(n)       | 55.6 | 44.6| 53.2| 2.7  | 81.3 | 78.9 | 2.8     |
| BITS1(PP)      | 55.2 | 44.0| 52.7| 2.7  | 79.2 | 77.0 | 2.8     |
| BITS2(n)       | 75.9 | 66.6| 75.2| 43.0 | 82.4 | 80.5 | 70.3    |
| BITS2(PP)      | 75.1 | 65.8| 74.3| 41.7 | 80.8 | 77.7 | 68.3    |
| BITS3(n)       | 76.0 | 66.3| 74.5| 40.8 | 82.4 | 78.7 | 69.9    |
| BITS3(PP)      | 75.2 | 65.4| 73.8| 40.6 | 80.9 | 77.1 | 68.0    |
| UBITS(n)       | 83.4 | 78.0| 82.0| 52.3 | 91.6 | 92.3 | 74.7    |
| UBITS(PP)      | 82.6 | 77.0| 81.2| 51.8 | 90.1 | 89.2 | 73.6    |
| Median model sizes |
| BITS1(PP)      | 136.0| 200.0|125.5|200.0|79.5 |200.0|116.5   |
| BITS2(PP)      | 75.0 | 76.0| 76.0|64.5 |76.0 |9.0  |66.0    |
| BITS3(PP)      | 88.0 | 88.0| 88.5|77.0 |86.0 |9.0  |79.0    |
| UBITS(n)       | 387.0| 386.0|386.5|387.0|384.0|383.0|379.0   |
| UBITS(PP)      | 232.0| 298.0|227.0|299.5|191.0|201.0|195.5   |
| HOLP(eBIC)     | 4.0  | 4.0 | 4.0 | 7.0 | 4.0 | 6.0 | 5.0     |
| SIS(eBIC)      | 4.0  | 2.0 | 4.0 | 3.0 | 4.0 | 5.0 | 5.0     |
| FR(eBIC)       | 6.0  | 6.0 | 6.0 | 14.0| 3.0 | 7.0 | 18.0    |

Table 3: Proportion of the times an important variable with coefficient \( \beta \) is picked up by a BITS algorithm in the compound symmetry setting with \( n = 50, p = 100 \).

| \( \beta \) | (0,.05] | (.05,0.1] | (.1,.15] | (.15,0.2] | (.2,.25] | (.25,.3] | (.3,.5] | (.5,1] | >1 |
|-------------|--------|----------|----------|-----------|---------|---------|---------|--------|----|
| BITS1       | 36.36  | 45.95    | 43.59    | 36.84     | 46.43   | 59.46   | 69.17   | 94.40  | 100 |
| BITS2       | 39.39  | 51.35    | 46.15    | 31.58     | 46.43   | 59.46   | 66.17   | 93.66  | 100 |
| BITS3       | 54.55  | 51.35    | 41.03    | 44.74     | 39.29   | 59.46   | 64.66   | 93.28  | 98.95 |
consisting of 282 founding lines. The response from the field trials are typically spatially correlated, thus we use a random row-column adjustment to obtain the adjusted phenotypes of the varieties. However, marker information of only $n = 3,951$ of these varieties are available from the panzea project (https://www.panzea.org/) which provides information on 546,034 single nucleotide polymorphisms (SNP) markers after removing duplicates and SNPs with minor allele frequency less than 5%. We use the starch content as our phenotype for conducting the association study. Because the inbred varieties are bi-allelic, we store the marker information in a sparse format by coding the minor alleles by one and major alleles by zero.

| Method | BITS1     | BITS2     | BITS3     | BITS(ALL) | HOLP(EBIC) | FR(EBIC) |
|--------|-----------|-----------|-----------|-----------|------------|----------|
| Mean (SE) | 182.9 (16.3) | 46.5 (6.4) | 32.1 (5.6) | 213.2 (18.0) | 1.18 (0.47) | 8.96 (1.09) |

Figure 1: Prediction accuracy on the test sets: correlation (top left), MSPE (top right) using least squares (LM), ridge estimates (Ridge), and Bayesian model averaging (SVEN). The means and standard deviations of model sizes are shown in the table.

In this study, we do a cross-validation by randomly splitting the whole data set with training set of size $n = 3,200$ and testing set of size 751. We run BITS with PP stopping rule with $w$ fixed at 0.1 but with three distinct values of $\lambda$: $p/n$ (BITS1), $n \log(n)/p$ (BITS2) and $n/p$ (BITS3). We also consider the union of these models. We compare these methods with HOLP and FR. The EBIC stopping criterion is also applied to all these methods for comparison. We repeat the process 100 times. In order to be able to use least squares estimates of the regression coefficients, we do not use screened model size same as $n$. However, HOLP and FR result in very small screened models (Figure 1) under EBIC based stopping rule. Indeed, out of 100 repetitions, 44 times HOLP with EBIC results in a null model.
In order to keep the comparisons fair, we also use HOLP and FR with same model size as the union of models from the BITS1, BITS2 and BITS3. For each of the three BITS methods, we use both the ordinary least squares estimates of the regression coefficients (denoted by ‘LM’) and the ridge estimates (denoted by ‘Ridge’) with the associated $\lambda$ because they are the posterior mode of the regression coefficient given the screened model (Figure 1). In addition, we perform a refined variable selection using SVEN (Li et al., 2023b) for each of these screened models (denoted by ‘SVEN’). SVEN allows prediction through Bayesian model averaging.

From the boxplots in Figures 1, it can be seen that models selected by BITS and FR with SVEN stopping rule yield very good prediction accuracies. In particular, union of BITS variables together with Bayesian model averaging yield more accurate MSPE than other BITS methods on an average. HOLP with EBIC stopping rule appears to be overtly conservative. Overall, HOLP with either EBIC or SVEN results in lowest prediction accuracies.

6. Discussion

In this paper, we propose a Bayesian iterative screening (BITS) method for screening variables in an ultra-high dimensional regression model that can accommodate prior information on the effect size and the model size. Despite being built on a Gaussian model assumption, BITS has been shown to be screening consistent even when the family is misspecified. In contrast to SIS, BITS does not require strong assumptions on marginal correlations. Compared to the frequentist iterative screening method FR, BITS naturally accommodates penalization on the effect size enhancing screening accuracy, particularly when important predictors are correlated among themselves. The proposed PP stopping rule, which is shown to be screening consistent, can provide informative screening by incorporating prior knowledge on the hyperparameters. BITS is implemented by a sophisticated algorithm that attains the same computational complexity as HOLP and allows fast statistical computations in ultra-high dimensional problems. BITS has been shown to have better performance than HOLP and FR in most simulation settings, especially when the BITS models from different shrinkages are united. Thus, in practice, it could be useful to take union of models from BITS using various degrees of shrinkage. Then Bayesian or other variable selection algorithms may find it easier to discover useful models. Finally, models from BITS are shown to have substantial posterior mass coverage in all simulation settings.
As a future project, we plan to establish the posterior screening consistency of BITS without the assumption of strong selection consistency and calibrate the stopping rule to return a set of variables that constitutes a subspace of models containing at least a prespecified posterior probability. BITS can be extended to accommodate larger class of models, for example generalized linear regression models. In theory, the iterative algorithm (2.5) is quite general and does not require Gaussianity assumption. We may use Laplace approximations to achieve fast statistical computations in generalized linear models. Also, our future projects include developing Bayesian screening methods for non-linear, partial linear and functional linear models.

**Supplementary Material**

Some useful notations and results. This section contains notations used in the proofs and some results.

Proofs of theorems. Proofs of the theorems stated in the paper appear here.

Proofs of lemmas and corollaries. This section contains proofs of several lemmas and some other results.

Further simulation results. Simulation results for further values of $n$ and $p$.

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Bayesian iterative screening in ultra-high dimensional linear regressions
Run Wang, Somak Dutta, and Vivekananda Roy
Department of Statistics, Iowa State University, USA

Supplementary Material

S1. Some useful notations and results
We use the following notations:

- $\tau^+$ denotes the largest eigenvalue of $X_\gamma^T X_\gamma/n$ for all $|\gamma| \leq K_n |t|$.
- $\Phi$ and $\phi$ denote the standard normal distribution and density function, respectively.

For any model $\gamma$ with $|\gamma| < n$,

- $\tilde{\beta}_\gamma = (X_\gamma^T X_\gamma + \lambda I)^{-1} X_\gamma^T \tilde{y}$ and $H_\gamma = X_\gamma (X_\gamma^T X_\gamma)^{-1} X_\gamma^T$.
- $\text{RSS}_\lambda(\gamma) = \tilde{y}^T \tilde{y} - \tilde{y}^T X_\gamma (X_\gamma^T X_\gamma + \lambda I)^{-1} X_\gamma^T \tilde{y}$.
- $\text{RSS}(\gamma) = \tilde{y}^T \tilde{y} - \tilde{y}^T X_\gamma (X_\gamma^T X_\gamma)^{-1} X_\gamma^T \tilde{y} = \tilde{y}^T (I - H_\gamma) \tilde{y}$.
- $\Omega(\gamma) = -\frac{|\gamma|}{2(n-1)} \log \lambda + \frac{1}{2(n-1)} \log |X_\gamma^T X_\gamma + \lambda I| + \frac{1}{2} \log \text{RSS}_\lambda(\gamma) - \frac{|\gamma|}{n-1} \log w - \frac{p - |\gamma|}{n-1} \log (1 - w)$ which is equal to $-\log f(\gamma|y)/(n-1)$ up to an additive constant that does not depend on $\gamma$.

First we state some useful results whose proofs are given in Section S3 of the supplement. These results are used in the proofs of Theorems 2 and 4.

Lemma 3. For any model $\gamma$ with $|\gamma| < n$, and any $i \notin \gamma$,

$$\text{RSS}(\gamma) - \text{RSS}(\gamma + e_i) = \frac{(X_i^T \tilde{y} - X_i^T H_\gamma \tilde{y})^2}{n - X_i^T H_\gamma X_i}.$$
Lemma 4. For any model $\gamma$ and $j \notin \gamma$, \( \log |X_{\gamma'}^T X_{\gamma'} + \lambda I| - \log |X_{\gamma}^T X_{\gamma} + \lambda I| \) lies between $\log \lambda$ and $\log(n + \lambda)$ where $\gamma' = \gamma + e_j$.

Lemma 5. Under conditions C2 and C3, there exists $c' > 0$ and $c'' > 0$ such that for all sufficiently large $n$,

$$\log(1 + nK_n|t|/\lambda) \leq 2c' \log n, \text{ and}$$

$$\frac{K_n\lambda}{2n\tau_+} + \frac{K_n \log(n + \lambda)}{2(n - 1)} - \frac{K_n \log \lambda}{2(n - 1)} \leq c'' \log n. \quad (S1)$$

Lemma 6. Suppose $|\gamma| < K_n|t|$ and $\gamma \nsubseteq t$ then $\max_{k \in \gamma \setminus \gamma} \{\Omega(\gamma) - \Omega(\gamma + e_k)\} \geq \max_{k \in \gamma \setminus \gamma} \{\text{RSS}(\gamma) - \text{RSS}(\gamma + e_k)\}/(2\|\tilde{y}\|^2) - \lambda/(2n\tau_+) - \log(n/\lambda + 1)/(2(n - 1)) + \log(w/(1 - w))/(n - 1)$.

Lemma 7. Suppose $|\gamma| < K_n|t|$ and $\gamma \nsubseteq t$, then with $s_n$ given in C3,

$$\max_{k \in t \cap \gamma} (X_k^T(I - H_\gamma)X_k\beta_t)^2 \geq ns_n^2.$$

Corollary 2. Suppose $|\gamma| < K_n|t|$, $\gamma \nsubseteq t$, and $\sigma \Upsilon_n < s_n$. Let

$$a_{\gamma',t} = (I - H_{\gamma'})X_t/\| (I - H_{\gamma'})X_t \| \text{ and } \Upsilon_n = \max_{l \in t} \max_{\gamma' : |\gamma'| < K_n|t|} |a_{\gamma',l}|.$$

Then $\max_{k \in t \cap \gamma} \{\text{RSS}(\gamma) - \text{RSS}(\gamma + e_k)\} \geq (s_n - \sigma \Upsilon_n)^2$.

S2. Proofs of theorems

Proof of Theorem 1. Under the orthogonal design,

$$f(\gamma + e_i|y) > f(\gamma + e_j|y) \iff (X_i^T \tilde{y})^2 > (X_j^T \tilde{y})^2,$$

which does not depend on $\gamma$. Now, for each $i \in t$, suppose $A_i$ denotes the event \{(X_i^T \tilde{y})^2 > \max_{j \notin t} (X_j^T \tilde{y})^2\}. Then the theorem will be proved if $P(\cap_{i \in t} A_i) \rightarrow 1$ as $n \rightarrow \infty$, for which it is sufficient to show that $\sum_{i \in t} P(A_i^c) \rightarrow 0$, as $n \rightarrow \infty$.

To that end, assume without loss that true $\sigma^2 = 1$ and notice that for $1 \leq l \leq p$, $U_l := n^{-1/2}X_l^T \epsilon$ are iid standard normal because $X^T X = nI_p$. Thus for all $i \in t$ and $j \notin t$, $X^T 1 = 0$ implies that $X_i^T \tilde{y} = n\beta_i + \sqrt{n}U_i$ and $X_j^T \tilde{y} = \sqrt{n}U_j$.

Thus, $A_i = \{(\sqrt{n}\beta_i + U_i)^2 > \max_{j \notin t} U_j^2\}$. Consequently, since $U_i$'s are iid standard normal, we have,

$$P(A_i^c) = 1 - P(A_i) = 1 - E \prod_{j \notin t} P(|U_j| \leq |\sqrt{n}\beta_i + U_i| \mid U_i)$$
Let $\gamma = \arg \min t \{ \gamma^{(i)} \cap t \neq \emptyset \}$ for $j \geq 2$, 
$$
\theta_j = \arg \min \{ (\gamma^{(i)} \setminus \gamma^{(\theta_j - 1)}) \cap t \neq \emptyset \}.
$$
We note that, 
$$
\{ \gamma^{(K_n|t|)} \not\supset t \} = \{ \theta_{|t|} > K_n|t| \} \subseteq \bigcup_{j=0}^{|t|-1} \{ \theta_{j+1} - \theta_j > K_n \}
= \bigcup_{j=0}^{|t|-1} \{ \theta_{j+1} - \theta_j > K_n, \text{ and } \theta_{i+1} - \theta_i \leq K_n \forall 0 \leq i < j \}.
$$

**Proof of Theorem 2.** Let $\theta_0 = 0$ and $\theta_1, \theta_2, \ldots, \theta_{|t|}$ denote the random inclusion times of the variables in $t$ in the models $\gamma^{(1)}, \gamma^{(2)}, \ldots$. That is, $\theta_1 = \arg \min_{i \geq 1} \{ \gamma^{(i)} \cap t \neq \emptyset \}$ and for $j \geq 2$, 
$$
\theta_j = \arg \min_{i > \theta_{j-1}} \{ (\gamma^{(i)} \setminus \gamma^{(\theta_{j-1})}) \cap t \neq \emptyset \}.
$$

Because $2\Phi(|\sqrt{n}\beta_i + U_i|) - 1 < 1$ and $1 - \Phi(x) \leq \phi(x)/x$ for all $x > 0$, the first term on the right side of (S3) is at most 
$$
P(|U| > \sqrt{2\log n}) \leq 2/(n\sqrt{4\pi \log n}). \quad (S4)
$$

Next, since $\sqrt{n}\beta_+ > \sqrt{\log n}$, for all sufficiently large $n$, $\sqrt{n}\beta_+ - 2\log n > c_n := 2\sqrt{\log n}$. Thus, the second term on the right side of (S3) is at most 
$$
E \left[ \{ 1 - (2\Phi(\sqrt{n}|\beta_i| - |U_i|) - 1)^n \} I(|U| \leq \sqrt{2\log n}) \right]
\leq 1 - (2\Phi(\sqrt{n}\beta_+ - 2\log n) - 1)^n \leq 1 - (2\Phi(c_n) - 1)^n
\leq 2n[1 - \Phi(c_n)]/c_n \leq \frac{1}{n \log n} \leq \frac{2}{n \sqrt{8\pi \log n}}, \quad (S5)
$$
where the third last inequality holds because $(1 - x)^n \geq 1 - nx$, for $x \leq 1$.

Thus, from (S3), (S4) and (S5) we have, for all sufficiently large $n$, that 
$$
\sum_{i \in t} P(A_i^c) \leq \sum_{i \in t} \left\{ \frac{2}{n \sqrt{4\pi \log n}} + \frac{2}{n \sqrt{8\pi \log n}} \right\} = \frac{2(\sqrt{2} + 1)|t|}{n \sqrt{8\pi \log n}}.
$$
The right hand side $\to 0$ as $n \to \infty$ because $|t| = O(n^a)$ for some $a < 1$. \qed
where \( \cup \) denotes union of disjoint sets. We now analyze the \( j \)th event \( \{ \theta_{j+1} - \theta_j > K_n, \theta_j \leq jK_n \} \). Note that, \( \theta_{j+1} - \theta_j > K_n \) implies that for each \( i = \theta_j, \theta_j + 1, \ldots, \theta_j + K_n - 1 \), it must be that a variable outside of \( t \) was selected in the \((i + 1)\)st iteration, that is, for each such \( i \), \( \Omega(\gamma(i)) - \Omega(\gamma(i+1)) > \max_{k \in t \backslash \gamma(i)} \{ \Omega(\gamma(i)) - \Omega(\gamma(i) + e_k) \} \); and also that \( i < K_n|t| \) and \( \gamma(i) \notin t \).

Thus using Lemma 6, Corollary 2, and (S2), we get

\[
\{ \theta_{j+1} - \theta_j > K_n, \theta_j \leq jK_n \} \cap \{ \sigma Y_n < s_n \} \quad \text{(S7)}
\]

\[
\subseteq \left\{ \sum_{i=\theta_j}^{\theta_j+K_n-1} (\Omega(\gamma(i)) - \Omega(\gamma(i+1))) \right\}
\]

\[
\leq \left\{ \sum_{i=\theta_j}^{\theta_j+K_n-1} (\Omega(\gamma(i)) - \Omega(\gamma(i+1))) \right\} + \frac{K_n}{2\|s\|^2} |s_n - \sigma Y_n|^2 - e'' \log n + \frac{K_n}{n-1} \log \frac{w}{1-w} \right\}
\]

However, on the other hand, on \( \{ \theta_{j+1} - \theta_j > K_n, \theta_j \leq jK_n \} \) we have using Lemma 4

\[
\sum_{i=\theta_j}^{\theta_j+K_n-1} (\Omega(\gamma(i)) - \Omega(\gamma(i+1))) \leq \frac{1}{2} \sum_{i=\theta_j}^{\theta_j+K_n-1} (\log(\text{RSS}_\lambda(\gamma(i))) - \log(\text{RSS}_\lambda(\gamma(i+1))))
\]

\[
= \frac{1}{2} \left\{ \log \lambda \left( \frac{1}{2(n-1)} - \frac{1}{2(n-1)} \right) \right\} + \frac{K_n}{n-1} \log \frac{w}{1-w}
\]

\[
< \frac{1}{2} \left\{ \log \|\tilde y\|^2 - \log(\text{RSS}_\lambda(\gamma(\theta_j))) \right\} + \frac{K_n}{n-1} \log \frac{w}{1-w}
\]

\[
\leq \frac{1}{2} \log(1 + nK_n|t|/\lambda) + \frac{K_n}{n-1} \log \frac{w}{1-w} \quad \text{(S8)}
\]

because \( \tau^+ \leq K_n|t| \) and

\[
\text{RSS}_\lambda(\gamma(\theta_j+K_n)) = \tilde y^T \left( I + \frac{1}{\lambda} X_{\gamma(\theta_j+K_n)} X_{\gamma(\theta_j+K_n)}^T \right)^{-1} \tilde y \geq \|\tilde y\|^2(1 + n\tau^+ / \lambda)^{-1}
\]

\[
\geq \|\tilde y\|^2(1 + nK_n|t|/\lambda)^{-1}.
\]
Thus applying (S1) from (S8) we get
\[ \sum_{i=\theta_j}^{\theta_j+K_n-1} (\Omega(\gamma^{(i)}) - \Omega(\gamma^{(i+1)})) \leq c' \log n + \frac{K_n}{n-1} \log \frac{w}{1-w}. \] (S9)

Hence, with \( c = 2(c' + c'') \), using (S7), (S9) and condition C3, for sufficiently large \( n \), for all \( j \),
\[ \{\theta_{j+1} - \theta_j > K_n, \theta_j \leq jK_n\} \cap \{\sigma \gamma_n < s_n\} \]
\[ \subseteq \{c' \log n \geq \frac{K_n}{2\|\tilde{y}\|^2}(s_n - \sigma \gamma_n)^2 - c'' \log n\} \cap \{\sigma \gamma_n < s_n\} \]
\[ \subseteq \left\{ \frac{K_n}{\|\tilde{y}\|^2}(s_n - \sigma \gamma_n)^2 \leq c \log n \right\} \cap \{\sigma \gamma_n < s_n\} \subseteq \left\{ s_n \left(1 - \sqrt{\|\tilde{y}\|^2/(nu_n)}\right) \leq \sigma \gamma_n < s_n \right\} \]
where \( u_n = \tau^2_+ \beta^4 K_n/(c\|t\|/\beta_t^2 \log n) \). Thus,
\[ \{\theta_{j+1} - \theta_j > K_n, \theta_j \leq jK_n\} \subseteq \{\theta_{j+1} - \theta_j > K_n, \theta_j \leq jK_n\} \cap \{\sigma \gamma_n < s_n\} \cup \{\sigma \gamma_n \geq s_n\} \]
\[ \subseteq \left\{ s_n \left(1 - \sqrt{\|\tilde{y}\|^2/(nu_n)}\right) \leq \sigma \gamma_n < s_n \right\} \cup \{\sigma \gamma_n \geq s_n\} \]
\[ = \left\{ s_n \left(1 - \sqrt{\|\tilde{y}\|^2/(nu_n)}\right) \leq \sigma \gamma_n \right\}. \]

Since for all sufficiently large \( n \), the above is true for all \( j \), we have from (S6) that
\[ \{\theta_{|t|} > K_n|t|\} \subseteq \left\{ \sigma \gamma_n \geq s_n \left(1 - \sqrt{\|\tilde{y}\|^2/(nu_n)}\right) \right\}. \] (S10)

Thus, for all sufficiently large \( n \), using the union bound,
\[ P(\theta_{|t|} > K_n|t|) \leq P\left( \sigma \gamma_n \geq s_n \left(1 - \sqrt{\|\tilde{y}\|^2/(nu_n)}\right) \right) \]
\[ \leq P\left( \sigma \gamma_n \geq s_n \left(1 - \sqrt{\|\tilde{y}\|^2/(nu_n)}\right), \|\tilde{y}\|^2 \leq nu_n(1 - \sigma \delta)^2 \right) + P(\|\tilde{y}\|^2 > nu_n(1 - \sigma \delta)^2) \]
\[ \leq P(\gamma_n \geq s_n \delta) + P(\|\tilde{y}\|^2 > nu_n(1 - \sigma \delta)^2) \]
\[ \leq \sum_{l \in \gamma: \gamma_l < K_n|t|} \sum_{\gamma_l \in \gamma/\gamma_l < K_n|t|} P(\|\tilde{y}\|^2 > nu_n(1 - \sigma \delta)^2) \]
\[ \leq \sum_{l \in \gamma: \gamma_l < K_n|t|} \sum_{\gamma_l \in \gamma/\gamma_l < K_n|t|} e^{1-q(s_n \delta)} + P(\|\tilde{y}\|^2 > nu_n(1 - \sigma \delta)^2) \]
\[ \leq \exp(1 - q(s_n \delta) + K_n|t| \log p + \log |t|) + P(\|\tilde{y}\|^2 > nu_n(1 - \sigma \delta)^2). \]

This proves the theorem. \( \Box \)
Proof of Theorem 3. Assume without loss that the true $\sigma^2 = 1$. First we shall show that $\mathbb{P}(T \geq |t|) \to 1$. As in the proof of Theorem 1 note that for any $i \in t$, $(X_i^\top \bar{y})^2 = (n\beta_i + \sqrt{n}U_i)^2$ where $U_i$'s are i.i.d $N(0, 1)$ variables. Thus for any $\gamma \subset t$, and $i \in t \cap \gamma^c$, $f(\gamma + e_i|y) < f(\gamma|y)$ is equivalent to,

$$
\log a_n + (n - 1) \log(RSS_\lambda(\gamma)) < (n - 1) \left\{ \log \left( RSS_\lambda(\gamma) - (X_i^\top \bar{y})^2/(n + \lambda) \right) \right\}
\iff \frac{(\sqrt{n} \beta_i + U_i)^2}{\log n} < \frac{1}{n + \lambda} \frac{n + \lambda}{n} RSS_\lambda(\gamma) \left( 1 - a_n^{\frac{1}{n-\lambda}} \right)
$$

(S11)

where $a_n = \lambda w^2/((n + \lambda)(1 - w)^2)$. But, $RSS_\lambda(\gamma) \leq \|\bar{y}\|^2 = n\|\beta_i\|^2 + 2\beta_i^\top X_i^\top \epsilon + \|\epsilon\|^2$ and hence $\|\bar{y}\|^2/n \to \|\beta_i\|^2 + 1$ almost surely. Recall that as in Theorem 1, $\lambda$ is assumed fixed here. Also, $\log a_n/\log n \to -(2c + 1)$ as $n \to \infty$,

$$
\frac{1}{n + \lambda} RSS_\lambda(\gamma) \left( 1 - a_n^{\frac{1}{n-\lambda}} \right) \leq \frac{\|\bar{y}\|^2 + n \log a_n (1 - e^{(\log a_n)/(n-1)})}{n - 1} \to (2c + 1)(\|\beta_i\|^2 + 1),
$$

in probability. Hence, $P(A_0) \to 1$, as $n \to \infty$ where

$$
A_0 = \left\{ \max_{\gamma \subseteq t} \frac{1}{n + \lambda} \frac{n + \lambda}{n} RSS_\lambda(\gamma) \left( 1 - a_n^{\frac{1}{n-\lambda}} \right) < c'' \right\}
$$

for some constant $c'' > 0$. Next denote $A = \cap_{i \in t} A_i$ where $A_i$'s are defined in the proof of Theorem 1. Then $P(A) \to 1$, as $n \to \infty$ and $\gamma(j) \subset t$ for $1 \leq j \leq |t|$ on $A$.

Since $\sqrt{n} \beta_i > \sqrt{\log n}$, we have $\sqrt{n} |\beta_i| - \sqrt{c'' \log n} > \sqrt{2 \log n}$ for all $i$, and for all large $n$. Hence, from (S11) note that for $1 \leq j < |t|$, and $i \in t \setminus \gamma(j)$, we have, by symmetry of $U_i$

$$
P \left( A_0 \cap A \cap \left\{ \max_{i \in t \setminus \gamma(j)} f(\gamma(j) + e_i|y) < f(\gamma(j)|y) \right\} \right) \leq P \left( (\sqrt{n} \beta_i + U_i)^2 < c'' \log n \right)
\leq P(U_i > \sqrt{n} |\beta_i| - \sqrt{c'' \log n}) \leq P(U_i > \sqrt{2 \log n}) \leq \frac{1}{n \sqrt{4 \pi \log n}}.
$$

(S12)

for sufficiently large $n$. Thus from (S11) and (S12) we have,

$$
P(T < |t|) \leq P \left( A_0 \cap A \cap \bigcup_{j=1}^{|t|-1} \left\{ \max_{i \in t \setminus \gamma(j)} f(\gamma(j) + e_i|y) < f(\gamma(j)|y) \right\} \right) + P(A_0^c) + P(A^c)
\leq \sum_{j=1}^{|t|-1} P \left( A_0 \cap A \cap \left\{ \max_{i \in t \setminus \gamma(j)} f(\gamma(j) + e_i|y) < f(\gamma(j)|y) \right\} \right) + P(A_0^c) + P(A^c)
$$
\[
\leq |t|/(n\sqrt{4\pi \log n}) + P(A_0^c) + P(A^c),
\]
so that \(\lim P(T < |t|) = 0.\)

Next, we show that \(P(T \geq |t| + 1) \to 0.\) To that end, suppose \(j \notin t.\) Then the probability of stopping the iteration exactly at \(|t|\) is \(P(\max_{j \notin t} f(t + e_j|y) < f(t|y)).\) Since for any \(j \notin t, (X_j^\top \tilde{y})^2 = nU_j^2\) where \(U_j\)’s are i.i.d \(N(0,1)\) variables, \(\max_{j \notin t} f(t + e_j|y) < f(t|y)\) is equivalent to

\[
\log a_n + (n-1) \log(RSS_\lambda(t)) < (n-1) \min_{j \notin t} \{\log (RSS_\lambda(t) - (X_j^\top \tilde{y})^2/(n+\lambda))\}
\]

\[
\iff \max_{j \notin t} \frac{U_j^2}{\log n} < \frac{1}{n+\lambda} \frac{n+\lambda}{n} RSS_\lambda(t) \left(1 - \frac{1}{n+1}\right), \tag{S13}
\]

where \(a_n = \lambda w^2/((n+\lambda)(1-w)^2)\) is as defined before. We will now show that the left side is less than 2 with probability tending to 1 and the right side converges to \(2c+1 > 2\) in probability. This will complete the proof.

First, as \(n \to \infty,\) we have

\[
P(\max_{j \notin t} U_j^2 > 2 \log n) \leq \sum_{j \notin t} P(U_j^2 > 2 \log n) \leq 2n \left(1 - \Phi(\sqrt{2\log n})\right) \leq \frac{1}{\sqrt{\pi \log n}} \to 0.
\]

Then, note that under the orthogonal design, for any \(\gamma \subseteq t,\)

\[
RSS_\lambda(t) = RSS(t) + \frac{\lambda}{n(n+\lambda)} \tilde{y}^\top X_t X_t^\top \tilde{y},
\]

and \(RSS(t)/n \to 1,\) in probability, so that \(RSS_\lambda(t)/(n-1) \to 1\) in probability. Consequently, as \(n \to \infty,\) with probability tending to one,

\[
\frac{1}{\log n} \frac{n+\lambda}{n} RSS_\lambda(t) \left(1 - \frac{1}{n+1}\right) = \frac{n+\lambda}{n-1} RSS_\lambda(t) \frac{1 - e^{(\log a_n)/(n-1)}}{\log a_n} \log n \to 2c+1 > 2.
\]

\[\square\]

**Proof of Theorem 4.** Let

\[
B_i = \left\{ \max_{k \notin \gamma(i)} (\Omega(\gamma^{(i)}) - \Omega(\gamma^{(i)} + e_k)) < 0 \right\} \cap \{\gamma^{(i)} \notin t\}.
\]

Thus BITS is stopped **prematurely** by the posterior probability criterion without including all variables in \(t\) iff \(B_i\) happens for some \(i.\) However, note that

\[
\cup B_i = \left\{ \cup_{i=1}^{K_n|t|} B_i \right\} \cup \{ \cup_{i>K_n|t|} B_i \}.
\]
We first analyze $\bigcup_{i=1}^{K_n |t|} B_i$. To that end, note that when $\gamma^{(i)}$ does not contain $t$,
\[
\max_{k \in t \setminus \gamma^{(i)}} (\Omega(\gamma^{(i)}) - \Omega(\gamma^{(i)} + \epsilon_k)) \leq \max_{k \notin \gamma^{(i)}} (\Omega(\gamma^{(i)}) - \Omega(\gamma^{(i)} + \epsilon_k)).
\]
Consequently, for $i \leq K_n |t|$, we have
\[
B_i \cap \{ \sigma Y_n < s_n \} \subseteq \left\{ \max_{k \in t \setminus \gamma^{(i)}} (\Omega(\gamma^{(i)}) - \Omega(\gamma^{(i)} + \epsilon_k)) < 0 \right\} \cap \{ \sigma Y_n < s_n \}
\]
\[
\subseteq \left\{ \frac{1}{2 \| \bar{y} \|^2} \max_{k \in t \setminus \gamma^{(i)}} (\text{RSS}(\gamma^{(i)} - \text{RSS}(\gamma^{(i)} + \epsilon_k))) < \frac{\lambda}{2n \tau_+} + \frac{\log(n + \lambda) - \log \lambda}{2(n-1)} - \frac{\log w}{n-1} \right\} \cap \{ \sigma Y_n < s_n \}
\]
\[
\subseteq \left\{ \frac{1}{2 \| \bar{y} \|^2} |s_n - \sigma Y_n|^2 < \frac{c'' \log n}{K_n} - \frac{1}{n-1} \log \frac{w}{1-w} \right\} \cap \{ \sigma Y_n < s_n \}
\]
which is independent of $i$. In the second set inequality above we have used Lemma 6 and the third inequality is due to Corollary 2 and (S2). Also, note that
\[
c'' \log n - \frac{K_n}{n-1} \log \frac{w}{1-w} < c'' \log n
\]
by condition C3 for some $c'' > 0$ for sufficiently large $n$. Hence, for sufficiently large $n$,
\[
\bigcup_{i=1}^{K_n |t|} B_i \subseteq \left\{ \{ \sigma Y_n < s_n \} \cap \bigcup_{i=1}^{K_n |t|} B_i \right\} \cup \{ \sigma Y_n \geq s_n \}
\]
\[
\subseteq \left\{ \frac{K_n}{2 \| \bar{y} \|^2} |s_n - \sigma Y_n|^2 < c'' \log n, \sigma Y_n < s_n \right\} \cup \{ \sigma Y_n \geq s_n \}
\]
\[
\subseteq \left\{ s_n \left( 1 - \sqrt{\| \bar{y} \|^2/(nu_n')} \right) \leq \sigma Y_n \right\}
\] (S14)
where $u_n' = \tau_+^2 \beta_+^4 K_n/(2c'' |t| \| \beta_t \|^2 \log n)$. Note from the (S10) that
\[
\bigcup_{i > K_n |t|} B_i \subseteq \{ \theta_{|t|} > K_n |t| \} \subseteq \left\{ s_n \left( 1 - \sqrt{\| \bar{y} \|^2/(nu_n)} \right) \leq \sigma Y_n \right\}. \quad \text{(S15)}
\]
Now let $c^* = \max\{ c, 2c'' \}$ and $u_n^* = \min\{ u_n, u_n' \} = \tau_+^2 \beta_+^4 K_n/(c^* |t| \| \beta_t \|^2 \log n)$. Then, for all sufficiently large $n$, combining (S14) and (S15) we finally get,
\[
P(\bigcup B_i) \leq P \left( \sigma Y_n \geq s_n \left( 1 - \sqrt{\| \bar{y} \|^2/(nu_n^*)} \right) \right)
\]
\[
\leq \exp(1 - q(s_n \delta) + K_n |t| \log p + \log |t|) + P(\| \bar{y} \|^2 > nu_n^*(1 - \sigma \delta)^2). \quad \square
\]
S3. Proofs of lemmas and corollaries

S3.1 Proof of Lemma 1

Proof. Since \( K_n = n^{\xi_0 + 4\xi_{\min}} (\log n)^2 \),
\[
\frac{|t||\beta_t|^2 \log n}{\tau_+^2 \beta_+^4} \leq \nu \nu^{-4} \tau_{\min}^{-2} C_\beta^2 n^{\xi_0 + 4\xi_{\min}} \log n < K_n.
\]

Also, since \( \lambda \) and \( w \) are fixed here, and \( \tau_+ \geq \tau_{\min} \),
\[
n \log n \min \left\{ \frac{1}{\lambda}, \left| \log \left( \frac{1}{w} - 1 \right) \right| \right\} \geq c_n \log n
\]
for some constant \( c_n \). Thus, if \( \xi_0 + 4\xi_{\min} < 1 \),
\[
\frac{|t||\beta_t|^2 \log n}{\tau_+^2 \beta_+^4} \leq K_n \leq n \log n \min \left\{ \frac{1}{\lambda}, \left| \log \left( \frac{1}{w} - 1 \right) \right| \right\}.
\]

Next, since \( \epsilon_i \overset{iid}{\sim} N(0, 1) \), \( q(\zeta) = \zeta^2 / 2 \). Therefore,
\[
q(s_n \delta) - K_n |t| \log p - \log |t| \geq \frac{n \tau_+^2 \beta_+^4 \delta^2}{2||\beta_t||^2|t|} - K_n |t| \log p - \log |t|
\geq 0.5 \delta^2 \nu^{-1} \nu^{-1} \tau_{\min}^{-2} C_\beta^{-2} n^{1-\xi_0-4\xi_{\min}} - \nu^2 n^{\xi_0+4\xi_{\min}} (\log n)^2
\geq -\nu \xi_0 \log n
\]  
(S16)

Note that (S16) \( \to \infty \) because \( \xi + 3\xi_0 + 8\xi_{\min} < 1 \).

S3.2 Proof of Lemma 2

Proof. Note that \( RSS_\lambda(\gamma) = nn_{\gamma, \gamma, \lambda} \). Suppose \( U_\gamma \) denotes the upper triangular Cholesky factor of \( X_\gamma^\top X_\gamma + \lambda I \). And let for \( i \notin \gamma, \gamma' = \gamma + e_i \). Then arranging the columns of \( X_{\gamma'} \) appropriately, we can assume that the Cholesky factor of \( X_{\gamma'}^\top X_{\gamma'} + \lambda I \) is given by
\[
U_{\gamma'} = \begin{pmatrix} U_\gamma & s \\ 0 & s_0 \end{pmatrix}
\]
so that \( U_{\gamma'}^{-\top} X_{\gamma'} \hat{y} = \left( U_{\gamma'}^{-\top} X_\gamma \hat{y} - s_0^\top U_{\gamma'}^{-\top} X_\gamma \hat{y} / s_0 \right) = \left( U_{\gamma'}^{-\top} X_\gamma \hat{y} / \sqrt{nn_{\gamma, \gamma, \lambda} / \sqrt{v_{\gamma, \lambda}}} \right) \)
where \( s = U_{\gamma'}^{-\top} X_{\gamma'} X_i \) and \( s_0^2 = X_i^\top X_i + \lambda - s^\top s = nn_{i, \gamma, \lambda} \). Also note that,
\[
RSS_\lambda(\gamma) - RSS_\lambda(\gamma') = ||U_{\gamma'}^{-\top} X_{\gamma'} \hat{y}||_2^2 - ||U_{\gamma}^{-\top} X_\gamma \hat{y}||_2^2 = nn_{\gamma, \gamma, \lambda}^2 / v_{\gamma, \lambda}
\]
\[ \Rightarrow \{ \text{RSS}_\lambda(\gamma) - \text{RSS}_\lambda(\gamma') \} / \text{RSS}_\lambda(\gamma) = R^2_{i, \gamma, \lambda} \]
\[ \Rightarrow \log \text{RSS}_\lambda(\gamma') - \log \text{RSS}_\lambda(\gamma) = \log \left( 1 - R^2_{i, \gamma, \lambda} \right). \]

Also,
\[ \log |X^\top_{\gamma'} X_{\gamma'} + \lambda I| - \log |X^\top_{\gamma} X_{\gamma} + \lambda I| = 2 \log s_0 = \log (nv_{i, \gamma, \lambda}). \]

Therefore,
\[ \log f(\gamma'|y) - \log f(\gamma|y) = \frac{1}{2} \log \lambda - \frac{1}{2} \left( \log |X^\top_{\gamma'} X_{\gamma'} + \lambda I| - \log |X^\top_{\gamma} X_{\gamma} + \lambda I| \right) \]
\[ - \frac{n - 1}{2} \left( \log \text{RSS}_\lambda(\gamma') - \log \text{RSS}_\lambda(\gamma) \right) + \log(w/(1-w)) \]
\[ = \frac{1}{2} \log(n\lambda w^2/(1-w)^2) - \frac{1}{2} (n - 1) \log \{1 - R^2_{i, \gamma, \lambda}\}, \]

which completes the proof.

S3.3 Proof of Lemma 3

Proof. Since
\[ \text{RSS}(\gamma) - \text{RSS}(\gamma + \epsilon_i) = (\bar{y}^\top X_{\gamma} \bar{y}^\top X_i) \left( \begin{array}{cc} X^\top_{\gamma} X_{\gamma} & X^\top_{\gamma} X_i \\ X^\top_i X_{\gamma} & n \end{array} \right)^{-1} \left( \begin{array}{c} X^\top_{\gamma} \bar{y} \\ X^\top_i \bar{y} \end{array} \right) - \bar{y}^\top X_{\gamma} (X^\top_{\gamma} X_{\gamma})^{-1} X^\top_{\gamma} \bar{y}, \]
the proof follows from the fact that
\[ \left( \begin{array}{cc} X^\top_{\gamma} X_{\gamma} & X^\top_{\gamma} X_i \\ X^\top_i X_{\gamma} & n \end{array} \right)^{-1} \]
\[ = \frac{1}{a} \left( a(X^\top_{\gamma} X_{\gamma})^{-1} + (X^\top_{\gamma} X_{\gamma})^{-1} X^\top_i X_{\gamma} (X^\top_{\gamma} X_{\gamma})^{-1} - (X^\top_{\gamma} X_{\gamma})^{-1} X^\top_i X_{\gamma} \right) \]
\[ \begin{array}{c} X^\top_{\gamma} X_{\gamma} \\ X^\top_i X_{\gamma} \end{array} \]

where \( a = n - X^\top_i X_{\gamma} (X^\top_{\gamma} X_{\gamma})^{-1} X^\top_{\gamma} X_{\gamma} \).

S3.4 Proof of Lemma 4

Proof. Note that,
\[ \log |X^\top_{\gamma'} X_{\gamma'} + \lambda I| - \log |X_{\gamma} X_{\gamma} + \lambda I| = \log(n+\log X^\top_j X_{\gamma}(X^\top_{\gamma} X_{\gamma} + \lambda I)^{-1} X^\top_j X_{\gamma}), \]
because \( X^\top_j X_{j} = n \). Since \( X^\top_j X_{\gamma}(X^\top_{\gamma} X_{\gamma} + \lambda I)^{-1} X^\top_j X_{\gamma} \geq 0 \) (equality holding iff \( X^\top_j X_{j} = 0 \)) and \( n - X^\top_j X_{\gamma}(X^\top_{\gamma} X_{\gamma} + \lambda I)^{-1} X^\top_j X_{\gamma} > 0 \), the result follows immediate.
S3.5 Proof of Lemma 5

Proof. To prove (S1) note that
\[
\log(1 + nK_n|t|/\lambda) \leq \max\{\log 2, \log(2nK_n|t|/\lambda) = O(\log n),
\]
since \(K_n|t| < n\) and \(|\log \lambda| = O(\log n)\). To prove (S2) note that \(K_n\lambda/(n\tau_+) = O(\log n)\) and \(K_n < n\).

\[\square\]

S3.6 Proof of Lemma 6

Proof. Note that for any \(k \notin \gamma\),
\[
\Omega(\gamma) - \Omega(\gamma + e_k) \\
\geq \frac{1}{2} \left( \log \text{RSS}_\lambda(\gamma) - \log \text{RSS}_\lambda(\gamma + e_k) \right) - \frac{\log(n + \lambda)}{2(n - 1)} + \frac{\log \lambda}{2(n - 1)} + \frac{1}{n - 1} \log \frac{w}{1 - w} \\
= \frac{1}{2} \left( \log \frac{\text{RSS}_\lambda(\gamma)}{\|\tilde{y}\|^2} - \log \frac{\text{RSS}_\lambda(\gamma + e_k)}{\|\tilde{y}\|^2} \right) - \frac{\log(n + \lambda)}{2(n - 1)} + \frac{\log \lambda}{2(n - 1)} + \frac{1}{n - 1} \log \frac{w}{1 - w} \\
\geq \frac{1}{2\|\tilde{y}\|^2} \left( \text{RSS}(\gamma) - \text{RSS}(\gamma + e_k) \right) - \frac{\log(n + \lambda)}{2(n - 1)} + \frac{\log \lambda}{2(n - 1)} + \frac{1}{n - 1} \log \frac{w}{1 - w} \\
+ \frac{1}{n - 1} \log \frac{w}{1 - w} \\
= \frac{1}{2\|\tilde{y}\|^2} \left( \text{RSS}(\gamma) - \text{RSS}(\gamma + e_k) \right) - \frac{\lambda}{2n\tau_+} - \frac{\log(n + \lambda)}{2(n - 1)} + \frac{\log \lambda}{2(n - 1)} + \frac{1}{n - 1} \log \frac{w}{1 - w}.
\]

In the above, the first inequality follows from the definition of \(\Omega(\gamma)\) and Lemma 4; the second inequality follows from the facts that \(\text{RSS}_\lambda(\gamma) < \|\tilde{y}\|^2\) for any model \(\gamma\) and that \(\log u - \log v \geq u - v\) for \(0 < v < u < 1\). Finally, the last inequality follows from the facts that \(\text{RSS}_\lambda(\gamma) \geq \text{RSS}(\gamma)\) for any \(\gamma\) and that for all \(\gamma'\) of size at most \((K_n + 1)|t|\) we have
\[
\text{RSS}_\lambda(\gamma') - \text{RSS}(\gamma') = \tilde{y}^T X_{\gamma'} \left( (X_{\gamma'}^T X_{\gamma'})^{-1} - (X_{\gamma'}^T X_{\gamma'} + \lambda I)^{-1} \right) X_{\gamma'}^T \tilde{y}
\]
because the nonzero eigenvalues of \( X_{\gamma'}X_{\gamma'}^\top \) and \( (X_{\gamma'}X_{\gamma'})^{-1} \) are the same. \( \square \)

**S3.7 Proof of Lemma 7**

**Proof.** Note that

\[
\| \beta_t \|_2^2 |t| \max_{k \in \ell \setminus \gamma}(X_k^\top (I - H_\gamma)X_t \beta_t)_2^2 \geq \| \beta_t \|_2^2 \sum_{k \in \ell \setminus \gamma}(X_k^\top (I - H_\gamma)X_t \beta_t)_2^2
\]

\[
= \| \beta_t \|_2^2 \sum_{k \in \ell}(X_k^\top (I - H_\gamma)X_t \beta_t)_2^2
\]

\[
\geq \left( \sum_{k \in \ell} \beta_k X_k^\top (I - H_\gamma)X_t \beta_t \right)_2^2
\]

\[
= \| (I - H_\gamma)X_t \beta_t \|_2^4 = \| X_t \beta_t - X_\gamma X_\gamma^\top X_\gamma X_\gamma^{-1} X_\gamma X_t \beta_t \|_2^4 = \| X_{\ell \setminus \gamma} \beta_{\ell \setminus \gamma} + X_\gamma \tilde{b} \|_2^4
\]

\[
\geq n^2 \tau_+^2 \beta_+^4,
\]

for some vector \( \tilde{b} \), where the first equality follows from the fact that \( (I - H_\gamma)X_k = 0 \) for any \( k \in \ell \cap \gamma \), the second inequality is the Cauch-Schwarz inequality, and the final inequality follows from the fact that the matrix \( [X_{\ell \setminus \gamma} \ X_\gamma] \) has less than \( (K_n + 1)|t| \) columns and that \( \| \beta_{\ell \setminus \gamma} \| \geq \beta_+ \). The proof follows because \( s_n = \sqrt{n} \tau_+^2 \beta_+^2 / (\| \beta_t \|_2 \sqrt{|t|}) \). \( \square \)

**S3.8 Proof of Corollary 1**

**Proof.** Since \( \tilde{y}^\top \tilde{y} \leq \beta_t^\top X_t^\top X_t \beta_t + \sigma^2 \epsilon^\top \epsilon + 2\sigma \epsilon^\top X_t \beta_t \), we have

\[
P(\| \tilde{y} \|_2^2 > nu_n) \leq P\left( \frac{\beta_t^\top X_t^\top X_t \beta_t}{n} + \frac{\sigma^2 \epsilon^\top \epsilon}{n} + \frac{2\sigma \epsilon^\top X_t \beta_t}{n} > u_n \right)
\]

\[
\leq P\left( \frac{\sigma^2 \epsilon^\top \epsilon}{n} > v_n \right) + P\left( \frac{2\sigma \epsilon^\top X_t \beta_t}{n} > 1 \right). \quad (S17)
\]
By Berry-Esseen theorem,
\[ P \left( \frac{\sigma^2 \epsilon^\top}{n} > v_n \right) \leq 1 - \Phi \left( \frac{\sqrt{n}v_n}{\sigma^2 \sqrt{\kappa}} \right) + \frac{c_1}{\sqrt{n}} \leq \frac{\sigma^2 \sqrt{\kappa}}{\sqrt{2\pi n} v_n} \exp \left( -\frac{n v_n^2}{2\sigma^4 \kappa} \right) + \frac{c_1}{\sqrt{n}}, \]
where \( v_n > 0 \) for all large \( n \). Since \( \text{Var} (\epsilon^\top X_t \beta_t) = \sigma^2 \beta_t^\top X_t^\top X_t \beta_t \), the proof follows as by the Chebyshev’s inequality we have
\[ P \left( \frac{2\sigma \epsilon^\top X_t \beta_t}{n} > 1 \right) \leq \frac{4\sigma^4 \beta_t^\top X_t^\top X_t \beta_t}{n^2}. \]
\[ \square \]

S3.9 Proof of Corollary 2

Proof. Let \( \tilde{\epsilon} = (I_n - n^{-1}1_n1_n^\top)\epsilon \). Note that \( H_\gamma 1_n = 0 \) since \( X^\top 1_n = 0 \). Thus,
\[ X_k^\top (I - H_\gamma) \tilde{\epsilon} = X_k^\top (I - H_\gamma) \epsilon. \]
Consequently, from Lemma 3 we have
\[ \max_{k \in \ell \setminus \gamma} \{\text{RSS}(\gamma) - \text{RSS}(\gamma + e_k)\} = \max_{k \in \ell \setminus \gamma} \frac{(X_k^\top (I - H_\gamma) \tilde{y})^2}{\| (I - H_\gamma) X_k \|^2} \]
\[ = \max_{k \in \ell \setminus \gamma} \frac{X_k^\top (I - H_\gamma) X_t \beta_t + \sigma X_k^\top (I - H_\gamma) \epsilon}{\| (I - H_\gamma) X_k \|^2} \]
\[ \geq \max_{k \in \ell \setminus \gamma} \frac{|X_k^\top (I - H_\gamma) X_t \beta_t|}{\| (I - H_\gamma) X_k \|} - \sigma \max_{k \in \ell \setminus \gamma} \frac{|X_k^\top (I - H_\gamma) \epsilon|}{\| (I - H_\gamma) X_k \|} \]
\[ \geq \frac{n \tau + \beta^2 |\beta_t|^{-1} |t|^{-1/2}}{\sqrt{n}} - \sigma \max_{k \in \ell} \max_{|\gamma| < K_n |t|} |a_{\gamma,t}|^2 \]
\[ = |s_n - \sigma \Upsilon_n|^2. \]
In the above, the first inequality follows from the fact that for any two sequences \((b_m)\) and \((c_m)\) of real numbers, \( \max_m |b_m - c_m| \geq \max_n |b_n| - \max_m |c_m| \); the last inequality follows from Lemma 7 and from the assumption that \( \sigma \Upsilon_n < s_n \). \( \square \)

S4. Further simulation results

In this section we provide simulation results from \((n, p) = (75, 200), (100, 2000), (150, 2000)\) The eight simulation models we consider here are described in Section 4.
### Table S1: n = 75, p = 200

| Method     | Ind. | CS   | AR   | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|------------|------|------|------|------|------|------|---------|-------|
| BITS1(n)   | 86.4 | 81.6 | 87.6 | 84.6 | 90.7 | 79.8 | 85.8    | 6.4   |
| BITS1(PP)  | 76.7 | 69.7 | 71.0 | 69.7 | 77.7 | 78.1 | 62.3    | 5.4   |
| BITS2(n)   | 86.0 | 80.8 | 86.6 | 86.0 | 90.1 | 79.8 | 86.4    | 5.6   |
| BITS2(PP)  | 76.4 | 69.1 | 71.7 | 72.6 | 74.8 | 77.6 | 62.4    | 4.0   |
| BITS3(n)   | 86.0 | 81.4 | 85.8 | 87.8 | 92.2 | 79.7 | 84.7    | 4.2   |
| BITS3(PP)  | 77.1 | 70.2 | 69.3 | 70.2 | 49.6 | 77.2 | 64.0    | 2.9   |
| UBITS(n)   | 90.9 | 87.7 | 92.7 | 90.8 | 95.3 | 82.0 | 92.4    | 7.6   |
| UBITS(PP)  | 79.3 | 75.3 | 75.1 | 80.4 | 81.6 | 79.4 | 72.0    | 6.1   |
| HOLP(n)    | 79.3 | 78.4 | 81.2 | 79.6 | 82.4 | 84.7 | 70.2    | 7.9   |
| HOLP(eBIC) | 40.1 | 33.1 | 36.9 | 48.0 | 35.8 | 50.1 | 13.7    | 0.1   |
| SIS(n)     | 76.7 | 60.7 | 81.1 | 55.6 | 87.3 | 53.1 | 69.4    | 0.0   |
| SIS(eBIC)  | 34.2 | 19.1 | 30.0 | 11.8 | 37.2 | 34.1 | 9.4     | 0.0   |
| FR(n-2)    | 84.6 | 77.8 | 79.6 | 86.3 | 51.9 | 87.0 | 70.8    | 35.8  |
| FR(eBIC)   | 60.7 | 46.4 | 48.3 | 56.8 | 25.9 | 58.0 | 30.1    | 0.0   |
| BITS1(n)   | 69.3 | 66.8 | 69.3 | 53.6 | 78.0 | 67.1 | 52.2    | 67.1  |
| BITS1(PP)  | 64.5 | 60.3 | 63.9 | 47.9 | 69.4 | 60.3 | 41.6    | 52.2  |
| BITS2(n)   | 70.2 | 66.6 | 69.1 | 55.4 | 77.1 | 66.4 | 55.5    | 66.0  |
| BITS2(PP)  | 65.0 | 60.3 | 63.6 | 49.0 | 68.6 | 59.6 | 42.5    | 51.3  |
| BITS3(n)   | 69.5 | 64.7 | 67.8 | 55.5 | 75.4 | 64.0 | 54.3    | 60.7  |
| BITS3(PP)  | 64.3 | 58.3 | 62.5 | 49.8 | 67.8 | 57.8 | 42.0    | 48.0  |
| UBITS(n)   | 92.4 | 92.6 | 92.6 | 86.4 | 98.2 | 88.2 | 95.2    | 98.2  |
| UBITS(PP)  | 87.1 | 86.2 | 87.0 | 80.5 | 91.6 | 82.0 | 83.8    | 86.3  |
| BITS1(PP)  | 17.5 | 23.0 | 18.0 | 17.0 | 28.0 | 20.0 | 22.0    | 42.0  |
| BITS2(PP)  | 19.0 | 24.0 | 19.0 | 16.0 | 28.0 | 20.0 | 23.0    | 39.0  |
| BITS3(PP)  | 19.5 | 26.5 | 16.0 | 15.0 | 13.5 | 9.0  | 26.0    | 34.0  |
| UBITS(n)   | 109.0| 108.0| 109.0| 101.0| 109.0| 99.0 | 107.0   | 93.0  |
| UBITS(PP)  | 27.0 | 40.0 | 25.0 | 25.0 | 41.0 | 32.0 | 33.0    | 55.0  |
| HOLP(eBIC) | 3.0  | 3.0  | 3.0  | 6.0  | 4.0  | 5.0  | 2.0     | 1.0   |
| SIS(eBIC)  | 3.0  | 2.0  | 2.0  | 3.0  | 4.0  | 3.0  | 2.0     | 1.0   |
| FR(eBIC)   | 6.0  | 4.0  | 5.0  | 9.0  | 2.0  | 5.0  | 6.0     | 1.0   |
| Method     | Ind. | CS  | AR  | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|------------|------|-----|-----|------|------|------|---------|-------|
| BITS1(n)   | 70.3 | 62.0| 75.3| 56.7 | 82.4 | 80.4 | 57.6    | 7.6   |
| BITS1(PP)  | 69.3 | 61.6| 69.3| 56.7 | 80.9 | 80.4 | 50.7    | 7.6   |
| BITS2(n)   | 71.4 | 62.2| 72.4| 66.0 | 82.0 | 77.6 | 59.3    | 0.3   |
| BITS2(PP)  | 70.6 | 60.0| 62.3| 59.0 | 59.2 | 77.2 | 44.1    | 0.3   |
| BITS3(n)   | 71.7 | 61.1| 70.6| 65.3 | 82.0 | 77.4 | 59.1    | 0.1   |
| BITS3(PP)  | 70.9 | 59.3| 62.4| 55.3 | 41.7 | 76.8 | 43.8    | 0.1   |
| UBITS(n)   | 75.2 | 68.9| 82.7| 71.2 | 84.8 | 83.8 | 70.0    | 7.7   |
| UBITS(PP)  | 73.9 | 68.1| 76.1| 72.2 | 82.2 | 83.4 | 60.8    | 7.7   |
| HOLP(n)    | 59.0 | 57.3| 67.0| 53.2 | 75.9 | 85.1 | 47.1    | 32.9  |
| HOLP(eBIC) | 32.8 | 25.8| 27.8| 30.4 | 31.9 | 56.0 | 11.0    | 9.6   |
| SIS(n)     | 58.4 | 40.4| 67.8| 20.4 | 75.7 | 53.4 | 47.0    | 0.0   |
| SIS(eBIC)  | 32.4 | 17.3| 27.8| 4.7  | 31.9 | 38.1 | 9.9     | 0.0   |
| FR(n-2)    | 71.0 | 61.0| 63.1| 59.2 | 31.8 | 79.1 | 44.0    | 4.2   |
| FR(eBIC)   | 60.2 | 44.2| 48.9| 36.2 | 25.4 | 57.6 | 28.5    | 0.0   |
| Mean posterior mass coverages |
| BITS1(n)   | 53.6 | 44.3| 51.2| 10.7 | 80.7 | 66.1 | 12.1    | 73.4  |
| BITS1(PP)  | 52.6 | 42.9| 50.1| 8.8  | 76.9 | 63.5 | 11.1    | 61.7  |
| BITS2(n)   | 64.6 | 54.8| 62.6| 22.9 | 76.4 | 64.9 | 39.5    | 46.8  |
| BITS2(PP)  | 63.4 | 53.3| 61.3| 22.0 | 73.4 | 62.7 | 37.3    | 41.5  |
| BITS3(n)   | 64.2 | 54.1| 60.1| 26.7 | 75.4 | 61.5 | 37.5    | 33.5  |
| BITS3(PP)  | 63.1 | 52.7| 59.0| 26.0 | 72.7 | 59.6 | 35.5    | 30.6  |
| UBITS(n)   | 77.7 | 75.3| 77.4| 49.8 | 91.0 | 83.2 | 62.5    | 93.5  |
| UBITS(PP)  | 76.1 | 73.2| 75.8| 47.5 | 88.1 | 80.0 | 59.8    | 85.2  |
| Median model sizes |
| BITS1(PP)  | 54.0 | 80.5| 51.0| 100.0| 40.0 | 92.0 | 51.5    | 100.0 |
| BITS2(PP)  | 38.0 | 39.0| 39.0| 36.5 | 44.0 | 36.0 | 37.5    | 48.0  |
| BITS3(PP)  | 45.0 | 45.0| 45.5| 40.5 | 45.0 | 10.0 | 44.0    | 40.5  |
| UBITS(n)   | 186.0| 186.0|186.0|182.0|183.0|181.0|182.0    |173.0 |
| UBITS(PP)  | 100.5| 130.0|100.0|145.0| 94.5|100.5| 95.0    |153.5 |
| HOLP(eBIC) | 3.0  | 2.0 | 2.0 | 5.0 | 1.0 | 5.0 | 2.0     | 2.0   |
| SIS(eBIC)  | 3.0  | 2.0 | 2.0 | 3.0 | 1.0 | 3.0 | 2.0     | 1.0   |
| FR(eBIC)   | 5.5  | 4.0 | 4.0 | 8.0 | 2.0 | 5.0 | 6.5     | 1.0   |
Table S3: n = 150, p = 2000

| Method     | Ind. | CS   | AR   | Fac. | Grp. | Ext. | Sp.Fac. | Spur. |
|------------|------|------|------|------|------|------|---------|-------|
| **Mean true positive rates** |      |      |      |      |      |      |         |       |
| BITS1(n)   | 79.4 | 69.7 | 87.1 | 69.9 | 93.7 | 84.2 | 79.3    | 5.9   |
| BITS1(PP)  | 77.0 | 67.6 | 76.2 | 69.8 | 89.3 | 84.2 | 69.0    | 5.9   |
| BITS2(n)   | 80.1 | 70.9 | 82.0 | 79.6 | 91.7 | 82.1 | 85.8    | 0.2   |
| BITS2(PP)  | 78.9 | 69.2 | 70.4 | 76.8 | 74.4 | 81.7 | 75.6    | 0.2   |
| BITS3(n)   | 80.0 | 70.3 | 81.3 | 80.6 | 91.2 | 81.9 | 85.7    | 0.2   |
| BITS3(PP)  | 78.9 | 68.8 | 71.0 | 75.9 | 51.0 | 81.4 | 75.6    | 0.2   |
| UBITS(n)   | 82.7 | 75.2 | 91.3 | 83.1 | 93.9 | 85.8 | 90.0    | 6.0   |
| UBITS(PP)  | 80.2 | 72.9 | 80.7 | 81.4 | 90.3 | 85.8 | 82.0    | 6.0   |
| HOLP(n)    | 67.4 | 63.8 | 71.7 | 65.2 | 87.6 | 88.8 | 58.2    | 26.2  |
| HOLP(eBIC) | 42.2 | 37.9 | 40.3 | 43.2 | 44.2 | 64.7 | 18.1    | 4.4   |
| SIS(n)     | 67.7 | 46.0 | 71.4 | 24.6 | 87.9 | 56.2 | 58.0    | 0.0   |
| SIS(eBIC)  | 41.4 | 22.2 | 38.0 | 5.8  | 43.9 | 43.4 | 17.0    | 0.0   |
| FR(n-2)    | 80.1 | 70.0 | 70.6 | 79.1 | 35.2 | 83.9 | 75.0    | 6.8   |
| FR(eBIC)   | 69.8 | 56.2 | 58.6 | 65.4 | 28.4 | 66.3 | 62.0    | 0.0   |
| **Mean posterior mass coverages** |      |      |      |      |      |      |         |       |
| BITS1(n)   | 69.4 | 62.9 | 69.5 | 16.3 | 84.1 | 76.3 | 26.1    | 76.5  |
| BITS1(PP)  | 67.8 | 60.6 | 67.9 | 15.9 | 80.1 | 72.7 | 25.0    | 64.1  |
| BITS2(n)   | 73.1 | 65.1 | 73.2 | 38.8 | 80.5 | 73.9 | 62.4    | 59.2  |
| BITS2(PP)  | 71.6 | 63.0 | 71.7 | 37.6 | 77.2 | 70.3 | 59.0    | 51.6  |
| BITS3(n)   | 72.9 | 64.2 | 71.7 | 40.2 | 78.7 | 70.2 | 62.3    | 44.1  |
| BITS3(PP)  | 71.3 | 62.3 | 70.3 | 39.1 | 75.9 | 67.3 | 59.1    | 39.5  |
| UBITS(n)   | 86.0 | 83.2 | 86.3 | 62.2 | 94.4 | 91.6 | 77.9    | 97.3  |
| UBITS(PP)  | 84.0 | 80.5 | 84.4 | 60.6 | 91.3 | 87.6 | 74.3    | 88.7  |
| **Median model sizes** |      |      |      |      |      |      |         |       |
| BITS1(PP)  | 43.0 | 69.0 | 48.0 | 150.0 | 48.5 | 72.5 | 45.0    | 150.0 |
| BITS2(PP)  | 56.0 | 56.5 | 56.0 | 44.0 | 65.5 | 10.0 | 45.0    | 74.0  |
| BITS3(PP)  | 68.0 | 68.0 | 68.0 | 55.0 | 69.5 | 9.0  | 58.0    | 62.0  |
| UBITS(n)   | 276.0 | 274.0 | 276.0 | 269.0 | 273.0 | 265.0 | 268.0    | 250.0 |
| UBITS(PP)  | 119.5 | 148.5 | 132.0 | 199.0 | 137.5 | 91.0 | 99.5    | 222.0 |
| HOLP(eBIC) | 4.0  | 3.0  | 3.0  | 8.0  | 4.0  | 6.0  | 4.0     | 2.0   |
| SIS(eBIC)  | 4.0  | 2.0  | 3.0  | 3.0  | 4.0  | 4.0  | 3.5     | 1.0   |
| FR(eBIC)   | 7.0  | 5.0  | 5.0  | 13.0 | 3.0  | 6.0  | 16.0    | 1.0   |