RaSE: A Variable Screening Framework via Random Subspace Ensembles

Ye Tian  
Department of Statistics  
Columbia University  
and  
Yang Feng  
Department of Biostatistics, School of Global Public Health  
New York University

Abstract

Variable screening methods have been shown to be effective in dimension reduction under the ultra-high dimensional setting. Most existing screening methods are designed to rank the predictors according to their individual contributions to the response. As a result, variables that are marginally independent but jointly dependent with the response could be missed. In this work, we propose a new framework for variable screening, Random Subspace Ensemble (RaSE), which works by evaluating the quality of random subspaces that may cover multiple predictors. This new screening framework can be naturally combined with any subspace evaluation criterion, which leads to an array of screening methods. The framework is capable to identify signals with no marginal effect or with high-order interaction effects. It is shown to enjoy the sure screening property and rank consistency. We also develop an iterative version of RaSE screening with theoretical support. Extensive simulation studies and real-data analysis show the effectiveness of the new screening framework.

Keywords: Variable screening; Random subspace method; Ensemble learning; Sure screening property; Rank consistency; High dimensional data; Variable selection

1
1 Introduction

With the rapid advancement of computing power and technology, high-dimensional data become ubiquitous in many disciplines such as genomics, image analysis, and tomography. With high-dimensional data, the number of variables $p$ could be much larger than the sample size $n$. What makes statistical inference possible is the sparsity assumption, which assumes only a few variables have contributions to the response. Under this sparsity assumption, there has been a rich literature on the topic of variable selection, including LASSO (Tibshirani, 1996), SCAD (Fan and Li, 2001), elastic net (Zou and Hastie, 2005), and MCP (Zhang, 2010). Despite the success of these methods in many applications, for the ultra-high dimensional scenario where the dimension $p$ grows exponentially with $n$, they may not work well due to the “curse of dimensionality” in terms of simultaneous challenges to computational expediency, statistical accuracy, and algorithmic stability (Fan et al., 2009).

To conquer these difficulties, Fan and Lv (2008) proposed a novel procedure called sure independence screening (SIS) with solid theoretical support. In the past decade, the power of feature screening has been well recognized and a myriad of screening methods have been proposed. The existing screening methods can be broadly classified into two categories, model-based methods and model-free ones. Model-based screening methods rely on specific models, such as SIS (Fan and Lv, 2008) and its extensions to generalized linear models (Fan et al., 2009), Cox model (Fan et al., 2010; Zhao and Li, 2012), non-parametric independence screening method based on additive models (Fan et al., 2011; Cheng et al., 2014) and screening via high-dimensional ordinary least-square projection (HOLP) (Wang and Leng, 2016). Recently, model-free approaches become more popular because of less stringent requirements. Examples of such approaches include the sure
independent ranking and screening (SIRS) (Zhu et al., 2011), the screening method based on distance correlation (DC-SIS) and its iterative version (Li et al., 2012; Zhong and Zhu, 2015), screening procedure via martingale difference correlation (MDC-SIS) (Shao and Zhang, 2014), screening via Kolmogorov filter (Mai and Zou, 2013, 2015), the screening approach for discriminant analysis (MV-SIS) (Cui et al., 2015), interaction pursuit via Pearson correlation (IP) and the distance correlation (IPDC) (Fan et al., 2016; Kong et al., 2017), the screening method based on ball correlation (Pan et al., 2018), the nonparametric screening under conditional strictly convex loss (Han, 2019), and the screening method via covariate information number (CIS) (Nandy et al., 2020).

For variables that are marginally independent but jointly dependent with the response, many existing screening methods could miss them. This issue has been recognized in the literature (Fan and Lv, 2008; Fan et al., 2009; Zhu et al., 2011; Zhong and Zhu, 2015) and iterative screening procedures were developed, which were shown to be effective empirically. However, to the best of our knowledge, there is not much theoretical development for the iterative screening methods. In addition, some iterative screening methods (e.g. iterative SIS) are coupled with a variable selection method like LASSO or SCAD, making its performance dependent on the specific choice of the regularization method. Besides, some other iterative screening methods (e.g. iterative SIRS and iterative DC-SIS) recruit variables step by step through residuals until a pre-specified number of variables are picked. Thus, their success hinges on a key tuning parameter, that is, how many variables to recruit in each step, making these procedures potentially less robust.

These issues mentioned above motivate us to propose a new screening framework which goes beyond marginal utilities. In the new framework, we investigate multiple features at the same time, via the random subspace method (Ho, 1998). Tian and Feng (2021)
proposed a new Random Subspace Ensemble classification method based on a similar idea, RaSE, according to a specific aggregation framework first introduced in Cannings and Samworth (2017). They advocated applying RaSE on sparse classification problems. The main idea of RaSE can be simply described as follows. First, \( B_1 B_2 \) random subspaces are generated from a specific distribution on subspaces, which are evenly divided into \( B_1 \) groups. Next, the best subspace within each group is picked according to some criterion and a base learner is trained in that subspace. Hence we obtain \( B_1 \) base learners, each of which corresponds to a subspace. Finally, these \( B_1 \) base learners are aggregated on average and the ensemble will be used in prediction. The vanilla RaSE algorithm is reviewed in Algorithm 3 in Appendix A.1. It’s important to note that there is a by-product of RaSE, which is the selected proportion of each variable within \( B_1 \) selected subspaces. In this work, we will use this selected proportion to do variable screening, and call this the RaSE screening framework.

We highlight the merits of RaSE screening framework as follows. First, by looking at different feature subspaces, variables marginally independent but jointly dependent with the response can be identified. Second, instead of proposing only a single screening approach, the flexible framework of RaSE allows us to use any criterion function for comparing subspaces, leading to an array of screening methods. One possible way to construct such a criterion function is to choose a base learner and a specific measure for comparing the subspaces. For example, if we know linear methods are suitable for the data, then we can apply RaSE by picking subspaces achieving lower BIC under linear models. If \( k \)-nearest neighbor (\( k \)NN) is believed to perform better, we can apply RaSE by choosing subspaces with the smallest cross-validation error on \( k \)NN. Third, under general conditions, we show the sure screening property and rank consistency for RaSE screening framework. Finally,
we develop a novel iterative RaSE screening framework with sure screening property established without the need to use a variable selection step or specifying the number of variables to recruit in each step.

The rest of this paper is organized as follows. Section 2 introduces the vanilla RaSE screening framework and its iterative version in detail, and discusses the relationship between RaSE and marginal screening methods. In Section 3, we present the theoretical properties for vanilla RaSE and iterative RaSE screening, including sure screening property and rank consistency. In Section 4, extensive simulation studies and real-data analysis are conducted to demonstrate the power of our new screening framework. We summarize our contributions and point out some promising future avenues in Section 5. The supplementary materials include all the technical proofs as well as additional details.

2 RaSE: A General Variable Screening Framework

In what follows, we consider predictors $\mathbf{x} = (x_1, \ldots, x_p)^T$ and response $y$. For regression problems, $y$ takes value from the real line $\mathbb{R}$, while for classification problems, $y$ takes value from an integer set $\{1, \ldots, K\}$, where $K > 1$ is a known integer. Denote the training data as $\{(\mathbf{x}_i, y_i)\}_{i=1}^n$. Denote by $S_{\text{Full}} = \{1, \ldots, p\}$ the full feature set. The signal set $S^* \subseteq S_{\text{Full}}$ is defined as the set $S$ with minimal cardinality satisfying $y|_{\mathbf{x}_S \perp \perp \mathbf{x}_{S_{\text{Full}} \setminus S}}$. Denote $p^* = |S^*|$. $[a]$ is used to represent the largest integer no larger than $a$.

To introduce the RaSE framework, we denote the $B_1 B_2$ random subspaces as $\{S_{b_1 b_2} : b_1 = 1 \ldots, B_1, b_2 = 1 \ldots, B_2\}$, the $b_1$-th group of subspaces as $\{S_{b_1 b_2}^{B_2} : b_2 = 1 \ldots, B_2\}$, and the selected $B_1$ subspaces as $\{S_{b_1\ast}^{B_1} : b_1 = 1 \ldots, B_1\}$. The objective function corresponding to the specific criterion to choose subspaces is written as $\text{Cr}_n : S \rightarrow \mathbb{R}$, where $S$ is the collection of all subspaces.
Assume a smaller value of $\text{Cr}_n$ leads to a better subspace. Although the original RaSE (Tian and Feng, 2021) was introduced to solve classification problems, we now consider the general prediction framework, including both classification and regression.

### 2.1 Vanilla RaSE screening framework

Following the idea of Tian and Feng (2021), we use the proportion of each feature among the selected $B_1$ subspaces as the importance measure. Therefore, a natural screening procedure is to rank variables based on this proportion vector, then pick the variables with the largest proportions. The RaSE screening framework is summarized in Algorithm 1.

**Algorithm 1: Vanilla RaSE screening**

**Input:** training data $\{(x_i, y_i)\}_{i=1}^n$, subspace distribution $\mathcal{D}$, criterion function $\text{Cr}_n$,
integers $B_1$ and $B_2$, number of variables $N$ to select

**Output:** the selected proportion of each feature $\hat{\eta}$, the selected subset $\hat{S}$

1. Independently generate random subspaces $S_{b_1b_2} \sim \mathcal{D}, 1 \leq b_1 \leq B_1, 1 \leq b_2 \leq B_2$

2. for $b_1 \leftarrow 1$ to $B_1$ do

3. Select the optimal subspace $S_{b_1*} = S_{b_1b_2*}$, where $b_2^* = \arg\min_{1 \leq b_2 \leq B_2} \text{Cr}_n(S_{b_1b_2})$

4. end

5. Output the selected proportion of each feature $\hat{\eta} = (\hat{\eta}_1, \ldots, \hat{\eta}_p)^T$ where

   $$\hat{\eta}_j = B_1^{-1} \sum_{b_1=1}^{B_1} 1(j \in S_{b_1*}), j = 1, \ldots, p$$

6. Output $\hat{S} = \{1 \leq j \leq p : \hat{\eta}_j \text{ is among the } N \text{ largest of all}\}$

In the algorithm, the subspace distribution $\mathcal{D}$ is chosen as a *hierarchical uniform distribution* over the subspaces by default. Specifically, with $D$ as the upper bound of the subspace size, we first generate the subspace size $d$ from the uniform distribution over
Then, the subspace $S_{11}$ follows the uniform distribution over all size-$d$ subspaces $\{S \subseteq S_{\text{Full}} : |S| = d\}$. In practice, the subspace distribution can be adjusted if we have prior information about the data structure.

Algorithm 1 is not the end of the story because it ranks all the variables but does not determine how many variables to keep. To facilitate the theoretical analysis, we define the final feature subset to be selected as

$$\hat{S}_\alpha = \{1 \leq j \leq p : \hat{\eta}_j \text{ is among the } \lfloor \alpha D/c_{2n} \rfloor \text{ largest of all}\},$$

(1)

where $c_{2n}$ is a constant (to be specified in the next section) depending on $n$, $B_2$, $D$, and the criterion $C_r$ which is a population counterpart of $C_r_n$. Here, $\alpha$ can be any constant larger than 1, which will appear in the upper bound introduced in the sure screening theorem of Section 3.

2.2 Iterative RaSE screening

As we mentioned in the introduction, the existing iterative screening methods have various tuning components such as the number of variables to recruit in each step and/or a specific variable selection method. We propose the iterative RaSE screening in Algorithm 2 to tackle these issues.

The main idea of iterative RaSE screening is to update the subspace distribution based on the selected proportion in the preceding steps and not to conduct variable screening until the final step. To understand the details in the algorithm, we introduce a new subspace distribution.

Note that each subspace $S$ can be equivalently represented as $J = (J_1, \ldots, J_p)^T$, where $J_j = 1(j \in S), j = 1, \ldots, p$. A subspace following the hierarchical restrictive multinomial...
Algorithm 2: Iterative RaSE screening (RaSE$_T$)

**Input:** training data $\{(x_i, y_i)\}_{i=1}^n$, initial subspace distribution $D^{[0]}$, criterion function $C_{r_n}$, integers $B_1$ and $B_2$, the number of iterations $T$, positive constant $C_0$, number of variables $N$ to select

**Output:** the selected proportion of each feature $\hat{\eta}^{[T]}$, the selected subset $\hat{S}^T$

```plaintext
1 for $t \leftarrow 0$ to $T$ do

2 Independently generate random subspaces $S_{b_1b_2}^{[t]} \sim D^{[t]}$, $1 \leq b_1 \leq B_1$, $1 \leq b_2 \leq B_2$

3 for $b_1 \leftarrow 1$ to $B_1$ do

4 Select the optimal subspace $S_{b_1*}^{[t]} = S_{b_1b_2}^{[t]}$, where $b_2* = \arg \min_{1 \leq b_2 \leq B_2} C_{r_n}(S_{b_1b_2}^{[t]})$

5 end

6 Update $\hat{\eta}^{[t]}$ where $\hat{\eta}_j^{[t]} = B_1^{-1} \sum_{b_1=1}^{B_1} 1(j \in S_{b_1*}^{[t]}), j = 1, \ldots, p$

7 Update $D^{[t+1]} \leftarrow$ hierarchical restrictive multinomial distribution $R(\mathcal{U}_0, p, \tilde{\eta}^{[t]})$, where $\tilde{\eta}_j^{[t]} \propto [\hat{\eta}_j^{[t]} 1(\hat{\eta}_j^{[t]} > C_0/\log p) + \frac{C_0}{p} 1(\hat{\eta}_j^{[t]} \leq C_0/\log p)]$ and $\sum_{j=1}^p \tilde{\eta}_j^{[t]} = 1$

8 end

9 Output the selected proportion of each feature $\hat{\eta}^{[T]}$

10 Output $\hat{S} = \{1 \leq j \leq p : \hat{\eta}_j^{[T]} \text{ is among the } N \text{ largest of all}\}$
```

**distribution** $R(\mathcal{U}, p, \tilde{\eta})$, where $\sum_{j=1}^p \tilde{\eta}_j = 1$ and $\tilde{\eta}_j \geq 0$, is equivalent to the procedure:

1. Draw $d$ from distribution $\mathcal{U}$ on $\{1, \ldots, D\}$;

2. Draw $J = (J_1, \ldots, J_p)^T$ from a restrictive multinomial distribution with parameter $(p, d, \tilde{\eta})$, where the restriction is $J_j \in \{0, 1\}$.

For example, the hierarchical uniform distribution belongs to this family where $\mathcal{U}$ is the
uniform distribution \( U_0 \) on \( \{1, \ldots, D\} \) and \( \tilde{\eta}_j = \frac{1}{p} \) for all \( j = 1, \ldots, p \).

With the hierarchical restrictive multinomial distribution in hand, we can depict the iterative algorithm more precisely. At iteration \( t \), the algorithm updates the subspace distribution of next round \( D^{t+1} \) by the hierarchical restrictive multinomial distribution \( \mathcal{R}(U_0, p, \tilde{\eta}^{[t]}) \), where \( \tilde{\eta}_j^{[t]} \propto [\tilde{\eta}_j^{[t]} \mathbb{1}(\tilde{\eta}_j^{[t]} > C_0 / \log p) + \frac{C_0}{p} \mathbb{1}(\tilde{\eta}_j^{[t]} \leq C_0 / \log p)] \) and \( \tilde{\eta}_j^{[t]} \) is the proportion of variable \( j \) in the \( B_1 \) selected subspaces \( \{S_{b_1}\}_{b_1=1}^{B_1} \).

### 2.3 Connections with marginal screening and interaction detection

Before closing this section and moving into theoretical analysis, we want to point out the connection of RaSE screening approach with the classical marginal screening methods as well as the important problem of interaction detection.

First of all, it is easy to observe that when \( D = 1 \) in Algorithm 1, with proper measure, RaSE screening method reduces to the marginal screening approaches. In this sense, RaSE screening method can be seen as an extension of classical marginal screening frameworks by evaluating subspaces instead of individual predictors. In addition, when there are signals with no marginal contribution, one intuitive idea is to screen all possible interaction terms, which demand extremely high computational costs. For example, screening all the order-\( d \) interactions leads to a computational cost of \( O(p^d) \). Instead of screening all possible interactions, RaSE randomly chooses some feature subspaces and explores their contributions to the response via a specific criterion. The carefully designed mechanism of generating random subspaces along with the iterative step greatly alleviate the requirement on computation.

Second, there has been a great interest in studying screening methods for interaction
The proposed RaSE screening framework works in a different fashion, by evaluating the contribution of variables through the joint contributions in different subspaces. A simulation example (Example 4) where we have 4-way interactions among predictors will be studied to show the effectiveness of RaSE.

3 Theoretical Analysis

In this section, we investigate the theoretical properties of RaSE screening method to help readers understand how it works and why it can succeed in practice. We are not claiming that the assumptions we make are the weakest and conclusions we obtain are the strongest.

Before moving forward, we first define some notations. For two numbers $a$ and $b$, we denote $a \vee b = \max(a, b)$ and $a \wedge b = \min(a, b)$. For two numerical sequences $\{a_n\}_{n=1}^\infty$ and $\{b_n\}_{n=1}^\infty$, we denote $a_n = o(b_n)$ or $a_n \ll b_n$ if $\lim_{n \to \infty} |a_n/b_n| = 0$. Denote $a_n = O(b_n)$ or $a_n \lesssim b_n$ if $\limsup_{n \to \infty} |a_n/b_n| < \infty$. When $a_n \lesssim b_n$ and $a_n \gtrsim b_n$ hold at the same time, we write it as $a_n \asymp b_n$. Denote Euclidean norm for a length-$p$ vector $\mathbf{x} = (x_1, \ldots, x_p)^T$ as $\|\mathbf{x}\|_2 = \sqrt{\sum_{j=1}^p x_j^2}$. $\mathbf{1}_p$ represents a length-$p$ vector with all entries 1. For a $p \times p'$ matrix $A = (a_{ij})_{p \times p'}$, define the 1-norm $\|A\|_1 = \sup_j \sum_{i=1}^p |a_{ij}|$, the operator norm $\|A\|_2 = \sup_{\|\mathbf{x}\|_2 = 1} \|A\mathbf{x}\|_2$, the infinity norm $\|A\|_\infty = \sup_i \sum_{j=1}^{p'} |a_{ij}|$ and the maximum norm $\|A\|_{\max} = \sup_{i,j} |a_{ij}|$. We also denote the minimal and maximal eigenvalues of a square matrix $A$ as $\lambda_{\min}(A)$ and $\lambda_{\max}(A)$, respectively. Besides, we use different probability notations $\mathbb{P}$, $\mathbb{P}$, $\mathbb{P}$ to represent probabilities w.r.t. randomness from subspaces, randomness from training samples, and all randomness, respectively. And we use the same fonts $\mathbb{E}$, $\mathbb{E}$, $\mathbb{E}$ to represent the corresponding expectations. In addition, throughout this section, we assume $p^* = |S^*|$ is fixed.
3.1 Sure screening property

First, note that the success of RaSE relies on the large selected proportions of all signals. According to Algorithm 1, the selected proportion of signal \( j \) depends on the comparison of two different types of subspaces, namely “covering signal \( j \)” or “not covering signal \( j \”).

To understand when RaSE can succeed, we also need to compare subspaces “covering a subset \( \bar{S}_j \supset j \)” or “not covering \( \bar{S}_j \)”, which is essential when signal \( j \) has no marginal effect.

Next, we analyze the joint distribution of these two types of subspaces given the number of \( B_2 \) subspaces covering some \( \bar{S}_j \supset j \), in the following useful lemma.

**Lemma 1.** Let \( \{S_{1b_2}\}_{b_2=1}^{B_2} \overset{i.i.d.}{\sim} \mathcal{R}(U_0, p, p^{-1}) \). For any set \( \bar{S}_j \supset j \) with cardinality \( |\bar{S}_j| \leq D \), let \( p_j = \mathbb{P}(S_{11} \supset \bar{S}_j) = D^{-1} \sum_{d=|\bar{S}_j|}^{D} \binom{D - |\bar{S}_j|}{d} \cdot 1(S_{1b_2} \supset \bar{S}_j) \). Given \( N_j := \#\{b_2 : S_{1b_2} \supset \bar{S}_j\} = k \), dividing \( \{S_{1b_2}\}_{b_2=1}^{B_2} \) into \( \{S_{1b_2}^{(j)}\}_{b_2=1}^{k} \) and \( \{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k} \), where \( S_{1b_2}^{(j)} \supset \bar{S}_j \) and \( S_{1b_2}^{(-j)} \not\supset \bar{S}_j \).

(i) \( \{S_{1b_2}^{(j)}\}_{b_2=1}^{k} \) independently follow the distribution

\[
\mathbb{P}(S^{(j)} = S) = \left[D \cdot p_j \left(\frac{p}{|S|}\right)\right]^{-1} \cdot 1(S \supset \bar{S}_j); \tag{2}
\]

(ii) \( \{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k} \) independently follow the distribution

\[
\mathbb{P}(S^{(-j)} = S) = \left[D(1 - p_j) \left(\frac{p}{|S|}\right)\right]^{-1} \cdot 1(S \not\supset \bar{S}_j); \tag{3}
\]

(iii) \( \{S_{1b_2}^{(j)}\}_{b_2=1}^{k} \perp \{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k} \).

The proof of Lemma 1 can be found in Appendix B. It shows us that given \( N_j := \#\{b_2 : S_{1b_2} \supset \bar{S}_j\} = k \), \( \{S_{1b_2}^{(j)}\}_{b_2=1}^{k} \) and \( \{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k} \) are independent. And each \( S_{1b_2}^{(j)}, S_{1b_2}^{(-j)} \) follows a “weighted” hierarchical uniform distribution by adjusting the sampling weight based on the cardinality of subspace.
Now, we introduce a concentration of \( \text{Cr}_n \) on its population version \( \text{Cr} \) for a collection of subsets. In particular, for any \( D \), there exists a sequence \( \{\epsilon_n := \epsilon(n, D)\}_{n=1}^{\infty} \) and positive constant \( c_{1n} \to 0 \) such that

\[
P \left( \sup_{S : |S| \leq D} |\text{Cr}_n(S) - \text{Cr}(S)| > \epsilon_n \right) \leq c_{1n} \tag{4}
\]

holds for any \( n \). Such a sequence \( \{\epsilon_n\}_{n=1}^{\infty} \) always exists, though we would like it to be small to have a uniform concentration as described in the following assumption, which is important to establish the sure screening property of RaSE.

**Assumption 1.** For any \( j = 1, \ldots, p \), there exists a subset \( \bar{S}_j \ni j \), and we denote \( \delta_j(S) := \delta_j(n, D, S) = \mathbb{P}_{S^{(j)}}(\text{Cr}(S) - \text{Cr}(S^{(j)}) < 2\epsilon_n|S) \), where \( S^{(j)} \) follows the distribution in (2) w.r.t. \( \bar{S}_j \). It holds that

\[
D \geq \sup_{j \in S^*} |\bar{S}_j|, B_2 \inf_{j \in S^*} p_j \gtrsim 1, \limsup_{n, D, B_2 \to \infty} \left\{ B_2 \sup_{j \in S^*} \mathbb{E}_{S^{(-j)}} \left[ \delta_j(S^{(-j)})^{\frac{1}{2}B_2p_j} \right] \right\} < \infty,
\]

where \( S^{(-j)} \) follows the distribution in (3) and \( p_j = \mathbb{P}(S_{11} \supseteq \bar{S}_j) = D^{-1} \sum_{d=|\bar{S}_j|}^{D} \frac{\binom{p}{d}}{\binom{p}{d}} \).

**Remark 1.** In Assumption 1, \( \delta_j \) measures the strength of signal \( j \) via comparing the two types of feature subspaces introduced in Lemma 1. From the assumption, we need a large \( B_2 \) when \( \delta_j \) is small.

**Theorem 1** (Sure screening property). Define

\[
c_{2n} := c_2(n, B_2, D) := \left( 1 - \sup_{j \in S^*} \mathbb{E}_{S^{(-j)}} \left[ \delta_j(S^{(-j)})^{\frac{1}{2}B_2p_j} \right] \right)^{B_2} \left( 1 - \exp \left\{ -\frac{3}{28} B_2 \inf_{j \in S^*} p_j \right\} \right).
\]

For any \( \alpha > 1 \), let \( \hat{S}_\alpha = \{1 \leq j \leq p : \hat{\eta}_j \text{ is among the } \lfloor \alpha D/c_{2n} \rfloor \text{ largest of all} \} \). Under Assumption 1, when \( B_1 \gg \log p^* \) and \( n \to \infty \), we have
(i) $P(S^* \subseteq \hat{S}_\alpha) \geq 1 - p^* \exp \left\{-2B_1 \epsilon_n^2 \left(1 - \frac{1}{\alpha}\right)^2 \right\} \to 1$;

(ii) The selected model size $|\hat{S}_\alpha| \lesssim D$.

Next, we would like to analyze the restriction on $B_2$ imposed by Assumption 1, which depends on $\delta_j$. We first introduce a useful notion called detection complexity.

**Definition 1** (Detection complexity). We say feature $j \in S^*$ is detectable in complexity $d$, if there exists a subset $\bar{S}_j \ni j$ with cardinality $d$ and another subset $S^0_j \subseteq S_{\text{Full}} \setminus \{j\}$ with cardinality $p^0_j$, such that

$$\inf_{S \in \mathcal{S}, S' \in \mathcal{S}' \setminus \mathcal{S}} [\text{Cr}(S) - \text{Cr}(S')] > 2\epsilon_n,$$

where $\mathcal{S} = \mathcal{S}(j, D) = \{S : |S| \leq D, |S \cap (S^* \cup S^0_j)| < d\}$, $\mathcal{S}' = \mathcal{S}'(j, D) = \{S : |S| \leq D, S \supseteq \bar{S}_j\}$, and $\epsilon_n$ satisfies (4). We define the detection complexity of $j$, which is denoted by $d_j$, as the minimal integer $d$ to make $j \in S^*$ detectable in complexity $d$.

**Remark 2.** The detection complexity $d_j$ actually indicates the difficulty to identify signal $j$. When $d_j = 1$, $\bar{S}_j$ is actually equal to $\{j\}$ and $\mathcal{S} = \{S : |S| \leq D, S \cap (S^* \cup S^0_j) = \emptyset\}$. It implies that the given criterion function performs better at subsets covering $j$ than at subsets not intersecting with $S^* \cup S^0_j$. $S^0_j$ is introduced to avoid cases that some noises might have strong marginal effects. This condition is similar to marginal conditions in literature, for examples, see Fan and Lv (2008); Fan et al. (2011); Zhu et al. (2011); Li et al. (2012); Shao and Zhang (2014); Cui et al. (2015); Pan et al. (2018); Nandy et al. (2020). The difference is that here we state it via subspaces instead of single features used in existing works. And when $d_j \geq 2$, the definition of detection complexity allows us to consider the joint contribution of multiple features. See Examples 1 and 6 in our numerical studies as examples.
Now we introduce an assumption under which the restriction on $B_2$ can be explicitly calculated.

**Assumption 2.** All signals in $S^*$ are detectable in complexity $d$, where $d = \max_{j \in S^*} d_j$.

Intuitively speaking, this assumption requires all signals to be detectable under the same level, which equals the largest detection complexity of signals. In some sense, it is necessary for the sure screening property. Signal $j$ with large detection complexity is associated with a larger set $\bar{S}_j$, requiring a larger $B_2$ to sample subsets that cover $\bar{S}_j$ with sufficiently high probability.

**Proposition 1.** Under Assumption 2, when $B_2 \asymp \left(\frac{p}{D}\right)^d$, Assumption 1 hold.

In the ideal case, in Assumption 1, we can set $\bar{S}_j = \{j\}$ for all $j \in S^*$, implying $d = 1$, which leads to the weakest restriction on $B_2$, that is, $B_2 \asymp \frac{p}{D}$. If a signal $j$ does not have marginal contribution to the response, we have $d_j \geq 2$, requiring a larger order of $B_2$ to satisfy Assumption 1. This motivates the iterative RaSE screening (Algorithm 2) which usually has a less stringent restriction on $B_2$, making the framework more applicable to high-dimensional settings.

Next, we study the sure screening property for iterative RaSE, and discuss how the restriction on $B_2$ can be relaxed. For simplicity, we only study the one-step iteration, i.e. the case when $T = 1$. It’s not very hard to generalize the conditions and conclusions to the general case when $T > 1$. To better state the results, we first generalize Lemma 1 to understand the distribution of two aforementioned types of subspaces after one iteration.

**Lemma 2.** For any set $\bar{S}_j \ni j$ with cardinality $|\bar{S}_j| \leq D$, let $\{S_{1b_2}\}_{b_2=1}^{B_2}$ i.i.d. some distribution $\mathcal{F}$ such that $P_{S_{11}}(S_{11} \supseteq \bar{S}_j) \in (0, 1)$. Given $N_j := \# \{b_2 : S_{1b_2} \supseteq \bar{S}_j\} = k$, dividing $\{S_{1b_2}\}_{b_2=1}^{B_2}$ into $\{S^{(j)}_{1b_2}\}_{b_2=1}^{k}$ and $\{S^{(-j)}_{1b_2}\}_{b_2=1}^{B_2-k}$, where $S^{(j)}_{1b_2} \supseteq \bar{S}_j$ and $S^{(-j)}_{1b_2} \nsubseteq \bar{S}_j$. 14
(i) \( \{S_{i_2}^{(j)}\}_{i_2=1}^k \) independently follow the distribution
\[
P(S^{(j)} = S) = P_{S_{11} \sim \mathcal{F}}(S_{11} = S) \cdot \frac{1(S \supseteq \bar{S}_j)}{P_{S_{11} \sim \mathcal{F}}(S_{11} \supseteq S_j)};
\]

(ii) \( \{S_{i_2}^{(-j)}\}_{i_2=1}^{B_2-k} \) independently follow the distribution
\[
P(S^{(-j)} = S) = P_{S_{11} \sim \mathcal{F}}(S_{11} = S) \cdot \frac{1(S \nsubseteq \bar{S}_j)}{P_{S_{11} \sim \mathcal{F}}(S_{11} \nsubseteq S_j)};
\]

(iii) \( \{S_{i_2}^{(j)}\}_{i_2=1}^k \updownarrow \{S_{i_2}^{(-j)}\}_{i_2=1}^{B_2-k} \).

We omit the proof of Lemma 2 as it is very similar to Lemma 1. Next, we introduce the following technical assumption analogous to Assumption 1.

**Assumption 3.** Suppose the signal set \( S^* \) can be decomposed as \( S^* = S^*_{[0]} \cup S^*_{[1]} \), where \( S^*_{[0]} \) and \( S^*_{[1]} \) satisfy the following conditions:

(i) (The first-step detection) For any \( j \in S^*_{[0]} \), denote \( \delta_j^{[0]}(S) = P_{S^{(j)}}(Cr(S) - Cr(S^{(j)})) < 2\epsilon_n|S| \), \( p^{[0]} = P(j \in S_{11}) = \frac{D+1}{2p} \), where \( S^{(j)} \) follows the distribution in (2) w.r.t. \( \bar{S}_j = \{j\} \). Then,
\[
B_2 \gtrsim \frac{p}{D}, \quad \limsup_{n,D,B_2 \to \infty} \left\{ B_2 \sup_{j \in S^*_{[0]}} E_{S^{(-j)}} \left[ \delta_j^{[0]}(S^{(-j)})\frac{1_{B_2p^{[0]}}}{2^{B_2p^{[0]}}} \right] \right\} < \infty,
\]
where \( S^{(-j)} \) follows the distribution in (3) w.r.t. \( \bar{S}_j \).

(ii) (The second-step detection) Denote \( \delta_j^{[1]}(S) = P_{S^{(j)}}(Cr(S) - Cr(S^{(j)})) < 2\epsilon_n|S| \), \( p^{[1]} = \frac{(D+1)C_0}{2(D+C_0)p} \), where \( S^{(j)} \) follows the distribution in (5) w.r.t. \( \bar{S}_j = \{j\} \), and \( C_0 \) is a constant from Algorithm 2. \( \Upsilon = \{R(U_0,p,\bar{\eta})\} \) is a family of hierarchical restrictive multinomial distributions satisfying
\[
\inf_{j \in S^*_{[0]}} \bar{\eta}_j \geq \frac{C^2}{(D+C^*)},
\]
for a constant $c_2^* > 0$. Then,

$$B_2 \gtrsim p, \limsup_{n,D,B_2 \to \infty} \left\{ B_2 \sup_{F \in \Upsilon} \sup_{j \in S^*} \mathbb{E}_{S(-j)} \left[ \delta_j^{[1]}(S^{(-j)})^{1/2}B_2p^{[l]} \right] \right\} < \infty,$$

where $S^{(-j)}$ follows the distribution in (6) w.r.t. $\bar{S}_j = \{j\}$ and $\{S_{b_{1,b_2}}\}_{b_1,b_2} \overset{i.i.d.}{\sim} F \in \Upsilon$.

**Remark 3.** Condition (i) is a relaxed version of Assumption 1, which replaces $S^*$ by a subset $S^*_0$. This can be seen as a first-step detection condition for RaSE screening method to capture $S^*_0$. The remaining signals in $S^*_1$ that might be missed in the first step will be captured in the second step. The family of distributions $\Upsilon$ is introduced to incorporate the randomness in the first step of RaSE screening. This type of stepwise detection condition is very common in the literature (Jiang and Liu, 2014; Li and Liu, 2019; Zhou et al., 2020; Tian and Feng, 2021).

**Theorem 2** (Sure screening property for one-step iterative RaSE screening). Define

$$c_2^{[l]} := c_2^{[l]}(n, B_2, D) := (1-c_{1n}) \left( 1 - \sup_{j \in S^*} \mathbb{E}_{S(-j)} \left[ \delta_j^{[l]}(S^{(-j)})^{1/2}B_2p^{[l]} \right] \right) \left( 1 - \exp \left\{ -\frac{3}{28}B_2(p^{[l]^2}) \right\} \right),$$

where $l = 0, 1$. For $\hat{S}_\alpha^{[1]} = \{1 \leq j \leq p : \hat{\eta}_j^{[1]} \text{ is among the } [\alpha D/c_{2n}] \text{ largest of all}\}$, where $\alpha > 1$, under Assumption 3, if $c_2^{[0]} > c_2^*$ and $B_1 \gg \log p^*$, we have

(i) $P(S^* \subseteq \hat{S}_\alpha^{[1]}) \geq 1 - p^* \exp \left\{ -2B_1(c_2^{[0]} - c_2^*)^2 \right\} - p^* \exp \left\{ -2B_1(c_2^{[1]^2})^2(1 - \frac{1}{\alpha})^2 \right\} \to 1,$

as $n \to \infty$;

(ii) $|\hat{S}_\alpha^{[1]}| \lesssim D$.

The lower bound in (i) comes from the two steps of Algorithm 2, which is very intuitive. The general iterative RaSE screening algorithm with any $T \geq 1$ can be studied similarly by imposing analogous conditions, which we leave as future work.
The restriction on $B_2$ can be discussed in a similar fashion as the vanilla RaSE screening for some specific scenarios. For instance, similar to Definition 1, we can define the detection complexity of the second step based on the distribution of subsets from the first step. If a similar assumption like Assumption 2 (see Assumption 5 in Appendix A.2 for the precise statement) holds, then we can expect that there exist $B_2 \asymp p/D$ in the first step and $B_2 \lesssim D|S_{[0]}| (\log p)^{|S_{[1]}|^{-1}} p$ in the second step to make Assumption 3 hold (see Proposition 3 in Appendix A.2 for a precise description), which relaxes the requirement shown in Proposition 1 ($B_2 \asymp (p/D)|S_{[0]}|^{-1}$) to a great extent. In Section 4, an array of simulations and real data analyses will show the effectiveness of iterative RaSE screening.

3.2 Rank consistency

Next, we study another important property of the RaSE screening, namely the rank consistency. First, we impose the following assumption.

**Assumption 4.** Suppose the following conditions hold:

1. Denote $\tilde{\delta}_j(S) = P_{S^{(j)}}(\text{Cr}(S) - 2\epsilon_n < \text{Cr}(S^{(j)}))|S|$ and $\delta_j(S) := \delta_j(n, D, S) = P_{S^{(j)}}(\text{Cr}(S) - \text{Cr}(S^{(j)}) < 2\epsilon_n)|S|$, where $S^{(j)}$ follows the distribution in (3) with respect to $\bar{S}_j = \{j\}$ while $S^{(j)}$ follows the distribution in (2) with respect to some subset $\bar{S}_j \ni j$. We have

$$
\gamma(n, D, B_2) := (1 - c_{1n}) \left(1 - 2\exp \left\{ -\frac{3}{28} B_2 \inf_{j \in S^*} p_j \right\} \right) \\
\cdot \left(1 - \sup_{j \in S^*} E_{S^{(j)}} \left[ \tilde{\delta}_j(S^{(j)})^{\frac{1}{2}} B_2 p_j \right] \right)^{B_2} + \left(1 - \sup_{j \notin S^*} E_{S^{(j)}} \left[ \tilde{\delta}_j(S^{(j)}) B_2 - \frac{3}{2} B_2 p_0 \right] \right)^{\frac{3}{2} B_2 p_0} - 1
$$

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where $S^{(j)}$ and $S^{(-j)}$ follow the distributions in (2) and (3), respectively.

(ii) $B_1 \gg \gamma(n, D_B, B_2)^{-2} \vee \log p$.

**Remark 4.** Condition (i) is introduced to make sure the signals are separable from the noises. Here, $\tilde{\delta}_j$ is a parallel definition to $\delta_j$, measuring the noise level via comparing the two types of feature subspaces introduced in Lemma 1. A related condition can be found in Assumption (C3) of Cui et al. (2015).

**Theorem 3** (Rank consistency). Under Assumption 4,

$$
P \left( \inf_{j \in S^*} \hat{\eta}_j > \sup_{j \notin S^*} \hat{\eta}_j \right) \geq 1 - p \exp \left\{ -\frac{1}{2} B_1 \gamma^2 (n, D_B, B_2) \right\} \to 1,$$

as $n, B_1, B_2 \to \infty$.

In addition, under Assumption 2 with $d = 1$, when $B_2$ is restricted to some level, we have Assumption 4 holds by default.

**Proposition 2.** Under Assumption 2 with $d = 1$, there exist constants $C_2 > C_1 > 0$, such that, when $B_2 \in (C_1 p/D, C_2 p/D)$, Assumption 4 holds.

### 4 Numerical Studies

In this section, we will investigate the performance of RaSE screening methods via extensive simulations and real data experiments. Each setting is replicated 200 times. In simulations, we evaluate different screening approaches by calculating the 5%, 25%, 50%, 75%, and
95% quantiles of the minimum model size (MMS) to include all signals. The smaller the quantile is, the better the screening approach is. For real data, since $S^*$ is unknown, we compare different methods by investigating the performance of the corresponding post-screening procedure. That is, after screening, we keep the same number of variables for each screening method, then the same model is fitted based on those selected variables and their prediction performance on an independent test data is reported.

We compare RaSE screening methods with SIS (Fan and Lv, 2008), ISIS (Fan and Lv, 2008; Fan et al., 2009), SIRS (Zhu et al., 2011), DC-SIS (Li et al., 2012), MDC-SIS (Shao and Zhang, 2014), MV-SIS (Cui et al., 2015), HOLP (Wang and Leng, 2016), IPDC (Kong et al., 2017), and CIS (Nandy et al., 2020).

All the experiments are conducted in R. We implement RaSE screening methods in RaSEn package. R package SIS is used to implement SIS. Corresponding to one-step iterative RaSE, we report the results of ISIS with two screening steps and one selection step (Saldana and Feng, 2018).\(^1\) R package screening (https://github.com/wwrechard/screening) is used to implement HOLP. We conduct SIRS, DC-SIS and MV-SIS through R package VariableSelection. IPDC is implemented by calling the function dcor in R package energy. We implement MDC-SIS through function mdd in R package EDMeasure to calculate the martingale difference divergence. CIS is implemented via R codes shared in Nandy et al. (2020).

We combine RaSE framework with various criteria to choose subspaces, including minimizing BIC (RaSE-BIC) and eBIC (RaSE-eBIC) in linear model or logistic regression model, minimizing the leave-one-out MSE/error in $k$-nearest neighbor ($k$NN) (RaSE-$k$NN), and minimizing the 5-fold cross-validation MSE/error in support vector machine (SVM).

\(^1\)For more details, please refer to the toy example in Appendix A.3.1.
with RBF kernel (RaSE-SVM). We add a subscript 1 to RaSE to denote the one-step iterative RaSE (e.g. RaSE$_1$-BIC). In practice, we can choose the criterion based on the model we prefer in the post-screening procedure. For example, if we would like to use linear model in post-screening, we could set minimizing BIC of linear model as the criterion. If we want to fit a non-linear model in post-screening, minimizing cross-validation error in $k$NN or SVM with RBF kernel can be good choices. Some exploratory analysis can help us choose a proper post-screening method.

For all RaSE methods, we fix $B_1 = 200$ and $B_2 = 20 \times [p/D]$, motivated by Proposition 1. In addition, following Weng et al. (2019), we fix $D = [\sqrt{n}]$, which is motivated from the fact that many estimators are $\sqrt{n}$-consistent. And we verify the effectiveness of this choice in Example 1. For Example 1, we also investigate the impact of $B_1$, $B_2$ and $D$ on the median MMS. For RaSE-$k$NN and RaSE$_1$-$k$NN, $k$ is set to be 5. For RaSE-eBIC and RaSE$_1$-eBIC, we set the penalty parameter $\gamma = 0.5$ (Chen and Chen, 2008, 2012).

All the codes used in numerical experiments can be found on GitHub (https://github.com/ytstat/RaSE-screening-codes).

4.1 Simulations

**Example 1** (Example II in Fan and Lv (2008)). We generate data from the following model:

$$y = 5x_1 + 5x_5 + 5x_3 - \frac{15}{\sqrt{2}}x_4 + \epsilon,$$

(7)

where $x = (x_1, \ldots, x_p)^T \sim N(0, \Sigma)$, $\Sigma = (\sigma_{ij})_{p \times p}$, $\sigma_{ij} = 0.5^{T(i \neq j)}$, $\epsilon \sim N(0, 1)$, and $\epsilon \perp \perp x$.

The signal set $S^* = \{1, 2, 3, 4\}$. $n = 100$ and $p = 1000$.

In this example, there is no correlation between $y$ and $x_4$, further leading to the independence due to normality, therefore methods based on the marginal effect will fail to capture
However, after projecting $y$ on the space which is perpendicular with any signals from $x_1$, $x_2$ and $x_3$, the correlation appears between the projected $y$ and $x_4$, which motivates the ISIS. Besides, the proposed RaSE methods are also expected to succeed since it works with feature subsets instead of a single variable.

| Method/MMS  | Example 1       |       |       |       |       | Example 2       |       |       |       |       |
|-------------|-----------------|-------|-------|-------|-------|-----------------|-------|-------|-------|-------|
|             | 5%   | 25%   | 50%   | 75%   | 95%   | 5%   | 25%   | 50%   | 75%   | 95%   |
| SIS         | 227  | 317   | 397   | 647   | 922   | 6    | 28    | 105   | 592   | 1855  |
| ISIS        | 14   | 15    | 15    | 25    | 172   | 861  | 1415  | 1825  | 1963  |
| SIRS        | 87   | 370   | 594   | 762   | 949   | 6    | 1158  | 1492  | 1774  | 1964  |
| DC-SIS      | 96   | 358   | 610   | 776   | 942   | 6    | 1083  | 1460  | 1752  | 1976  |
| HOLP        | 912  | 949   | 969   | 986   | 999   | 45   | 196   | 576   | 1252  | 1906  |
| IPDC        | 224  | 442   | 700   | 869   | 980   | 59   | 210   | 386   | 678   | 1517  |
| MDC-SIS     | 146  | 287   | 512   | 734   | 937   | 6    | 20    | 93    | 999   | 1908  |
| CIS         | 203  | 434   | 601   | 780   | 940   | 2000 | 2000  | 2000  | 2000  | 2000  |
| RaSE-BIC    | 5    | 12    | 37    | 126   | 650   | 6    | 358   | 1514  | 1821  | 1956  |
| RaSE$_1$-BIC| 4    | 4     | 4     | 16    | 55    | 13   | 834   | 1507  | 1797  | 1969  |
| RaSE-eBIC   | 6    | 21    | 42    | 489   | 852   | 8    | 26    | 1323  | 1789  | 1935  |
| RaSE$_1$-eBIC| 4   | 4     | 4     | 4     | 14    | 907  | 1485  | 1739  | 1878  | 1971  |
| RaSE-kNN    | 22   | 88    | 233   | 312   | 883   | 5    | 5     | 6     | 76    | 1190  |
| RaSE$_1$-kNN| 6   | 80    | 422   | 694   | 921   | 5    | 5     | 5     | 13    | 1846  |
| RaSE-SVM    | 13   | 59    | 150   | 336   | 842   | 5    | 5     | 5     | 6     | 68    |
| RaSE$_1$-SVM| 4   | 4     | 82    | 126   | 542   | 5    | 5     | 5     | 5     | 11    |

Table 1: Quantiles of MMS in Examples 1 and 2.

We present the results in the left panel of Table 1. From the results, it can be seen that all the marginal screening methods do not perform well in the sense that they need a large model to cover all 4 signals. ISIS performs much better because it can detect the signals with a smaller model than SIS with one step iteration. For RaSE screening methods
with no iteration, as analyzed in Proposition 1, we have \( d = 2 \) since \( x_4 \) has no marginal contribution to \( y \), leading to a theoretical requirement \( B_2 \propto (p/D)^2 \), where \( (p/D)^2 = 10^4 \). Despite the current small \( B_2 \) setting, RaSE-BIC and RaSE-eBIC still perform better than SIS and other marginal screening methods. After one iteration, RaSE_1-BIC and RaSE_1-eBIC improve a lot compared to their vanilla counterparts, with RaSE_1-eBIC achieving the best performance.

Note that iterations can usually improve the performance of vanilla RaSE at small quantiles, but possibly lead to worse performance at large quantiles. See RaSE-kNN and RaSE_1-kNN for examples. This phenomenon happens because iterative RaSE is very aggressive and the success of the second step is based on the accurate capture of some signals in the first step. If the first step fails to identify enough signals but captures many noises, these noises will be selected more frequently in the second step.

To further study the impact of \((B_1, B_2)\), we run this example for 200 times under different \((B_1, B_2)\) settings, where we range \( B_1 \) from 100 to 1000 with increment 100 and \( B_2 \) from 1000 to 97000 with increment 6000. The median of MMS with RaSE-BIC and RaSE_1-BIC is summarized in Figure 1. It shows that in general, larger \((B_1, B_2)\) leads to better performance. The performance is stable in terms of \( B_1 \) when \( B_2 \) is large. On the other hand, the performance improves continuously as \( B_2 \) grows. In particular, for RaSE-BIC, when \( B_2 \geq 10^4 \), it can capture \( S^* \) very well, which agrees with Proposition 1. These results indicate that we can further improve the performance of RaSE screening if we have sufficient computational resources. RaSE_1-BIC can always achieve a great performance with a small \( B_2 \), showing its effectiveness in relaxing the restriction on \( B_2 \).

We also run this example 200 times to plot the median of MMS for RaSE-BIC and RaSE_1-BIC under different \((D, B_2)\) while fixing \( B_1 = 200 \) in Figure 3 in Appendix A.3,
where $D$ ranges from 2 to 40 with increment 2 and $B_2$ from 200 to 5000 with increment 300. The subfigure (a) shows that for RaSE-BIC, for a given $B_2$, the impact of $D$ is not monotonic. RaSE-BIC has a good and stable performance when $D$ is around $\sqrt{n} = 10$, which verifies the effectiveness of our choice for $D$. The subfigure (b) shows that the performance of RaSE$_1$-BIC is very robust with respect to $D$, as long as $D$ and $B_2$ are not very small.

To compare the computational time of different methods, we list the average running time in 200 replications of Example 1 in Table 2. All codes were run on NYU Greene clusters (2x Intel Xeon Platinum 8268 24C 205W 2.9GHz Processor) with 40 cores and
It can be seen that RaSE methods have heavier computational burdens than other screening methods since their success leverages generating a large number of subspaces. This can be alleviated with parallel computing and more powerful machines.

| Other methods | SIS | ISIS | SIRS | DC-SIS | HOLP | IPDC | MDC-SIS | CIS |
|---------------|-----|------|------|--------|------|------|---------|-----|
| Time (s)      | 0.01| 0.67 | 0.28 | 1.30   | 0.02 | 0.49 | 0.28    | 1.18|
| RaSE methods  | BIC | BIC1 | eBIC | eBIC1  | kNN  | kNN1 | SVM     | SVM1|
| Time (s)      | 1.99| 4.03 | 2.01 | 3.94   | 6.74 | 13.66| 150.41  | 305.77|

Table 2: Average (over 200 replications) computational time in seconds for various methods in Example 1. For simplicity, for RaSE methods, we use criteria to differentiate them and the subscript “1” denotes the one-step iterative version of the corresponding RaSE-based methods.

**Example 2** (Latent clusters). We generate data from the following linear model:

\[ y = 0.5(\tilde{x}_1 + \tilde{x}_2 + \tilde{x}_3 + \tilde{x}_4 + \tilde{x}_5 + \epsilon), \]  

where \( \tilde{x} = (\tilde{x}_1, \ldots, \tilde{x}_p)^T \sim N(0, \Sigma), \epsilon \sim t_2, \Sigma = (\sigma_{ij})_{p \times p} = (0.5^{|i-j|})_{p \times p}, \) and \( \epsilon \perp \tilde{x} \).

Generate \( z \sim \text{Unif}([-3, 3]) \perp \tilde{x} \) and \( x = \tilde{x} + z1_p \). The signal set \( S^* = \{1, 2, 3, 4, 5\} \).

\( n = 200 \) and \( p = 2000 \).

Figure 2 shows the scatterplots of \( y \) vs. \( x_1 \) (left panel) and \( y \) vs. \( x_{10} \) (right panel).

We expect the methods based on Pearson correlation to deteriorate due to the partial cancellation of signals by the averaging of two clusters. For such kind of data, \( k\text{NN} \) could

\(^2\) For SIS, ISIS, SIRS, DC-SIS and HOLP, since the package implementing them does not provide the option to use multi-cores, we ran them with a single core only.
be a favorable approach. The performances of various methods are presented in the right panel of Table 1. SIS and MDC-SIS perform well at 5% and 25% quantiles. RaSE-kNN and RaSE-SVM perform quite well with their performances further improved by their respective one-step iterative versions.

Example 3 (Example 1.c in Li et al. (2012)). We generate data from the following model:

\[
y = 2\beta_1 x_1 x_2 + 3\beta_2 1(x_{12} < 0)x_2 + \epsilon,
\]

where \(\beta_j = (-1)^j U(4 \log n/\sqrt{n} + |Z|), j = 1, 2, U \sim \text{Bernoulli}(0.4), Z \sim N(0, 1), \epsilon \sim N(0, 1), x \sim N(0, \Sigma)\) where \(\Sigma = (\sigma_{ij})_{p \times p} = (0.8^{i-j})_{p \times p}\), \(U \perp Z, \epsilon \perp x\), and \((U, Z) \perp (\epsilon, x)\). Note that we regenerate \((U, Z)\) for each replication, so the results might differ from those in Li et al. (2012).

The signal set \(S^* = \{1, 2, 12, 22\}\). \(n = 200\) and \(p = 2000\).

The left panel of Table 3 exhibits the results of different screening methods. Due to the interaction term and indicator function, approaches based on linear models like SIS,
| Method/MMS | Example 3 | | | | | | Example 4 | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | 5% | 25% | 50% | 75% | 95% | 5% | 25% | 50% | 75% | 95% |
| SIS | 184 | 810 | 1370 | 1732 | 1957 | 264 | 570 | 709 | 885 | 984 |
| ISIS | 362 | 1008 | 1482 | 1775 | 1945 | 293 | 626 | 810 | 911 | 978 |
| SIRS | 54 | 741 | 1294 | 1634 | 1920 | 487 | 737 | 867 | 935 | 992 |
| DC-SIS | 25 | 456 | 1222 | 1638 | 1923 | 44 | 304 | 603 | 814 | 949 |
| HOLP | 326 | 954 | 1475 | 1774 | 1975 | 316 | 586 | 767 | 886 | 974 |
| IPDC | 128 | 429 | 920 | 1397 | 1899 | 7 | 19 | 68 | 158 | 528 |
| MDC-SIS | 52 | 165 | 504 | 1331 | 1872 | 189 | 482 | 736 | 889 | 979 |
| CIS | 4 | 5 | 8 | 55 | 548 | 5 | 33 | 136 | 352 | 789 |
| RaSE-BIC | 637 | 1242 | 1619 | 1842 | 1959 | 355 | 693 | 825 | 914 | 986 |
| RaSE1-BIC | 714 | 1196 | 1550 | 1839 | 1974 | 424 | 661 | 824 | 918 | 981 |
| RaSE-eBIC | 484 | 1137 | 1496 | 1794 | 1951 | 302 | 553 | 784 | 913 | 987 |
| RaSE1-eBIC | 725 | 1330 | 1617 | 1806 | 1948 | 480 | 686 | 860 | 930 | 986 |
| RaSE-kNN | 5 | 33 | 168 | 1321 | 1855 | 5 | 15 | 68 | 290 | 889 |
| RaSE1-kNN | 4 | 5 | 8 | 125 | 1528 | 4 | 8 | 51 | 446 | 910 |
| RaSE-SVM | 4 | 18 | 504 | 1282 | 1848 | 4 | 15 | 132 | 468 | 938 |
| RaSE1-SVM | 4 | 4 | 5 | 14 | 1141 | 4 | 30 | 232 | 645 | 898 |

Table 3: Quantiles of MMS in Examples 3 and 4.

ISIS, HOLP, and RaSE with BIC and eBIC do not perform very well. CIS and RaSE1-kNN achieve a very good performance at 5%, 25% and 50% quantiles. RaSE-kNN performs well at 5% and 25% quantiles but worse at others. RaSE-SVM performs well at the first two quantiles. The iteration step improves the performances of RaSE-kNN and RaSE-SVM significantly, and RaSE1-SVM outperforms all the other methods except at 95% quantile.

**Example 4 (Interactions).** We generate data from the following model:

\[
y = 3\sqrt{|x_1|} + 2\sqrt{|x_1|x_2^2 + 4 \sin(x_1) \sin(x_2) \sin^2(x_3) + 12 \sin(x_1)|x_2| \sin(x_3)x_4^2 + 0.5\epsilon},
\]

where \(x_1, \ldots, x_p \overset{i.i.d.}{\sim} N(0, 1), \epsilon \sim N(0, 1), \) and \(\epsilon \perp x\). The signal set \(S^* = \{1, 2, 3, 4\}\).
This example evaluates the capability of different screening methods in terms of selecting high-order interactions. The results are summarized in the right panel of Table 3. It can be observed that RaSE-kNN, RaSE$_1$-kNN, RaSE-SVM, RaSE$_1$-SVM, IPDC, and CIS achieve an acceptable performance, particularly for the lower quantiles. IPDC and CIS perform better at 75% and 95% quantiles than all RaSE methods but worse at the other three quantiles than RaSE$_1$-kNN. The remaining methods do not perform well on any of the 5 quantiles. It shows that RaSE framework equipped with minimizing cross-validation MSE on $k$NN or kernel SVM is promising to capture high-order interactions.

**Example 5** (Gaussian mixture, Example 1 in Cannings and Samworth (2017)). We generate data from the following model:

$$y \sim \text{Bernoulli}(0.5), \quad x|y = r \sim \frac{1}{2} N(\mu_r, \Sigma) + \frac{1}{2} N(-\mu_r, \Sigma), r = 0, 1,$$

where $\mu_0 = (2, -2, 0, \ldots, 0)^T$, $\mu_1 = (2, 2, 0, \ldots, 0)^T$, $\Sigma$ is an identity matrix. The signal set $S^* = \{1, 2\}$. $n = 200$ and $p = 2000$.

From the scatterplots in Figure 4 in Appendix A.3, the marginal screening methods are expected to fail because all signals are marginally independent with $y$. The only way to capture the signals is to measure the joint contribution of $(x_1, x_2)$. We summarize the results in the left panel of Table 4.

The table shows that the marginal methods fail as we expected. RaSE with BIC and eBIC fail as well because the data points from the two classes are not linearly separable (Figure 4). SIRS, RaSE$_1$-kNN and RaSE$_1$-SVM achieve the best performance with very accurate feature ranking.
Table 4: Quantiles of MMS in Examples 5 and 6.

| Method/MMS | Example 5 | | Example 6 | |
|-----------|-----------|--|-----------|--|-----------|-----------|
|           | 5% | 25% | 50% | 75% | 95% | 5% | 25% | 50% | 75% | 95% |
| SIS       | 515 | 1090 | 1414 | 1746 | 1947 | 170 | 471 | 910 | 1436 | 1932 |
| ISIS      | 445 | 1001 | 1470 | 1784 | 1967 | 7   | 7   | 7   | 8    | 8    |
| SIRS      | 2   | 2    | 2    | 2    | 2    | 821 | 1242 | 1551 | 1813 | 1966 |
| DC-SIS    | 451 | 960  | 1385 | 1706 | 1913 | 765 | 1155 | 1526 | 1775 | 1947 |
| MV-SIS    | 379 | 957  | 1366 | 1692 | 1895 | 199 | 706  | 1258 | 1660 | 1909 |
| HOLP      | 495 | 1065 | 1381 | 1712 | 1936 | —   | —   | —   | —    | —    |
| IPDC      | 495 | 1010 | 1344 | 1673 | 1908 | 879 | 1425 | 1722 | 1884 | 1988 |
| MDC-SIS   | 462 | 1038 | 1332 | 1708 | 1948 | 163 | 498  | 1064 | 1628 | 1917 |
| CIS       | 2000| 2000 | 2000 | 2000 | 2000 | 229 | 736  | 1195 | 1652 | 1941 |
| RaSE-BIC  | 506 | 1081 | 1487 | 1804 | 1946 | 8   | 14   | 20  | 26   | 1525 |
| RaSE1-BIC | 464 | 968  | 1360 | 1692 | 1927 | 5   | 5    | 5   | 6    | 14   |
| RaSE-eBIC | 425 | 1045 | 1424 | 1705 | 1965 | 26  | 346  | 894 | 1406 | 1919 |
| RaSE1-eBIC| 480 | 988  | 1370 | 1727 | 1938 | 5   | 7    | 10  | 14   | 1184 |
| RaSE-kNN  | 2   | 3    | 5    | 6    | 8    | 38  | 202  | 294 | 1470 | 1925 |
| RaSE1-kNN | 2   | 2    | 2    | 2    | 2    | 27  | 376  | 967 | 1486 | 1828 |
| RaSE-SVM  | 2   | 4    | 6    | 8    | 26   | 11  | 39   | 118 | 343  | 1743 |
| RaSE1-SVM | 2   | 2    | 2    | 2    | 2    | 5   | 5    | 118 | 1133 | 1792 |

Example 6 (Multinomial logistic regression, Case 2 in Section 4.5 of Fan et al. (2009)).

We first generate $\tilde{x}_1, \ldots, \tilde{x}_4 \overset{i.i.d.}\sim \text{Unif}([-\sqrt{3}, \sqrt{3}])$ and $\tilde{x}_5, \ldots, \tilde{x}_p \overset{i.i.d.}\sim N(0, 1)$, then let $x_1 = \tilde{x}_1 - \sqrt{2}\tilde{x}_5$, $x_2 = \tilde{x}_2 + \sqrt{2}\tilde{x}_5$, $x_3 = \tilde{x}_3 - \sqrt{2}\tilde{x}_5$, $x_4 = \tilde{x}_4 + \sqrt{2}\tilde{x}_5$ and $x_j = \tilde{x}_j$ for $j = 5, \ldots, p$.

The response is generated from

$$P(y = r|\tilde{\mathbf{x}}) \propto \exp\{f_r(\tilde{\mathbf{x}})\}, r = 1, \ldots, 4,$$

where $f_1(\tilde{\mathbf{x}}) = -a\tilde{x}_1 + a\tilde{x}_4$, $f_2(\tilde{\mathbf{x}}) = a\tilde{x}_1 - a\tilde{x}_2$, $f_3(\tilde{\mathbf{x}}) = a\tilde{x}_2 - a\tilde{x}_3$ and $f_4(\tilde{\mathbf{x}}) = a\tilde{x}_3 - a\tilde{x}_4$ with $a = 5/\sqrt{3}$. The signal set $S^* = \{1, 2, 3, 4, 5\}$. $n = 200$ and $p = 2000$. 

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In this example, \( x_5 \) is marginally independent of \( y \), therefore the marginal methods are expected to fail to capture \( x_5 \). Results are summarized in the right panel of Table 4.

We observe that ISIS, RaSE\(_1\)-BIC, and, RaSE\(_1\)-eBIC lead to better performances. Without iteration, RaSE-BIC still performs competitively compared to other non-iterative approaches. Similar to Example 1, the iteration usually improves the performance of vanilla RaSE at small quantiles, but leads to worse performance at large quantiles possibly due to the aggressiveness of iterative RaSE.

To justify the effectiveness of RaSE methods in dealing with more complicated predictors, we add two additional examples in Appendix A.3.2. In Example 7, we consider realistic predictors, with the same conditional model \( y|x \) as in Example 1. In Example 8, we use a mix of continuous and discrete variables, with the same conditional model as in Example 2. While we have similar findings as in Examples 1 and 2, the performance of most approaches become slightly worse, showing the challenges for analyzing real data.

4.2 Real data experiments

In this section, we investigate the performance of RaSE screening methods on two real data sets. Each data set is randomly divided into training data and test data. As suggested by Fan and Lv (2008), we select variables via different screening methods on training data, then the LASSO, \( k \)NN and SVM are fitted based on the selected variables on training data, and finally we evaluate different screening methods based on their corresponding post-screening performance on test data. As benchmarks, we also fit LASSO, \( k \)NN and SVM models on the training data without screening. Following Fan and Lv (2008), we choose the top \( \lceil n/\log n \rceil \) variables for all screening methods, i.e. let \( N = \lceil n/\log n \rceil \) in Algorithms 1 and 2. Note that we could also choose \( \lceil \alpha D \rceil \) variables for any \( \alpha > 1 \), which is motivated by (1).
Another possibility is to use data-driven strategies. For instance, we could sample out a separate validation data set and use the post-screening validation MSE/classification error to determine $N$.\footnote{For RaSE methods, sometimes there might be less than $n/\log n$ variables which have positive selected proportion. In this case, we randomly choose from the remaining variables with 0 selected proportions to have the desired number of selected variables.} We randomly divide the whole data set into 90% training data and 10% test data in each of 200 replications, and apply various screening methods on training data. Each time, both training and test data are standardized by using the center and scale of training data.

4.2.1 Colon cancer data set

This data set was collected by Alon et al. (1999) and consists of 2000 genes measured on 62 patients, of which 40 are diagnosed with colon cancer (class 1) and 22 are healthy (class 0). The information on each gene is represented as a continuous variable. The prediction results are summarized in the left panel of Table 5.

The table shows that SIS, ISIS, MDC-SIS, CIS, RaSE-BIC, RaSE$_1$-BIC, RaSE-eBIC, and RaSE$_1$-eBIC improve the performance of vanilla LASSO. In addition, RaSE-BIC with LASSO achieves the best performance among all post-screening procedures based on LASSO. Besides, RaSE-$k$NN with $k$NN and RaSE$_1$-$k$NN with $k$NN lead to better results than those of vanilla $k$NN. RaSE-SVM and RaSE$_1$-SVM also improve the performance of vanilla SVM, demonstrating the effectiveness of RaSE to improve various vanilla methods.

For results of RaSE methods, we also gather the top 10 selected features in 200 replications and calculate the percentages of selection of these top features out of 200 replications. The 10 features with the highest percentages (selection rates) are plotted in Figure 5 in
Appendix A.3. We notice that the first few features have high or moderately high selection rates (100% or > 50%, respectively), implying that they are frequently selected in different replications. These results demonstrate that RaSE-based variable screening methods are reasonably stable.

4.2.2 Rat eye expression data set

This data set was used by Scheetz et al. (2006); Fan et al. (2011); Wang and Leng (2016); Zhong and Zhu (2015); Nandy et al. (2020) among others. It contains the gene expression values corresponding to 18976 probes from the eyes of 120 twelve-week-old male F2 rats. Among the 18976 probes, TRIM32 is the response, which is responsible to cause Bardet-Biedl syndrome. We follow Wang and Leng (2016) to focus on the top 5000 genes with the highest sample variance. Therefore, the final sample size is 120 and there are 5000 predictors. The right panel of Table 5 shows the test average mean squared error (MSE) coupled with the standard deviation for each post-screening procedure.

The results show that SIS, ISIS, RaSE-BIC and RaSE-eBIC with LASSO achieve comparable performance, which are better than that of the vanilla LASSO. RaSE-kNN with kNN and RaSE$_{1}$-kNN with kNN enhance the vanilla kNN method as well. RaSE-SVM with SVM and RaSE$_{1}$-SVM with SVM only slightly improve the vanilla SVM for this data set. Note that MV-SIS is not directly applicable to this data set. It is possible to discretize all the variables to make MV-SIS work. See Section 4.2 in Cui et al. (2015) for details.

Similar to the colon data set, we also demonstrate the stability of RaSE methods in Figure 6.
| Screening | Post-screening | Cancer       | Eye          |
|-----------|----------------|--------------|--------------|
| —         | LASSO          | 0.1792(0.1427) | 0.0103(0.0091) |
| SIS       |                | 0.1633(0.1407) | 0.0091(0.0068) |
| ISIS      |                | 0.1767(0.1444) | 0.0091(0.0068) |
| SIRS      |                | 0.2800(0.1734) | 0.0132(0.0123) |
| DC-SIS    |                | 0.3000(0.1998) | 0.0124(0.0118) |
| MV-SIS    |                | 0.2958(0.1826) | —            |
| HOLP      |                | 0.1825(0.1491) | 0.0228(0.0269) |
| IPDC      |                | 0.1917(0.1464) | 0.0129(0.0132) |
| MDC-SIS   |                | 0.1600(0.1406) | 0.0103(0.0071) |
| CIS       |                | 0.1550(0.1332) | 0.0194(0.0231) |
| RaSE-BIC  |                | 0.1192(0.1277) | 0.0090(0.0066) |
| RaSE1-BIC |                | 0.1417(0.1324) | 0.0123(0.0104) |
| RaSE-eBIC |                | 0.3083(0.2118) | 0.0092(0.0069) |
| RaSE1-eBIC|                | 0.1458(0.1397) | 0.0122(0.0098) |
| —         | kNN            | 0.2258(0.1653) | 0.0166(0.0206) |
| RaSE-kNN  |                | 0.1533(0.1340) | 0.0131(0.0158) |
| RaSE1-kNN |                | 0.1867(0.1500) | 0.0133(0.0161) |
| —         | SVM            | 0.2025(0.1503) | 0.0160(0.0243) |
| RaSE-SVM  |                | 0.1375(0.1277) | 0.0158(0.0231) |
| RaSE1-SVM |                | 0.1858(0.1477) | 0.0158(0.0232) |

Table 5: Average test classification error rate with standard deviations (in parentheses) for colon cancer data set and average test mean square errors (MSEs) with standard deviations (in parentheses) for rat eye expression data set. We boldface the values corresponding to the best performances and italicize the values corresponding to the subsequent two best performances.
5 Discussion

In this article, we propose a very general screening framework named RaSE screening, based on the random subspace ensemble method. We can equip it with any criterion function for comparing subspaces. By comparing subspaces instead of single predictors, RaSE screening can capture signals without marginal effects on response. Besides, an iterative version of the RaSE screening framework is introduced to enhance the performance of vanilla RaSE and relax the restriction on $B_2$. In the theoretical analysis, we establish sure screening property for both vanilla and iterative RaSE frameworks under some general conditions. The rank consistency is also proved for the vanilla RaSE. We investigate the relationship between the signal strength and the appropriate choice of $B_2$, which shows that in some sense the weaker the signal is, a larger $B_2$ is necessary for RaSE to succeed. In the numerical studies, the effectiveness of RaSE and its iterative version is verified through multiple simulation examples and real data analyses.

The success of RaSE leverages on proper choices of Cr (the criterion), $B_1$ (the number of subspace groups), $B_2$ (the number of subspace candidates in each group), and $D$ (the maximum subspace size). While we have studied their impacts on the performance of RaSE, there exists potential improvement for choosing these “tuning” parameters. For example, the subspace distribution at each iteration step could be further generalized, e.g., we can choose $D$ from the empirical distribution of the sizes of the selected $B_1$ subspaces.

There are many other interesting problems worth further studying. The first question is that whether there is an adaptive way to automatically select the number of iterations ($T$). A possible solution is cross-validation and to stop the iteration process when the performance of RaSE on validation data stops improving further. Another interesting topic is to use different $B_2$ values in different iteration steps, which might further speed up
the computation.

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References
Alon, U., Barkai, N., Notterman, D. A., Gish, K., Ybarra, S., Mack, D., and Levine, A. J. (1999). Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays. Proceedings of the National Academy of Sciences, 96(12):6745–6750.

Cannings, T. I. and Samworth, R. J. (2017). Random-projection ensemble classification. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 79(4):959–1035.

Chen, J. and Chen, Z. (2008). Extended bayesian information criteria for model selection with large model spaces. Biometrika, 95(3):759–771.

Chen, J. and Chen, Z. (2012). Extended bic for small-n-large-p sparse glm. Statistica Sinica, pages 555–574.

Cheng, M.-Y., Honda, T., Li, J., and Peng, H. (2014). Nonparametric independence screening and structure identification for ultra-high dimensional longitudinal data. The Annals of Statistics, 42(5):1819–1849.

Cui, H., Li, R., and Zhong, W. (2015). Model-free feature screening for ultrahigh dimensional discriminant analysis. Journal of the American Statistical Association, 110(510):630–641.

Fan, J., Feng, Y., and Song, R. (2011). Nonparametric independence screening in sparse ultra-high-dimensional additive models. Journal of the American Statistical Association, 106(494):544–557.

Fan, J., Feng, Y., and Wu, Y. (2010). High-dimensional variable selection for cox’s proportional hazards model. In Borrowing strength: Theory powering applications—a Festschrift for Lawrence D. Brown, pages 70–86. Institute of Mathematical Statistics.
Fan, J. and Li, R. (2001). Variable selection via nonconcave penalized likelihood and its oracle properties. *Journal of the American statistical Association*, 96(456):1348–1360.

Fan, J. and Lv, J. (2008). Sure independence screening for ultrahigh dimensional feature space. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 70(5):849–911.

Fan, J., Samworth, R., and Wu, Y. (2009). Ultrahigh dimensional feature selection: beyond the linear model. *The Journal of Machine Learning Research*, 10:2013–2038.

Fan, Y., Kong, Y., Li, D., and Lv, J. (2016). Interaction pursuit with feature screening and selection. *arXiv preprint arXiv:1605.08933*.

Han, X. (2019). Nonparametric screening under conditional strictly convex loss for ultrahigh dimensional sparse data. *Annals of Statistics*, 47(4):1995–2022.

Hao, N. and Zhang, H. H. (2014). Interaction screening for ultrahigh-dimensional data. *Journal of the American Statistical Association*, 109(507):1285–1301.

Ho, T. K. (1998). The random subspace method for constructing decision forests. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 20(8):832–844.

Jiang, B. and Liu, J. S. (2014). Variable selection for general index models via sliced inverse regression. *The Annals of Statistics*, 42(5):1751–1786.

Kong, Y., Li, D., Fan, Y., and Lv, J. (2017). Interaction pursuit in high-dimensional multi-response regression via distance correlation. *The Annals of Statistics*, 45(2):897–922.

Li, R., Zhong, W., and Zhu, L. (2012). Feature screening via distance correlation learning. *Journal of the American Statistical Association*, 107(499):1129–1139.

Li, Y. and Liu, J. S. (2019). Robust variable and interaction selection for logistic regression and general index models. *Journal of the American Statistical Association*, 114(525):271–286.

Mai, Q. and Zou, H. (2013). The kolmogorov filter for variable screening in high-dimensional binary classification. *Biometrika*, 100(1):229–234.

Mai, Q. and Zou, H. (2015). The fused kolmogorov filter: A nonparametric model-free screening method. *The Annals of Statistics*, 43(4):1471–1497.
Nandy, D., Chiaromonte, F., and Li, R. (2020). Covariate information number for feature screening in ultrahigh-dimensional supervised problems. *Journal of the American Statistical Association*, pages 1–40. DOI: https://doi.org/10.1080/01621459.2020.1864380.

Pan, W., Wang, X., Xiao, W., and Zhu, H. (2018). A generic sure independence screening procedure. *Journal of the American Statistical Association*.

Saldana, D. F. and Feng, Y. (2018). Sis: an r package for sure independence screening in ultrahigh dimensional statistical models. *Journal of Statistical Software*, 83(2):1–25.

Scheetz, T. E., Kim, K.-Y. A., Swiderski, R. E., Philp, A. R., Braun, T. A., Knudtson, K. L., Dorrance, A. M., DiBona, G. F., Huang, J., and Casavant, T. L. (2006). Regulation of gene expression in the mammalian eye and its relevance to eye disease. *Proceedings of the National Academy of Sciences*, 103(39):14429–14434.

Shalev-Shwartz, S. and Ben-David, S. (2014). *Understanding machine learning: From theory to algorithms*. Cambridge university press.

Shao, X. and Zhang, J. (2014). Martingale difference correlation and its use in high-dimensional variable screening. *Journal of the American Statistical Association*, 109(507):1302–1318.

Tian, Y. and Feng, Y. (2021). Rase: Random subspace ensemble classification. *Journal of Machine Learning Research*, 22(45):1–93.

Tibshirani, R. (1996). Regression shrinkage and selection via the lasso. *Journal of the Royal Statistical Society: Series B (Methodological)*, 58(1):267–288.

Wang, X. and Leng, C. (2016). High dimensional ordinary least squares projection for screening variables. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 3(78):589–611.

Weng, H., Feng, Y., and Qiao, X. (2019). Regularization after retention in ultrahigh dimensional linear regression models. *Statistica Sinica*, 29(1):387–407.

Zhang, C.-H. (2010). Nearly unbiased variable selection under minimax concave penalty. *The Annals of Statistics*, 38(2):894–942.

Zhao, S. D. and Li, Y. (2012). Principled sure independence screening for cox models with ultra-high-dimensional covariates. *Journal of multivariate analysis*, 105(1):397–411.
Zhong, W. and Zhu, L. (2015). An iterative approach to distance correlation-based sure independence screening. *Journal of Statistical Computation and Simulation*, 85(11):2331–2345.

Zhou, T., Zhu, L., Xu, C., and Li, R. (2020). Model-free forward screening via cumulative divergence. *Journal of the American Statistical Association*, 115(531):1393–1405.

Zhu, L.-P., Li, L., Li, R., and Zhu, L.-X. (2011). Model-free feature screening for ultrahigh-dimensional data. *Journal of the American Statistical Association*, 106(496):1464–1475.

Zou, H. and Hastie, T. (2005). Regularization and variable selection via the elastic net. *Journal of the royal statistical society: series B (statistical methodology)*, 67(2):301–320.
Appendix A  Additional Details of This Paper

A.1 Vanilla RaSE algorithm in Tian and Feng (2021)

See Algorithm 3.

Algorithm 3: Random subspace ensemble classification (RaSE)

**Input:** training data \( \{(x_i, y_i)\}_{i=1}^n \), new data \( x \), subspace distribution \( D \), criterion \( C \), integers \( B_1 \) and \( B_2 \), type of base classifier \( T \)

**Output:** predicted label \( C_n^{RaSE}(x) \), the selected proportion of each feature \( \hat{\eta} \)

1. Independently generate random subspaces \( S_{b_1 b_2} \sim D, 1 \leq b_1 \leq B_1, 1 \leq b_2 \leq B_2 \)
2. for \( b_1 \leftarrow 1 \) to \( B_1 \) do
3.   Select the optimal subspace \( S_{b_1*} \) from \( \{S_{b_1 b_2}\}_{b_2=1}^{B_2} \) according to \( C \) and \( T \)
4.   Train \( C_n^{S_{b_1*}-T} \) in subspace \( S_{b_1*} \)
5. end
6. Construct the ensemble decision function \( \nu_n(x) = \frac{1}{B_1} \sum_{b_1=1}^{B_1} C_n^{S_{b_1*}-T}(x) \)
7. Set the threshold \( \hat{\alpha} \) according to minimize training error
8. Output the predicted label \( C_n^{RaSE}(x) = 1(\nu_n(x) > \hat{\alpha}) \), the selected proportion of each feature \( \hat{\eta} = (\hat{\eta}_1, \ldots, \hat{\eta}_p) \) where \( \hat{\eta}_l = B_1^{-1} \sum_{b_1=1}^{B_1} I(l \in S_{b_1*}), l = 1, \ldots, p \)

A.2 Additional analysis on iterative RaSE

Assumption 5. We assume the following conditions hold:
(i) For any \( j \in S_{[0]}^* \) and \( d \geq 1 \), we have
\[
Cr(S) - Cr(S') > 2\epsilon_n,
\]
for any \( S \) and \( S' \) satisfying \( |S \cap S^*| < d, |S' \cap S^*| \geq d, \) \( S' \ni j \), and \( S \not
\ni j \).

(ii) For any \( j \in S_{[1]}^* \) and \( d \geq |S_{[0]}^*| + 1 \), we have
\[
Cr(S) - Cr(S') > 2\epsilon_n,
\]
for any \( S \) and \( S' \) satisfying \( |S \cap S^*| < d, |S' \cap S^*| \geq d, \) \( S' \ni j \), and \( S \not
\ni j \).

Remark 5. By using the definition of detection complexity, Assumption 5 can be stated as
follows.

(i) Any \( j \in S_{[0]}^* \) is detectable in any complexity \( d \geq 1 \) w.r.t. any \( \bar{S}_j \ni j \) and \( \bar{S}_0^0 = \emptyset \).

(ii) Any \( j \in S_{[1]}^* \) is detectable in any complexity \( d \geq |S_{[0]}^*| + 1 \) w.r.t. any \( \bar{S}_j \ni j \) and \( \bar{S}_0^0 = \emptyset \).

Proposition 3. Under Assumption 5:

(i) When \( B_2 \asymp (p/D)^{|S_{[0]}^*|+1} \), Assumption 1 holds.

(ii) Let \( D \geq p^* \). There exist \( B_2 \asymp p/D \) in the first step, and \( B_2 \lesssim D^{|S_{[0]}^*|} (\log p)^{|S_{[1]}^*|} p \) in
the second step, such that Assumption 3 holds.

A.3 More numerical experiment results

A.3.1 Further illustration of ISIS used in numerical studies

As described at the beginning of Section 4, we report the results of ISIS with two screening
steps and one selection step. To facilitate readers’ understanding, we would like to explain
the details via the following toy example. Suppose we have $n = 10$ observations with $p = 10$ predictors, i.e. features 1-10. ISIS first screens 10 variables and selects the top $[n / \log n] \approx 4$ variables (screening step 1), which follows by fitting a LASSO model on these four variables and select those with non-zero coefficients (selection step 1). Suppose in screening step 1, the feature ranking is 4, 3, 1, 2, 6, 5, 7, 8, 10, 9. ISIS selects features 1-4 while in selection step 1, only features 1 and 4 have non-zero coefficients and are selected. Then ISIS screens on the remaining 8 features, and outputs the ranking of them (screening step 2). Suppose the ranking is 3, 7, 5, 9, 2, 6, 8, 10. In this case, the final output ranking from ISIS is 4, 1, 3, 7, 5, 9, 2, 6, 8, 10. The details can be summarized as follows:

- **Screening step 1**: 4, 3, 1, 2, 6, 5, 7, 8, 10, 9. Choose features 4, 3, 1, 2 to fit the LASSO.
- **Selection step 1**: 4, 1. (LASSO selects features 4 and 1)
- **Screening step 2**: 3, 7, 5, 9, 2, 6, 8, 10. (by screening on the remaining 8 features.)
- **Final output ranking**: 4, 1, 3, 7, 5, 9, 2, 6, 8, 10.

### A.3.2 Additional simulations

**Example 7** (Example 1 with realistic predictors, motivated by Model (3)(d) in Nandy et al. (2020)). In each replication, we randomly sample $p = 2000$ predictors from 18976 variables in rat eye expression data set, which is used in our real data example in Section 4.2.2. Then we generate the response from the same model (7) in Example 1. Here the sample size $n = 120$, as in the rat eye expression data set.

The goal of this example is to demonstrate the effectiveness of RaSE for realistic predictors. The performances of different approaches are summarized in the left panel of Table
leading to similar findings as in Example 1 with RaSE$_1$-eBIC still achieving the best overall performance. Note that HOLP seems to have a much better performance than that in Example 1.

| Method/MMS | Example 7 | Example 8 |
|------------|-----------|-----------|
|            | 5% 25% 50% 75% 95% | 5% 25% 50% 75% 95% |
| SIS        | 173 660 1184 1634 1907 | 7 41 221 599 1847 |
| ISIS       | 15 18 24 115 896 | 114 850 1392 1806 1969 |
| SIRS       | 564 1174 1537 1798 1944 | 6 1226 1602 1864 1960 |
| DC-SIS     | 675 1177 1552 1823 1958 | 61 1153 1620 1831 1976 |
| HOLP       | 4 11 44 151 657 | 63 270 604 1217 1847 |
| IPDC       | 487 936 1334 1642 1940 | 220 588 940 1411 1841 |
| MDC-SIS    | 110 602 1150 1617 1922 | 7 36 148 1218 1915 |
| CIS        | 264 703 1222 1644 1936 | 2000 2000 2000 2000 2000 |
| RaSE-BIC   | 4 11 34 98 1131 | 8 949 1512 1797 1954 |
| RaSE$_1$-BIC | 4 4 4 53 101 | 18 1228 1618 1872 1966 |
| RaSE-eBIC  | 4 19 59 822 1829 | 7 448 1619 1780 1965 |
| RaSE$_1$-eBIC | 4 4 6 10 40 | 1068 1527 1753 1896 1984 |
| RaSE-kNN   | 12 109 270 1447 1911 | 5 5 10 326 1740 |
| RaSE$_1$-kNN | 4 33 658 1412 1834 | 5 5 5 842 1858 |
| RaSE-SVM   | 7 61 204 937 1802 | 5 5 8 94 1504 |
| RaSE$_1$-SVM | 4 32 72 880 1707 | 5 5 5 6 675 |

Table 6: Quantiles of MMS in Examples 7 and 8.

**Example 8** (Example 2 with mixed types of covariates). We generate $\tilde{x}' \sim N(0, \Sigma)$ where $\Sigma = (\sigma_{ij})_{(4p/5)\times(4p/5)} = (0.5^{i-j})_{(4p/5)\times(4p/5)}$, $\tilde{x}' \in \mathbb{R}^{4p/5}$, and $p = 2000$. And we generate $\tilde{x}'' \sim \text{Unif}(\{-2,-1,0,1,2\})$, where $\tilde{x}'' \in \mathbb{R}^{p/5}$. Then we construct $\tilde{x}$ by letting $\tilde{x}_S = \tilde{x}'$ and $\tilde{x}_S = \tilde{x}''$, where $S = \{5,10,\ldots,1995,2000\}$. Generate $z \sim \text{Unif}(\{-3,3\}) \perp \tilde{x}$ and $x = \tilde{x} + z1_p$. The response is generated from the same model (8) in Example 8. The signal
set $S^* = \{1, 2, 3, 4, 5\}$. $n = 200$.

This example is used to verify the effectiveness of RaSE in dealing with mixed types of covariates, which is very common in applications. Results are summarized in the right panel of Table 6, which are similar to those of Example 2. MDC-SIS and SIS still achieve a good performance at 5% and 25% quantiles, with RaSE$_1$-SVM outperforming all other methods.

Figure 3: Median MMS to capture $S^*$ ($|S^*| = 4$) as $(D, B_2)$ varies for RaSE-BIC (a) and RaSE$_1$-BIC (b) in Example 1.

**A.3.3 Additional figures**

See Figures 4, 5 and 6. The full name of variables in Figure 5 can be found at [http://genomics-pubs.princeton.edu/oncology/affydata/names.html](http://genomics-pubs.princeton.edu/oncology/affydata/names.html)
Figure 4: Scatterplots of $x_2$ vs. $x_1$ and $x_6$ vs. $x_5$ for Example 5 ($n = 200$).

Appendix B  Proofs

In this section we use $C$ to represent a positive constant which is irrelevant to $n, D, B_1$ and $B_2$. It might take different values at different places.

B.1 Proof of Lemma 1

For arbitrary subsets $A_1^{(j)}, \ldots, A_k^{(j)}, A_1^{(-j)}, \ldots, A_{B_2-k}^{(-j)}$, we have

$$
P(S_{11}^{(j)} = A_1^{(j)}, \ldots, S_{1k}^{(j)} = A_k^{(j)}, S_{11}^{(-j)} = A_1^{(-j)}, \ldots, S_{1(B_2-k)}^{(-j)} = A_{B_2-k}^{(-j)} | N_j = k) = \frac{P(S_{11}^{(j)} = A_1^{(j)}, \ldots, S_{1k}^{(j)} = A_k^{(j)}, S_{11}^{(-j)} = A_1^{(-j)}, \ldots, S_{1(B_2-k)}^{(-j)} = A_{B_2-k}^{(-j)}) \cdot \prod_{i=1}^{k} 1(A_i^{(j)} \geq \bar{S}_j) \cdot \prod_{i=1}^{B_2-k} 1(A_i^{(-j)} \not\geq \bar{S}_j)}{P(N_j = k)}
$$
Figure 5: Features with the 10 highest selection rates (percentages in 200 replications) in the colon cancer data set.
Figure 6: Features with the 10 highest selection rates (percentages in 200 replications) in the rat eye expression data set.
\[
\frac{(B_2^k)}{B_2^k} \prod_{i=1}^{B_2^k} \frac{1}{D_i^k} \prod_{i=1}^{B_2-k} \frac{1}{D_i^k} \cdot \prod_{i=1}^{B_2} 1(A_i^{(j)} \supseteq \bar{S}_j) \cdot \prod_{i=1}^{B_2} 1(A_i^{(-j)} \supseteq \bar{S}_j)
\]

where the last equation is the joint density under conditions (i)-(iii). The second equality
in (i) and (ii) can be easily derived by basic algebra. This completes the proof.

### B.2 Proof of Theorem 1

**Lemma 3** (Chernoff’s bound). For \( N \sim \text{Bin}(B_2, p_0) \), where \( p_0 \in (0, 1) \), it holds

\[
P(N > (1 + \lambda)B_2p_0) \leq \exp \left\{ -\frac{\lambda^2}{2 + \frac{2}{3} \lambda} B_2p_0 \right\}, \lambda > 0,
\]

\[
P(N < (1 - \lambda)B_2p_0) \leq \exp \left\{ -\frac{\lambda^2}{2 + \frac{2}{3} \lambda} B_2p_0 \right\}, \lambda \in (0, 1).
\]

*Proof.* See Shalev-Shwartz and Ben-David (2014). \( \square \)

**Lemma 4** (Hoeffding’s inequality). Let \( N_j \sim \text{Bin}(B_2, p_0) \), where \( p_0 \in (0, 1) \), then for arbitrary \( x \in (0, p_0) \), there holds that

\[
\max \{P(N_j < B_2(p_0 - x)), P(N_j > B_2(p_0 + x))\} \leq \exp\{-2B_2x^2\}.
\]

Next we prove Theorem 1 by applying the lemmas above. Denote the training data as
\( \mathcal{D} = \{(x_i, y_i)\}_{i=1}^{n} \) and event \( \{\sup_{S : |S| \leq D} |\text{Cr}_{n}(S) - \text{Cr}(S)| \leq \epsilon_n\} \) as \( \mathcal{A} \). Let \( j \) be an arbitrary feature in \( S^* \). Because of Lemma 1, it holds

\[
P(j \in S_1* | N_j = k, \mathcal{A})
\]
where (B.9) holds due to Jensen inequality. It follows that

\[
P(j \in S_1|N_j = k) \geq P(j \in S_1|N_j = k, A)P(A) \geq (1 - c_1 n)(1 - E_{S^{(-j)}}[\delta_j(S^{(-j)})^k])^{B_2 - k}.
\]

Then we have

\[
P(j \in S_1) = \sum_{k=1}^{B_2} P(j \in S_1|N_j = k)P(N_j = k)
\geq (1 - c_1 n) \sum_{k=1}^{B_2} (1 - E_{S^{(-j)}}[\delta_j(S^{(-j)})^k])^{B_2 - k} \cdot P(N_j = k)
\]
\[
\sum_{k \geq \frac{1}{2} B_2 p_0} (1 - \mathbf{E}_{S(-j)}[\delta_j(S(-j))^{k}])^{B_2 - k} \cdot \mathbf{P}(N_j = k)
\]
\[
\geq (1 - c_{1n})(1 - \mathbf{E}_{S(-j)}[\delta_j(S(-j))^{\frac{1}{2} B_2 p_0}])^{B_2} \cdot \mathbf{P}\left(N_j \geq \frac{1}{2} B_2 p_j\right). \tag{B.12}
\]

By letting \( \lambda = \frac{1}{2} \) in Lemma 3, we have
\[
\mathbf{P}\left(N_j \geq \frac{1}{2} B_2 p_j\right) \geq 1 - \exp\left\{-\frac{3}{28} B_2 p_j\right\}. \tag{B.13}
\]

Combining (B.12) and (B.13), we obtain
\[
\eta_j = \mathbf{P}(j \in S_1) \geq c_{2n}.
\]

Again, by Lemma 4 and union bounds, it holds
\[
\mathbf{P}(S^* \subseteq \hat{S}_\alpha) \geq \mathbf{P}\left(\bigcap_{j \in S^*} \{\hat{\eta}_j \geq \frac{c_{2n}}{\alpha}\}\right)
\]
\[
\geq 1 - \sum_{j \in S^*} \mathbf{P}\left(\hat{\eta}_j - \eta_j < - \left(1 - \frac{1}{\alpha}\right) \eta_j\right)
\]
\[
\geq 1 - \sum_{j \in S^*} \exp\left\{-2B_1 \eta_j^2 \left(1 - \frac{1}{\alpha}\right)^2\right\}
\]
\[
\geq 1 - p^* \exp\left\{-2B_1 c_{2n}^2 \left(1 - \frac{1}{\alpha}\right)^2\right\}, \tag{B.14}
\]

which leads to conclusion (i).

For (ii), since \( \limsup_{n,D,B_2 \to \infty} \left\{B_2 \sup_{j \in S^*} \mathbf{E}_{S(-j)}[\delta_j(S(-j))^{\frac{1}{2} B_2 p_0}]\right\} < \infty, c_{1n} \to 0 \) and \( B_2 \inf_{j \in S^*} p_j \gtrsim 1 \), it’s easy to show that
\[
\liminf_{n,D,B_2 \to \infty} c_{2n} > 0,
\]
yielding \( |\hat{S}_\alpha| \lesssim D \), which completes our proof.
B.3 Proof of Proposition 1

Lemma 5. \( p_j = P(S_{11} \supseteq \bar{S}_j) = D^{-1} \sum_{d=|\bar{S}_j|}^{D} \frac{(p-|\bar{S}_j|)}{d} \asymp \left( \frac{p}{D} \right)^{|\bar{S}_j|} \), where \( S_{11} \) follows the distribution in (2) w.r.t. \( \bar{S}_j \).

Proof of Lemma 5. First, notice that
\[
p_j = \frac{1}{D} \sum_{d=|\bar{S}_j|}^{D} \frac{(p-|\bar{S}_j|) \cdot (p-d+1)}{p \cdots (p-d+1)} \cdot d \cdots (d-|\bar{S}_j|+1) \leq \frac{1}{D} \sum_{d=|\bar{S}_j|}^{D} \frac{D^{(|\bar{S}_j|)}}{(p-D+1)^{|\bar{S}_j|}} \lesssim \left( \frac{p}{D} \right)^{|\bar{S}_j|}.
\]

On the other hand,
\[
p_j \geq \frac{1}{D p^{||\bar{S}_j||}} \cdot \left( 1 - \frac{|\bar{S}_j|}{p-D} \right)^D \sum_{d=|\bar{S}_j|}^{D} d \cdots (d-|\bar{S}_j|+1) \geq \frac{1}{D p^{||\bar{S}_j||}} \cdot \left( 1 - \frac{|\bar{S}_j|}{p-D} \right)^D \sum_{r=1}^{D-|\bar{S}_j|+1} r \cdots (r+|\bar{S}_j|-1) \gtrsim \left( \frac{p}{D} \right)^{|\bar{S}_j|},
\]
where the last inequality is because \( D \ll p, \ |\bar{S}_j| \leq p^* \) and \( p^* \) is fixed. \( \square \)

Lemma 6. Under Assumption 2, we have
\[
P_{S^{(-j)}}(|S^{(-j)} \cap (S^* \cup S_0^j)| \geq |\bar{S}_j|) \lesssim \left( \frac{D}{p} \right)^{|\bar{S}_j|},
\]
where \( S^{(-j)} \) follows the distribution in (3).

Proof of Lemma 6. By Lemma 5, when \( n \) is sufficiently large, \( \inf_{j \in S^*} p_j < \frac{1}{2} \). Then for any integer \( t \in [0, p^* + p_0^j] \), we have
\[
P_{S^{(-j)}}(|S^{(-j)} \cap (S^* \cup S_0^j)| = t)
\]
\[
\sum_{d=t}^{D} \frac{1}{D} \left( \frac{1}{d} \right) \binom{p}{d} \left( p - p^* - p_j \right) \left( p^* + p_j^0 \right) \left( p - d - t \right) \left( p + p_j^0 \right) \frac{1}{d - t} \left( p^* + p_j^0 \right) \left( p - d - t + 1 \right) \\
\leq 2 \sum_{d=t}^{D} \frac{1}{D} \left( p - p^* - p_j^0 \right) \cdots \left( p - p^* - p_j^0 - (d + t - 1) \right) \cdot \left( p^* + p_j^0 \right) d \cdots (d - t + 1) \\
\leq \left( \frac{p}{D} \right)^t \left( 1 - \frac{p^* + p_j^0}{p} \right)^D \frac{1}{(p - D + 1)} \cdot D^t \\
\leq \frac{2(p^* + p_j^0)}{(p - D + 1)^t} \\
\lesssim \left( \frac{D}{p} \right)^t.
\]

Therefore,

\[
\mathbf{P}_{S(-j)} \left( |S^{(-j)} \cap (S^* \cup S_j^0)| \geq |\bar{S}_j| \right) \lesssim \mathbf{P}_{S(-j)} \left( |S^{(-j)} \cap (S^* \cup S_j^0)| = |\bar{S}_j| \right) \lesssim \left( \frac{D}{p} \right)^{|\bar{S}_j|}.
\]

Now let's prove Proposition 1. Due to Assumption 2, for any \( j \) there exists a set \( \bar{S}_j \supset j \) with cardinality \( d \) to make \( j \) detectable. By Lemmas 5 and 6, it's easy to see that

\[
B_2 \sup_{j \in S^*} \mathbf{E}_{S^{(-j)}} \left[ \delta_j (S^{(-j)})^{\frac{1}{2}B_2 p_j} \right] \leq B_2 \sup_{j \in S^*} \mathbf{P}_{S^{(-j)}} \left( |S^{(-j)} \cap (S^* \cup S_j^0)| \geq d \right) \lesssim B_2 \left( \frac{D}{p} \right)^d < \infty,
\]

\[
B_2 \inf_{j \in S^*} p_j \gtrsim B_2 \left( \frac{p}{D} \right)^d \gtrsim 1,
\]

implying that conditions in Assumption 2 hold.

**B.4 Proof of Theorem 2**

Akin to the argument in the proof of Theorem 1, we can prove that

\[
\mathbf{P} \left( \bigcap_{j \in S_{[0]}^*} \left\{ n_j^{[0]} \geq c_2^* \right\} \right) \geq 1 - p^* \exp \left\{ -2B_1 (c_2^{[0]} - c_2^*)^2 \right\}.
\]
For convenience, denote event $\cap_{j \in S_{[0]}^*} \{ \hat{\eta}_{[0]}^j \geq c_2^* \}$ as $B$. Write $\# \{ b_2 : j \in S_{10b_2}^{[1]} \}$ as $N_j$, then similar to (B.10) and (B.11), since

$$\inf_{i \in S_{[0]}^*} \tilde{\eta}_i \geq \frac{c_2^*}{(D + C_0)},$$

the subspace distribution family satisfies the condition in Assumption 3.(ii), it follows

$$P(j \in S_{1}^{[1]} | N_j = k, B) \geq (1 - c_{1n})(1 - (\delta_{[1]}^j)^k) B_{2-k}.$$

Similar to (B.12), it follows that

$$P(j \in S_{1}^{[1]} | \hat{\eta}^0 \in B)$$

$$= \sum_{k=1}^{B_2} P(j \in S_{1}^{[1]} | N_j = k, B) P(N_j = k | \hat{\eta}^0 \in B)$$

$$\geq (1 - c_{1n}) \sum_{k=1}^{B_2} (1 - E_{s(-j)}[\delta_j(S(-j)^k)] B_{2-k} \cdot P(N_j = k | \hat{\eta}^0 \in B)$$

$$\geq (1 - c_{1n}) \sum_{k \geq \frac{1}{2} B_2 p_{j}^{[1]}} (1 - E_{s(-j)}[\delta_j(S(-j)^k)] B_{2-k} \cdot P(N_j = k | \hat{\eta}^0 \in B)$$

$$\geq (1 - c_{1n})(1 - E_{s(-j)}[\delta_j(S(-j)^{\frac{1}{2} B_2 p_{j}^{[1]}})] B_{2} \cdot P \left( N_j \geq \frac{1}{2} B_2 p_{j}^{[1]} | \hat{\eta}^0 \in B \right), \quad (B.15)$$

where $p_{j}^{[1]} = P_{S_{1}^{[1]} \sim R(\ell_{6p, p}, \hat{\eta}^0)} (j \in S_{1}^{[1]} | \hat{\eta}^0 \in B)$. Notice that $N_j \sim Bin(B_2, p_{j}^{[1]})$ when $\hat{\eta}^0$ is given. Therefore, by Lemma 3, analogous to the proof of Theorem 1, we can obtain

$$P \left( N_j \geq \frac{1}{2} B_2 p_{j}^{[1]} | \hat{\eta}^0 \in B \right) \geq 1 - \exp \left\{ -\frac{3}{28} B_2 p_{j}^{[1]} \right\}. \quad (B.16)$$

Therefore, together with (B.16), equation (B.15) leads to

$$P(j \in S_{1}^{[1]} | \hat{\eta}^0 \in B)$$

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\[ \geq (1 - c_1n)(1 - \mathbf{E}_{S(-j)}[\delta_j(S^{(-j)})^{1/2}B_2p_j^{[1]}])B_2 \left( 1 - \exp \left\{ -\frac{3}{28}B_2p_j^{[1]} \right\} \right). \]

Therefore, given \( \eta^{[0]} \in \mathcal{B} \), it follows that

\[ \eta_j^{[1]} = P(j \in S_j^{[1]}|\hat{\eta}^{[0]} \in \mathcal{B}) \geq c_2n. \]

And for any \( j \), it’s straightforward to see that

\[ P_{S_1^{[1]} \sim \mathcal{R}(U_0,p,\hat{\eta}^{[0]})}(j \in S_1^{[1]}|\hat{\eta}^{[0]} \in \mathcal{B},|S_1^{[1]}| = d) \geq 1 - \left[ 1 - \frac{C_0}{D + C_0} \right] \cdot \left[ 1 - \frac{C_0}{D + C_0 - \frac{c_2n}{p}} \right] \cdots \]

\[ \geq \frac{C_0d}{(D + C_0)p}, \]

yielding that

\[ p_j^{[1]} = P_{S_1^{[1]} \sim \mathcal{R}(U_0,p,\hat{\eta}^{[0]})}(j \in S_1^{[1]}|\hat{\eta}^{[0]} \in \mathcal{B}) \geq \frac{1}{D} \sum_{d=1}^{D} \frac{C_0d}{(D + C_0)p} \geq \frac{(D + 1)C_0}{2(D + C_0)p} = p^{[1]}. \quad \text{(B.17)} \]

Analogous to (B.14), applying Hoeffding’s inequality and union bounds, we obtain

\[ P(S^* \subseteq S_\alpha^{[1]}) \geq P \left( \bigcap_{j \in S^*} \left\{ \hat{\eta}_j^{[1]} \geq \frac{c_2^{[1]}}{\alpha} \right\} \right| \hat{\eta}^{[0]} \in \mathcal{B}) P(\hat{\eta}^{[0]} \in \mathcal{B}) \]

\[ \geq 1 - \sum_{j \in S^*} P \left( \hat{\eta}_j^{[1]} - \eta_j^{[1]} < - \left( 1 - \frac{1}{\alpha} \right) \frac{c_2^{[1]}}{\alpha} \right| \hat{\eta}^{[0]} \in \mathcal{B}) - P(\hat{\eta}^{[0]} \notin \mathcal{B}) \]

\[ \geq 1 - p^* \exp \left\{ -2B_1(c_2^{[0]} - c_2^*)^2 \right\} - p^* \exp \left\{ -2B_1(c_2^{[1]})^2 \left( 1 - \frac{1}{\alpha} \right)^2 \right\}, \]

which completes the proof of conclusion (i). The proof of conclusion (ii) is similar to that of Theorem 1, and we omit it here.
B.5 Proof of Theorem 3

Similar to (B.10), for any \( j \notin S^* \), we have

\[
P(j \in S_{1*} | N_j = k, A)
= P \left( \inf_{1 \leq b_2 \leq k} \text{Cr}(S_{1b_2}^{(j)}) < \inf_{1 \leq b_2 \leq B_2 - k} \text{Cr}(S_{1b_2}^{(-j)}) | N_j = k, A \right)
\leq P \left( \inf_{1 \leq b_2 \leq k} \text{Cr}(S_{1b_2}^{(j)}) - 2\epsilon_n < \inf_{1 \leq b_2 \leq B_2 - k} \text{Cr}(S_{1b_2}^{(-j)}) | N_j = k, A \right)
= P \left( \inf_{1 \leq b_2 \leq k} \text{Cr}(S_{1b_2}^{(j)}) - 2\epsilon_n < \inf_{1 \leq b_2 \leq B_2 - k} \text{Cr}(S_{11}^{(-j)}) | N_j = k \right)
= 1 - \mathbb{E}_{\{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k}} \left[ P \left( \inf_{1 \leq b_2 \leq k} \text{Cr}(S_{1b_2}^{(j)}) - 2\epsilon_n \geq \inf_{1 \leq b_2 \leq B_2 - k} \text{Cr}(S_{11}^{(-j)}) | N_j = k, \{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k} \right) \right]
\leq 1 - P \left( \text{Cr}(S^{(j)}) - 2\epsilon_n \geq \inf_{1 \leq b_2 \leq B_2 - k} \text{Cr}(S_{11}^{(-j)}) | N_j = k, \{S_{1b_2}^{(-j)}\}_{b_2=1}^{B_2-k} \right)^k
= 1 - (1 - \mathbb{E}_{S^{(j)}} \left[ P_{S^{(-j)}}(\text{Cr}(S^{(j)}) - 2\epsilon_n \geq \text{Cr}(S^{(-j)}) | S^{(j)} B_2 - k) \right])^k
= 1 - (1 - \mathbb{E}_{S^{(j)}} \left[ \tilde{\delta}_j(S^{(j)}) B_2 - k \right])^k.
\]

Then we have

\[
P(j \in S_{1*} | N_j = k) \leq P(j \in S_{1*} | N_j = k, A) \mathbb{P}(A) + \mathbb{P}(A^c)
\leq (1 - c_{1n}) \left\{ 1 - \left( 1 - \mathbb{E}_{S^{(j)}} \left[ \tilde{\delta}_j(S^{(j)}) B_2 - k \right] \right)^k \right\} + c_{1n},
\]

which combined with Lemma 3 yields

\[
\gamma' := \inf_{j \in S^*} P(j \in S_{1*}) - \sup_{j \notin S^*} P(j \in S_{1*})
\]
\[
\geq \inf_{j \in S^*} \sum_{k=1}^{B_2} P(j \in S_1 | N_j = k) P(N_j = k) - \sup_{j \notin S^*} \sum_{k=1}^{B_2} P(j \in S_1 | N_j = k) P(N_j = k)
\]

\[
\geq (1 - c_{1n}) \inf_{j \in S^*} \sum_{k=1}^{B_2} \left( 1 - \mathbb{E}_{S(-j)} [\delta_j (S(-j)^k)] \right)^{B_2 - k} P(N_j = k)
\]

\[
+ (1 - c_{1n}) \inf_{j \notin S^*} \sum_{k=1}^{B_2} \left( 1 - \mathbb{E}_{S(-j)} [\tilde{\delta}_j (S(j)^{B_2 - k})] \right)^{k} \cdot P(N_j = k) - c_{1n}
\]

\[
\geq (1 - c_{1n}) \inf_{j \notin S^*} \sum_{k \geq 2 B_2 p_j} \left( 1 - \mathbb{E}_{S(-j)} [\tilde{\delta}_j (S(j)^{B_2 - k})] \right)^{k} \cdot P(N_j = k) - c_{1n}
\]

\[
\geq \left[ \left( 1 - \sup_{j \in S^*} \mathbb{E}_{S(-j)} [\delta_j (S(-j)^{\frac{1}{2}B_2 p_j})] \right)^{B_2} + \left( 1 - \sup_{j \notin S^*} \mathbb{E}_{S(j)} [\tilde{\delta}_j (S(j)^{B_2 - \frac{1}{2}B_2 p[0]})] \right)^{\frac{1}{2}B_2 p[0]} \right] - 1
\]

\[
\cdot (1 - c_{1n}) \left( 1 - 2 \exp \left\{ -\frac{3}{28} B_2 \inf_{j \in S^*} p_j \right\} \right) - c_{1n}
\]

\[
= \gamma.
\]

Denote \( \gamma'' = \inf_{j \in S^*} \eta_j - \sup_{j \notin S^*} \eta_j \). Then we have

\[
\sup_{j \notin S^*} \eta_j = \sup_{j \notin S^*} P(j \in S_1) = (1 - \gamma'') \inf_{j \in S^*} P(j \in S_1) = (1 - \gamma'') \inf_{j \in S^*} \eta_j.
\]

By Hoeffding’s inequality and union bounds, it follows

\[
P \left( \inf_{j \in S^*} \hat{\eta}_j > \sup_{j \notin S^*} \hat{\eta}_j \right)
\]

\[
\geq P \left( \sup_{j \notin S^*} \hat{\eta}_j < \left( 1 - \frac{1}{2} \gamma'' \right) \inf_{j \in S^*} \eta_j < \inf_{j \in S^*} \hat{\eta}_j \right)
\]

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\[ \geq 1 - \mathbb{P} \left( \bigcup_{j \notin S^*} \left\{ \hat{\eta}_j - \eta_j \geq \frac{\gamma''}{2} \inf_{j \in S^*} \eta_j \right\} \right) - \mathbb{P} \left( \bigcup_{j \in S^*} \left\{ \hat{\eta}_j - \eta_j \leq -\frac{\gamma''}{2} \inf_{j \in S^*} \eta_j \right\} \right) \]
\[ \geq 1 - \sum_{j \notin S^*} \mathbb{P} \left( \hat{\eta}_j - \eta_j \geq \frac{\gamma'}{2} \right) - \sum_{j \in S^*} \mathbb{P} \left( \hat{\eta}_j - \eta_j \leq -\frac{\gamma'}{2} \right) \]
\[ \geq 1 - \sum_{j \notin S^*} \exp \left\{ -\frac{1}{2} B_1 \gamma'^2 \right\} - \sum_{j \in S^*} \exp \left\{ -\frac{1}{2} B_1 \gamma'^2 \right\} \]
\[ \geq 1 - p \exp \left\{ -\frac{1}{2} B_1 \gamma'^2 \right\} \]
\[ \geq 1 - p \exp \left\{ -\frac{1}{2} B_1 \gamma'^2 (n, D, B_2) \right\}, \]
which converges to 1 due to Assumption 4 as \( n, B_1, B_2 \to \infty \). This completes the proof.

### B.6 Proof of Proposition 2

By the definition of \( \gamma(n, D, B_2) \), it suffices to show that there exist constants \( C_2 > C_1 > 0 \), such that

\[ \left( 1 - \sup_{j \in S^*} \mathbb{E}_{S(j)} \left[ \delta_j(S(j))^{\frac{1}{2} B_2 p_j} \right] \right)^{B_2} + \left( 1 - \sup_{j \notin S^*} \mathbb{E}_{S(j)} \left[ \tilde{\delta}_j(S(j))^{B_2 - \frac{3}{2} B_2 p_0} \right] \right)^{\frac{3}{2} B_2 p_0} > 1, \]
as well as \( B_2 \inf_{j \in S^*} p_j \gtrsim 1 \). Without loss of generality, assume feature \( 1 \in S^* \).

In fact, when \( B_2 \in \left( \frac{C_1 p}{D}, \frac{C_2 p}{D} \right) \), by the proof of Proposition 1,

\[ \left( 1 - \sup_{j \in S^*} \mathbb{E}_{S(j)} \left[ \delta_j(S(j))^{\frac{1}{2} B_2 p_j} \right] \right)^{B_2} \gtrsim e^{-C_2}. \]

On the other hand,

\[ \sup_{j \notin S^*} \mathbb{E}_{S(j)} \left[ \tilde{\delta}_j(S(j))^{B_2 - \frac{3}{2} B_2 p_0} \right] \leq \sup_{j \notin S^*} \left[ \mathbb{P}_{S(j)}(S(j) \cap (\{1\} \cup S^0) \neq \emptyset) + \mathbb{P}_{S(j)}(1 \notin S(j))^{B_2 - \frac{3}{2} B_2 p_0} \right] \]

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\[
\begin{aligned}
\lesssim & \frac{D}{p} + \left(1 - \frac{D}{p}\right)^{B_2 - \frac{2}{3}B_2p[0]} \\
\lesssim & e^{-C_1}.
\end{aligned}
\]

Therefore, \(\exists C > 0\), such that

\[
\left(1 - \sup_{j \notin S^*} \mathbb{E}_{S(j)} \left[\tilde{\delta}_j(S(j))B_2 - \frac{3}{2}B_2p[0]\right]\right)^{\frac{3}{2}B_2p[0]} \geq (1 - Ce^{-C_1})C_2.
\]

Let \(C_1 = C_2/2\), the inequality above leads to

\[
\left(1 - \sup_{j \notin S^*} \mathbb{E}_{S(j)} \left[\tilde{\delta}_j(S(j))\frac{1}{2}B_2p[j]\right]\right)^{B_2} + \left(1 - \sup_{j \notin S^*} \mathbb{E}_{S(j)} \left[\tilde{\delta}_j(S(j))B_2 - \frac{3}{2}B_2p[0]\right]\right)^{\frac{3}{2}B_2p[0]} \\
\geq e^{-C_2} + (1 - Ce^{-C_2})C_2 \\
> 1,
\]

when \(C_2\) is small than some constant, which finishes our proof.

### B.7 Proof of Proposition 3

Note that \(d = |S^*[0]| + 1\) and Assumption 2 holds. Therefore conclusion (i) holds due to Proposition 1. Let’s prove (ii). The \(B_2\) requirement in first step is derived from Proposition 1 since \(\sup_{i \in S^*[0]} d_i = 1\). We only need to calculate the restriction on \(B_2\) in the second step. By the proof of Theorem 2, \(\inf_{i \in S^*[0]} \tilde{\eta}_i \geq c_0^2\). Recalling Algorithm 2, we denote \(\tilde{S}^*[0] = \{i : \hat{\eta}_i[0] > C_0/\log p\} \setminus S^*[0]\). Then similar to (B.17), we know that

\[
\inf_{i \in \tilde{S}^*[0]} \tilde{\eta}_i[0] \gtrsim D^{-1}, \quad \inf_{i \in S^*[0]} \tilde{\eta}_i[0] \gtrsim (\log p)^{-1}, \quad \inf_{i \in S^*[1]} \tilde{\eta}_i[0] \gtrsim p^{-1}. \quad (B.18)
\]
• If \( j \notin \tilde{S}^*_0 \cup S^*_0 \), similar to the proof of Proposition 1, to guarantee Assumption 3, we need

\[
B_2 \mathbb{P}(S_{11}^\ast \supseteq S^*_0 \cup \tilde{S}^*_0 \cup \{j\}) \geq B_2 \mathbb{P}(S_{11}^\ast \cap S^\ast = S^*_0 \cup \tilde{S}^*_0 \cup \{j\}) \gtrsim 1, \text{ (B.19)}
\]

\[
B_2 \mathbb{P}(|S^{(-j)} \cap S^\ast| > |S^*_0 \cup \tilde{S}^*_0|) \lesssim B_2 \mathbb{P}(|S_{11}^\ast \cap S^\ast| > |S^*_0 \cup \tilde{S}^*_0|) \lesssim 1. \text{ (B.20)}
\]

Note that

\[
\mathbb{P}(|S_{11}^\ast \cap S^\ast| > |S^*_0 \cup \tilde{S}^*_0|) \leq \sum_{i \in S^* \setminus \tilde{S}^*_0} \mathbb{P}(S_{11}^\ast \cap S^\ast = S^*_0 \cup \tilde{S}^*_0 \cup \{i\}) \lesssim \mathbb{P}(S_{11}^\ast \cap S^\ast = S^*_0 \cup \tilde{S}^*_0 \cup \{j\}),
\]

which combined with (B.19) and (B.20) leads to \( B_2 \simeq (\mathbb{P}(S_{11}^\ast \cap S^\ast = S^*_0 \cup \tilde{S}^*_0 \cup \{j\}))^{-1} \). Then because of (B.18), it holds that

\[
\mathbb{P}(S_{11}^\ast \cap S^\ast = S^*_0 \cup \tilde{S}^*_0 \cup \{j\}) \geq D^{-1} \sum_{d=|S^*_0 \cup \tilde{S}^*_0|+1}^{D} \prod_{i \in S^* \setminus \tilde{S}^*_0 \cup \{j\}} \bar{n}^{[0]}_i \gtrsim D^{-1} \sum_{d=|S^*_0 \cup \tilde{S}^*_0|+1}^{D} D^{-|S^*_0|} (\log p)^{-|\tilde{S}^*_0|} p^{-1}
\]

\[
\gtrsim D^{-1} \sum_{d=|S^*_0 \cup \tilde{S}^*_0|+1}^{D} D^{-|S^*_0|} (\log p)^{-|\tilde{S}^*_0|} p^{-1},
\]

leading to \( B_2 \lesssim D^{|S^*_0|} (\log p)^{|\tilde{S}^*_0|} p \leq D^{|S^*_0|} (\log p)^{|S^*_{11}|} p^{-1} \).

• If \( j \in \tilde{S}^*_0 \cup S^*_0 \) and there exists \( j_0 \in S^*_{[1]} \setminus (\tilde{S}^*_0 \cup S^*_0) \), then

\[
B_2 \mathbb{P}(|S^{(-j)} \cap S^\ast| \geq |S^*_0 \cup \tilde{S}^*_0|) \lesssim B_2 \mathbb{P}(|S_{11}^\ast \cap S^\ast| > |S^*_0 \cup \tilde{S}^*_0|)
\]

\[
\lesssim B_2 \sum_{i \in S^*_{[1]} \setminus \tilde{S}^*_0} \mathbb{P}(S_{11}^\ast \cap S^\ast = S^*_0 \cup \tilde{S}^*_0 \setminus \{j\} \cup \{i\})
\]

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\[ \lesssim B_2 \mathbf{P}(S_{11}^{[i]} \cap S^* = S_{[0]}^* \cup \tilde{S}_{[0]}^* \backslash \{j\} \cup \{j_0\}), \]

and

\[ B_2 \mathbf{P}(S_{11}^{[i]} \supseteq S_{[0]}^* \cup \tilde{S}_{[0]}^*) \geq B_2 \mathbf{P}(S_{11}^{[i]} \cap S^* = S_{[0]}^* \cup \tilde{S}_{[0]}^*), \]

leading to \((\mathbf{P}(S_{11}^{[i]} \cap S^* = S_{[0]}^* \cup \tilde{S}_{[0]}^* \backslash \{j\} \cup \{j_0\}))^{-1} \lesssim B_2 \lesssim (\mathbf{P}(S_{11}^{[i]} \cap S^* = S_{[0]}^* \cup \tilde{S}_{[0]}^* \backslash \{j\} \cup \{j_0\}))^{-1} \lesssim D^{\|S_{[0]}^*\|} (\log p)^{\|S_{11}^{[i]}\|^{-1}} p. \]

Similar to the previous calculation, it can be shown that \((\mathbf{P}(S_{11}^{[i]} \cap S^* = S_{[0]}^* \cup \tilde{S}_{[0]}^* \backslash \{j\} \cup \{j_0\}))^{-1} \lesssim D^{\|S_{[0]}^*\|} (\log p)^{\|S_{11}^{[i]}\|^{-1}} p. \]

- If \(j \in \tilde{S}_{[0]}^* \cup S_{[0]}^* \) and \(S_{[1]}^{[i]} \backslash (\tilde{S}_{[0]}^* \cup S_{[0]}^*) = \emptyset\), we have \(\mathbf{P}(|S^{(-j)} \cap S^*| \geq |S_{[0]}^* \cup \tilde{S}_{[0]}^*|) = 0\) because \(S_{[0]}^* \cup \tilde{S}_{[0]}^* = S^*\). Therefore it is sufficient to require \(B_2 \gtrsim (\mathbf{P}(S_{11}^{[i]} \cap S^* = S_{[0]}^* \cup \tilde{S}_{[0]}^*))^{-1} = (\mathbf{P}(S_{11}^{[i]} \supseteq S^*))^{-1}\), where \(\mathbf{P}(S_{11}^{[i]} \supseteq S^*) \gtrsim (D \land \log p)^{-p^*}\), implying that there exists \(B_2 \lesssim (D \lor \log p)^{p^*} \lor p = p\) satisfying Assumption 3.

Above all, we complete the proof of Proposition 3.