Robust Variable and Interaction Selection for Logistic Regression and Multiple Index Models

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Abstract

We propose Stepwise cOnditional likelihood variable selection for Discriminant Analysis (SODA) to detect both main and quadratic interaction effects in logistic regression and quadratic discriminant analysis (QDA) models. In the forward stage, SODA adds in important predictors evaluated based on their overall contributions, whereas in the backward stage SODA removes unimportant terms so as to optimize the extended Bayesian Information Criterion (EBIC). Compared with existing methods on QDA variable selections, SODA can deal with high-dimensional data with the number of predictors much larger than the sample size and does not require the joint normality assumption on predictors, leading to much enhanced robustness. We further extend SODA to conduct variable selection and model fitting for multiple index models. Compared with existing variable selection methods based on the Sliced Inverse Regression (SIR) (Li 1991), SODA requires neither the linearity nor the constant variance condition and is much more robust. Our theoretical analyses establish the variable-selection consistency of SODA under high-dimensional settings, and our simulation studies as well as real-data applications demonstrate superior performances of SODA in dealing with non-Gaussian design matrices in both classification problems and multiple index models.

1 Introduction

Classification, also known as "supervised learning", is a fundamental building block of statistical machine learning. Applications of statistical classification methods include, for example, cancer diagnosis (Tibshirani et al. 2002), text categorization (Joachims 1998), computer vision (Phillips 1998), protein interaction predictions (Chowdhary et al. 2009), etc. Well-known classification methods include logistic regression, naive Bayes classifier, K-nearest-neighbors, support vector machines (Boser et al. 1992), and random forests (Breiman 2001). As important players in this field, linear and quadratic discriminant analysis (LDA and QDA) (Anderson 1958) are widely used. Compared with LDA, QDA is able to exploit interaction effects of predictors.

With rapid technical advances in data collection, it has become common that the number of predictors is much larger than the number of observations, which is also known as the “large \( p \) small \( n \)” problem.
problem. For example, in gene expression microarray analysis, usually $n$ is in hundreds of samples, whereas $p$ is in thousands of genes (Efron 2010). In a typical genome-wide association study, $n$ is in the order of a few thousands of subjects, and $p$ is from several thousands to millions of SNP markers (Waldmann et al. 2013). Vanilla LDA or QDA are infeasible when $p > n$ since the sample covariance matrices are consequently singular. Even in low-dimensional scenarios, including many irrelevant predictors can significantly impair the classification accuracy.

A number of variable selection methods have been developed for high-dimensional classification problems, of which many focused on imposing regularizations on the LDA model. For example, Witten and Tibshirani (2011) proposed to use fused Lasso to penalize discriminant vectors in Fisher’s discriminant problem. Cai and Liu (2011) proposed to estimate the product of precision matrix and the difference between two mean vectors directly through a constrained $L_1$ minimization. Han et al. (2013) relaxed the normal assumption of LDA to entertain Gaussian Copula models. More developments on high-dimensional LDA can be found in Guo et al. (2007), Fan and Fan (2008), Clemmensen et al. (2011), Shao et al. (2011), Mai et al. (2012) and Fan et al. (2013).

Aforementioned methods work for LDA models with only linear main effects. In many applications, however, interaction effects may be significant and scientifically interesting. On the other hand, in moderate to high dimensional situations, including in the model too many noise variables and their interaction terms can lead to an over-fitting problem more severe than that of linear discriminant models, resulting in a much impaired prediction accuracy. In recent years, there has been a significant surge of interest in detecting interaction effects for regression or classification problems (Simon and Tibshirani 2012; Bien et al. 2013; Jiang and Liu 2014; Fan et al. 2015), which both improves the classification accuracy and is of scientific interest. In this article, we use the term “interaction” to refer to all second-order effects, including both two-way interactions $X_i X_j$ with $i \neq j$ and quadratic terms $X_i^2$.

To motivate later developments, we consider a two-class Gaussian classification problem with both linear and interaction effects with 3 true predictors. The oracle Bayes rule is to classify an observation to class 1 if $Q (\mathbf{X}) > 0$, and to class 0 otherwise, where

$$Q (\mathbf{X}) = 1.627 + X_1 - 0.6 X_1^2 - 0.6 X_3^2 - 0.7 X_1 X_2 - 0.7 X_2 X_3. \quad (1)$$

We simulated 100 independent datasets, each having 100 observations in every class. Figure 1 shows the scatterplot of $(X_1, X_2)$ for one simulated dataset. For each simulated dataset, we applied LDA, logistic regression, and QDA to train classifiers, and the classification accuracy was estimated by using 1000 additional testing samples generated from the Oracle model. As shown in Table 1, both LDA and logistic regression with only linear terms had poor prediction powers, whereas QDA improved the classification accuracy dramatically. We further tested the classification accuracy of QDA when $k$ additional noise predictors were included $(k = 1, \ldots, 50)$, each being drawn independently from $\mathcal{N} (0, 1)$. Figure 1 shows that the classification error rate of QDA increased dramatically as the number of noise predictors increased, demonstrating the necessity of developing methods capable of selecting both main effect and interaction terms efficiently.
Figure 1: A two-class Gaussian classification problem, where Class 1 samples were drawn from $N(\mu_1, \Omega_1^{-1})$, and Class 2 from $N(\mu_2, \Omega_2^{-1})$. We set $\mu_1 = -\mu_2 = (0.5, 0, 0)$, $\Omega_1 = I_3 - \Omega$, and $\Omega_2 = I_3 + \Omega$, where $\Omega$ has entries $\omega_{22} = 1$, $\omega_{11} = \omega_{33} = -0.60$, $\omega_{12} = \omega_{23} = -0.35$, and $\omega_{13} = 0$. **Left**: Scatterplot of $(X_1, X_2)$ overlaid with corresponding theoretical contours for one simulated dataset. **Right**: QDA classification error rate versus number of noise predictors.

| Method                  | LDA   | Logistic regression | QDA       | QDA with 50 noise predictors |
|-------------------------|-------|---------------------|-----------|-----------------------------|
| Test error %            | 34.81 | 34.88 (1.38)        | 15.65 (0.84) | 37.33 (1.78)              |

Table 1: Means (standard deviations) of testing error rates for different classification methods over 100 replications.

However, a direct application of Lasso on logistic regression with all second-order terms is prohibitive for moderately large $p$ (e.g., $p \geq 1000$). To cope with this difficulty, Fan et al. (2015) proposed innovated interaction screening (IIS) based on transforming the original $p$-dimensional predictor vector by multiplying the estimated precision matrix for each class. IIS first reduces the number of predictors to a smaller order of $p$, and then identifies both important main effects and interactions using the elastic net penalty (Zou and Hastie 2005). The performance of the resulting method, IIS-SQDA, relies heavily on the estimation of the $p \times p$ dimensional precision matrix, which is usually a hard problem under high-dimensional settings. Murphy et al. (2010), Zhang and Wang (2011), and Maugis et al. (2011) proposed stepwise procedures for QDA variable selection. These methods were shown to be consistent under the multivariate Gaussian assumption on the design matrix. In practice, however, performances of these methods can be much compromised when the normality assumption is violated, especially when predictors follow heavier-tailed distributions or when they are correlated in non-linear manners (see Section 4).

In order to gain robustness and computational efficiency, we propose the method Stepwise cOnditional likelihood variable selection for Discriminant Analysis (SODA) under the logistic re-
gression framework, which starts with a forward stepwise selection procedure to add in predictors with main and/or interaction effects so as to reduce the number of candidate predictors to a smaller order of \( n \), and finishes with a backward stepwise elimination procedure for further narrowing down individual main and interaction effects. The criterion used for both forward addition and backward elimination is the extended Bayesian information criterion (EBIC) (Chen and Chen 2008).

Although stepwise variable selection methods have been widely known and used for regression problems, stepwise selection of interaction terms has been rare. Available methods typically consider adding interaction terms only among those predictors that have been selected for their main effects. In comparison, in each forward addition step, SODA evaluates the overall contribution of a predictor including both its main effects and its interactions with selected predictors. Under some regularity conditions, we establish the screening consistency of the forward step and the individual term selection consistency of the backward step of SODA under high-dimensional settings.

An interesting and powerful extension of SODA is for variable selection in multiple index models (Li 1991; Cook 2007; Jiang and Liu 2014), which assume that the response \( Y \) (may be either discrete or continuous) depends on a subspace of \( X \) through an unknown (nonlinear) link function. The most popular method for estimating the subspace is the sliced inverse regression (SIR) method (Li 1991). We note that after slicing (discretizing) the response variable \( y \), we can apply SODA effectively for variable selection and model fitting. We call this extension the Sliced SODA (S-SODA). Compared with variable selection methods based on SIR (see Jiang and Liu (2014) for references), S-SODA does not require the linearity condition and enjoys much improved robustness without much sacrifice in sensitivity.

The rest of the article is organized as follows. SODA and S-SODA are presented in full detail in Section 2. Theoretical properties of SODA are studied in Section 3. Simulation results are shown in Section 4 to compare performances of SODA and S-SODA with those of other methods. In Section 5 we further apply SODA to a couple of real examples to evaluate its empirical performances, and in Section 6 conclude the article with a short discussion. Detailed theoretical proofs and additional empirical results are provided in the Supplemental Materials.

2 Variable and Interaction Selection for Discrete Response Models

2.1 Quadratic logistic regression model and its extended BIC

We consider the \( K \)-class classification problem. Let \( Y \in \{1, \ldots, K\} \) denote the class label, let \( X = (X_1, X_2, \ldots, X_p)^T \) be a vector of \( p \) predictors, and let \( \{(x_i, y_i) : i = 1, \ldots, n\} \) denote \( n \) independent observations on \((X, Y)\). When \( p \) is large, usually only a small proportion of predictors have predictive power on \( Y \). Let \( \mathcal{P} \) denote the set of relevant predictors, and let \( \mathcal{P}^c = \{1, \ldots, p\} \setminus \mathcal{P} \) be noise ones. That is,

\[
P(Y \mid X_{\mathcal{P}}, X_{\mathcal{P}}^c) = P(Y \mid X_{\mathcal{P}}).
\]
We consider the following logistic model:

\[
p(Y = k \mid X, \theta) = \frac{\exp \left[ \delta_k(X \mid \theta) \right]}{1 + \sum_{l=1}^{K-1} \exp \left[ \delta_l(X \mid \theta) \right]}, \quad k = 1, \ldots, K, \tag{2}
\]

where \(\delta_k(X \mid \theta)\) is the discriminant function for class \(k\) and \(\theta\) denotes the vector of parameters.

Choosing class \(K\) as the baseline class so that \(\delta_K(X \mid \theta) = 0\), we assume that

\[
\delta_k(X \mid \theta) = \alpha_k + \beta_k^T X + X^T A_k X, \quad \text{for } k = 1, \ldots, K - 1. \tag{3}
\]

Since \(X\) is conditioned on, we do not need to model the distribution of \(X_p\) or \(X_{p^c}\), which is both convenient and robust for variable selection. Special cases of this model include:

- Multinomial logistic regression (with \(A_k = 0\) for all \(k\))
- Linear/quadratic discriminant analysis, where \(p(X_p \mid Y)\) is multivariate normal distribution
- Discriminant analyses where \(p(X_p \mid Y)\) is in the multivariate exponential family,

\[
p(X_p = x \mid Y = k, \eta) = h(x) g(\eta_k) \exp(\eta_k^T x).
\]

To see the connection between QDA and model (2), it is noted that for QDA models,

\[
\alpha_k = \log(\pi_k / \pi_K) - \frac{1}{2} \left( \log |\Sigma_k| - \log |\Sigma_K| + \mu_k^T \Sigma_k^{-1} \mu_k - \mu_K^T \Sigma_K^{-1} \mu_K \right),
\]

\[
\beta_k^T = \mu_k^T \Sigma_k^{-1} - \mu_K^T \Sigma_K^{-1},
\]

\[
A_k = -\frac{1}{2} \left( \Sigma_k^{-1} - \Sigma_K^{-1} \right), \quad \text{for } k = 1, \ldots, K - 1.
\]

Let \(\mathcal{M}\) and \(\mathcal{I}\) denote subsets of main effects and interaction pairs, respectively, and let \(\mathcal{M}_0\) and \(\mathcal{I}_0\) denote the corresponding true sets defined as

\[
\mathcal{M}_0 = \{ j : \exists k \text{ s.t. } \beta_{k,j} \neq 0 \} \quad \text{and} \quad \mathcal{I}_0 = \{ (i,j) : \exists k \text{ s.t. } A_{k,i,j} \neq 0 \},
\]

with \(k\) indicating the class label. Let \(\mathcal{A} = \mathcal{M}_0 \cup \mathcal{I}_0\) denote the true set of all effects, and let \(\mathcal{S} = \mathcal{M} \cup \mathcal{I}\). The true set of relevant predictors \(\mathcal{P}\) can be derived from \(\mathcal{A}\) as

\[
\mathcal{P} = \mathcal{M}_0 \cup \{ j : \exists i \text{ s.t. } (i,j) \in \mathcal{I}_0 \}.
\]

Our main objective is to infer \(\mathcal{A}\), with a special interest in terms in \(\mathcal{I}_0\).

Let \(\theta_S\) denote the collection of all coefficients in model (3), whose 0’s correspond to terms not in \(\mathcal{S}\), and let \(\theta_{k,S}\) denote the corresponding coefficients for class \(k\). For a dataset \(\{(x_i, y_i) : i = 1, \ldots, n\}\), the log-likelihood for \(\theta_S\) is denoted as \(l_n(\theta_S)\). Let \(Z = (1, X, X \otimes X)\) be the augmented version of \(X\), containing intercept 1, main effects, and all interaction terms of \(X\). Let \(z_i\) be the \(i\)-th obser-
vation of $Z$. Then $l_n(\theta_S)$ takes the form of a logistic regression model in $Z$:

$$l_n(\theta_S) = \sum_{i=1}^{n}\left\{\theta_i^T y_i^S z_i - \log \left(1 + \sum_{i=1}^{K-1}\exp\left(\theta_i^T z_i\right)\right)\right\}.$$ 

Let $\tilde{\theta}_S$ denote the MLE of $\theta_S$. By Lemma 2 in the appendix, with high probability $l_n(\theta_S)$ is convex and $\tilde{\theta}_S$ can be obtained by Newton-Raphson algorithm. Let $\theta_0$ denote the true parameter vector. Theorem 1 illustrates the consistency of $\tilde{\theta}_S$ for any reasonable set $S$.

**Theorem 1.** Under Conditions C1 $\sim$ C4 in Section 3, as $n \to \infty$,

$$\max_{S \supseteq A, |S| \leq Q} \|\tilde{\theta}_S - \theta_0\|_2 = O_p\left(n^{-1/2+\xi}\right),$$

for any constants $0 < \xi < 1/2$ and $Q \geq |A|$ independent of $n$.

In high-dimensional settings, the classic Bayesian information criterion (BIC) (Schwarz et al. 1978) is too liberal and tends to select many false positives (Broman and Speed 2002). Chen and Chen (2008) proposed extended BIC (EBIC) and showed it to be consistent for linear regression models under high-dimensional settings. The EBIC for set $S$ is specified as

$$\text{EBIC}_{\gamma}(S) = -2 l_n(\tilde{\theta}_S) + |S| \log n + 2\gamma |S| \log p,$$

where $|S|$ is the size of set $S$, and $\gamma$ is a tuning parameter. The selection of $\gamma$ may depend on the relative sizes of $n$ and $p$, and some heuristics on determining $\gamma$ practically is discussed in section 2.5. Let $\tilde{S}_{\text{EBIC}}$ be the selected set of predictors minimizing the EBIC, and let $Q$ be any positive constant greater than constant $p_0$ in condition (C1) in section 3. Then,

$$\tilde{S}_{\text{EBIC}} = \arg \min_{S: |S| \leq Q} \text{EBIC}_{\gamma}(S),$$

where $|S|$ denotes the size of set $S$. The asymptotic property of $\tilde{S}_{\text{EBIC}}$ is shown by the following theorem.

**Theorem 2. (EBIC criterion consistency)** Under Conditions C1 $\sim$ C4 in Section 3, $\tilde{S}_{\text{EBIC}}$ is a consistent estimator of $A$, i.e.,

$$\Pr\left(\tilde{S}_{\text{EBIC}} = A\right) \to 1, \text{ as } n \to \infty,$$

for any $\gamma > 2 - 1/(2\kappa)$.

By treating our model as a logistic regression on $(Z, Y)$, Theorem 2 follows directly from the asymptotic consistency of EBIC for generalized linear models (GLM), which was proved in Chen and Chen (2012) and Foygel and Drton (2011) in both fixed and random design contexts. We thus omit its proof. Different from Chen and Chen (2012) and Foygel and Drton (2011), here we require
\[ \gamma > 2 - 1/(2\kappa) \] instead of \[ \gamma > 1 - 1/(2\kappa) \] to penalize additional model flexibility caused by the inclusion of interaction terms.

2.2 SODA: a stepwise variable and interaction selection procedure

In practice it is infeasible to enumerate all possible \( S \) to find the one that minimizes the EBIC. For a closely related generalized linear model variable selection problem, Chen and Chen (2012) and Foygel and Drton (2011) used Lasso (Tibshirani 1996) to obtain a solution path of predictor sets, and chose the optimal set on the path with the lowest EBIC. However, this method also fails under the high-dimensional setting for QDA, in which there are \( O(p^2) \) candidate interaction terms. Furthermore, Lasso’s variable selection consistency for logistic regression requires the incoherence condition (Ravikumar et al. 2010), which can be easily violated due to correlations between interaction terms and their corresponding main effect terms. The IIS procedure proposed in Fan et al. (2015) requires the estimation of the \( p \times p \) precision matrix, which is by itself a challenging problem. If the related and unrelated predictors are moderately correlated, IIS’s marginal screening strategy has difficulties in filtering out noise predictors. We propose here the stepwise procedure SODA, consisting of three stages: (1) a preliminary forward main effect selection; (2) forward variable selection (considering both main and interaction effects), and (3) backward elimination.

1. Preliminary main effect selection: This step is the same as that in the standard stepwise regression method. Let \( \mathcal{M}_t \) denote the selected set of main effects at step \( t \). SODA starts with \( \mathcal{M}_1 = \emptyset \) and iterates the operations below until termination.

   (a) For each predictor \( j \notin \mathcal{M}_t \), create a new candidate set \( \mathcal{M}_{t,j} = \mathcal{M}_t \cup \{j\} \).

   (b) Find the predictor \( j \) with lowest \( \text{EBIC}_\gamma (\mathcal{M}_{t,j}) \). If \( \text{EBIC}_\gamma (\mathcal{M}_{t,j}) < \text{EBIC}_\gamma (\mathcal{M}_t) \), continue with \( \mathcal{M}_{t+1} = \mathcal{M}_{t,j} \), otherwise terminate with \( \tilde{\mathcal{M}}_F \) and go to 2.

2. Forward variable addition (both main and interaction effects): Let \( \mathcal{C}_t \) denote the selected set of predictors at step \( t \), and let \( \mathcal{S}_t = \tilde{\mathcal{M}}_F \cup \mathcal{C}_t \cup (\mathcal{C}_t \times \mathcal{C}_t) \) denote the set of terms induced by \( \mathcal{C}_t \). SODA starts with \( \mathcal{C}_1 = \emptyset \) and iterates the operations below until termination.

   (a) For each \( j \notin \mathcal{C}_t \), create a candidate set \( \mathcal{C}_{t,j} = \mathcal{C}_t \cup \{j\} \) and let \( \mathcal{S}_{t,j} = \tilde{\mathcal{M}}_F \cup \mathcal{C}_{t,j} \cup (\mathcal{C}_{t,j} \times \mathcal{C}_{t,j}) \).

   (b) Find the predictor \( j \) with lowest \( \text{EBIC}_\gamma (\mathcal{S}_{t,j}) \). If \( \text{EBIC}_\gamma (\mathcal{S}_{t,j}) < \text{EBIC}_\gamma (\mathcal{S}_t) \), continue with \( \mathcal{C}_{t+1} = \mathcal{C}_{t,j} \), otherwise terminate with \( \tilde{\mathcal{C}}_F \) and go to 3.

3. Backward elimination: Let \( \mathcal{S}_t \) denote the selected set of individual terms at step \( t \) of backward stage. SODA starts with \( \mathcal{S}_1 = \tilde{\mathcal{M}}_F \cup \tilde{\mathcal{C}}_F \cup (\tilde{\mathcal{C}}_F \times \tilde{\mathcal{C}}_F) \) and iterate the operations below until termination.

   (a) For each main or interaction term \( j \in \mathcal{S}_t \) (e.g. \( j = 1 \) or \( j = (1, 2) \)), create a candidate set \( \mathcal{S}_{t,j} = \mathcal{S}_t \setminus \{j\} \).
(b) Find term $j$ with lowest $\text{EBIC}_\gamma(S_{t,j})$. If $\text{EBIC}_\gamma(S_{t,j}) < \text{EBIC}_\gamma(S_t)$, remove term $j$, otherwise terminate and retain set $\tilde{S} = S_t$.

Stepwise methods had been primary tools for conducting variable selection in regression problems long before the recent development of Lasso-type methods. The forward stepwise procedure has also been considered for variable screening for linear regressions in high-dimensional settings (Wasserman and Roeder 2009; Wang 2009). When considering interactions, a standard approach typically examines only those among the variables that have been deemed significant due to their main effects. However, Stage 2 of SODA for forward variable addition is different. After the preliminary selection of Stage 1, in Stage 2 SODA keeps track of a new set of variables $C_t$, of which all main and quadratic terms are considered together. In other words, at each step SODA evaluates the EBIC for the overall effect of adding one predictor. Thus, choosing one variable to add in the forward variable selection stage is of order $O(p)$, and the whole stage is of order $O(ps)$, where $s$ is the number of truly relevant predictors. A naive method that searches through all individual terms is of order $O(p^2s^2)$. Another important feature of SODA is that each backward step only eliminates one individual term instead of all terms related to one predictor. In other words, SODA selects individual main and interaction effect terms without any nesting requirements.

Our theory shows that the forward variable addition step is sufficient for SODA to achieve the screening consistency. However, the number of parameters and the EBIC penalization in this forward step increases quadratically with the cardinality of $C_t$. Therefore it can be hard to add predictors with only weak main effects. To optimize the empirical performance, we include the preliminary main effect selection stage to identify predictors with only weak main effects.

### 2.3 Sliced SODA (S-SODA) for general index models

In his seminal work on nonlinear dimension reduction, Li (1991) proposed a semi-parametric index model of the form

$$Y = f \left( \beta_1^T X, \beta_2^T X, \ldots, \beta_d^T X, \varepsilon \right),$$

where $f$ is an unknown function and $\varepsilon$ is random error independent of $X$, and the sliced inverse regression (SIR) method to estimate the central dimension reduction subspace (CDRS) spanned by the directions $\beta_1, \ldots, \beta_d$. Since the estimation of CDRS does not automatically lead to variable selection, several methods have been developed to do simultaneous dimension reduction and variable selection for index models. For example, Li et al. (2005) designed a backward subset selection method, and Li (2007) developed the sparse SIR (SSIR) algorithm to obtain shrinkage estimates of the SDR directions under $L_1$ norm. Motivated by stepwise regression for linear models, Zhong et al. (2012) proposed a forward stepwise variable selection procedure called correlation pursuit (COP) for index models. Lin et al. (2015) showed the necessary and sufficient condition for SIR to be consistent in high-dimensional settings and introduced a diagonal thresholding method, DT-SIR, for variable selection. Lin et al. (2016) proposed a new formulation of the SIR estimation and a direct application of Lasso for variable selection with index models.
The aforementioned SIR-based methods consider primarily the information from the first conditional moment, \( E(X \mid Y) \), and tend to miss important variables with second-order effects. In order to overcome this problem, Jiang and Liu (2014) proposed SIRI, which utilizes both the first and the second conditional moments to select variables. SIRI derives its procedure from a likelihood-ratio test perspective by assuming the following working model:

\[
X_P \mid s(Y) = h \sim \mathcal{N}(\mu_h, \Sigma_h), \quad h = 1, \ldots, H. \tag{8}
\]

where \( P \) denote the set of true predictors. Jiang and Liu (2014) showed that SIRI is a consistent variable selection procedure for model (8), and also for a more general class of models satisfying the following linearity and constant variance conditions. In fact, all the aforementioned methods require either the linearity condition or the constant variance condition, or both.

**Linearity condition:** \( E(X_{Pc} \mid X_P) \) is linear in \( X_P \).

**Constant variance condition:** \( \text{Cov}(X_{Pc} \mid X_P) \) is a constant.

When the linearity and constant variance conditions approximately hold, SIRI and other SIR-related methods usually enjoy excellent empirical performances. However, when either condition is violated, the performances of these methods deteriorate rapidly. This issue motivates us to develop sliced-SODA (S-SODA), a modification of SODA. As a working model, S-SODA can be seen as assuming only the first half of model (8) without any distributional assumption on \( X_{Pc} \):

\[
X_P \mid s(Y) = h \sim \mathcal{N}(\mu_h, \Sigma_h), \quad h = 1, \ldots, H. \tag{9}
\]

Note that model (9) is essentially the QDA model, and we can apply SODA as a consistent variable selection procedure. More precisely, S-SODA starts by sorting the samples in ascending order of \( y_i \), and equally partitioning them into \( H \) slices (the discretization step). It then applies SODA to data \( \{(s_i, x_i)\}_{i=1}^n \), where \( s_i \) denote the slice index for \( y_i \). S-SODA finally outputs all the selected main and interaction terms.

### 2.4 Post-selection prediction for continuous response

S-SODA conducts variable selection for semi-parametric model (7) without knowing the true functional form of the link function. After variable selection, it is of interest to predict the response variable \( \tilde{y} \) for a new observation of predictors \( \tilde{x} \). Suppose our training data consist of \( n \) independent observations \( \{(y_i, x_i)\}_{i=1}^n \). Let \( \tilde{S} \) denote the selected set of terms by S-SODA, and let \( \tilde{P} \) denote the set of predictors with any term in \( \tilde{S} \), which is the S-SODA estimate of \( P \). Let \( \hat{\mu} = (\hat{\mu}_1, \ldots, \hat{\mu}_H) \), \( \hat{\Sigma} = (\hat{\Sigma}_1, \ldots, \hat{\Sigma}_H) \), where \( \hat{\mu}_h \) and \( \hat{\Sigma}_h \) are respectively the sample mean vector and covariance matrix of \( X_{P} \) in slice \( h \). Note that \( \hat{\mu} \) and \( \hat{\Sigma} \) are MLEs of parameters in model (9). Inverting model
(9) by the Bayes rule, we have

\[
\Pr (s (Y) = h \mid \mathbf{X}_\tilde{P}, \boldsymbol{\mu}, \Sigma) = \frac{N (\mathbf{X}_\tilde{P} \mid \mu_h, \Sigma_h)}{\sum_{l=1}^{H} N (\mathbf{X}_\tilde{P} \mid \mu_l, \Sigma_l)}, \quad h = 1, \ldots, H.
\]

We consider the conditional expectation \( \mathbb{E} [Y \mid \mathbf{X}_\tilde{P}] \) as prediction of \( Y \) given \( \mathbf{X}_\tilde{P} \). Note that

\[
\mathbb{E} [Y \mid \mathbf{X}_\tilde{P}] = \sum_{h=1}^{H} \mathbb{E} [Y \mid s (Y) = h, \mathbf{X}_\tilde{P}] \Pr (s (Y) = h \mid \mathbf{X}_\tilde{P}, \boldsymbol{\mu}, \Sigma)
\]

\[
= \frac{\sum_{h=1}^{H} \mathbb{E} [Y \mid s (Y) = h, \mathbf{X}_\tilde{P}] \cdot N (\mathbf{X}_\tilde{P} \mid \mu_h, \Sigma_h)}{\sum_{l=1}^{H} N (\mathbf{X}_\tilde{P} \mid \mu_l, \Sigma_l)}.
\]

We use a plug-in estimator of \( \mathbb{E} [Y \mid \mathbf{X}_\tilde{P}] \), denoted as \( \hat{Y} = \hat{\mathbb{E}} [Y \mid \mathbf{X}_\tilde{P}] \), where

\[
\hat{Y} = \hat{\mathbb{E}} [Y \mid \mathbf{X}_\tilde{P}] = \sum_{h=1}^{H} \hat{M}_h \cdot N (\mathbf{X}_\tilde{P} \mid \hat{\mu}_h, \hat{\Sigma}_h) / \sum_{l=1}^{H} N (\mathbf{X}_\tilde{P} \mid \hat{\mu}_l, \hat{\Sigma}_l),
\] (10)

where \( \hat{M}_h \) is the sample mean of response \( Y \) in slice \( h \). \( \hat{M}_h \) can be considered as the zero-th order approximation to \( \mathbb{E} [Y \mid s (Y) = h, \mathbf{X}_\tilde{P}] \), in the sense that \( \hat{M}_h \) is independent of \( \mathbf{X}_\tilde{P} \). A more sophisticated model is to consider the first-order approximation that models \( \mathbb{E} [Y \mid s (Y) = h, \mathbf{X}_\tilde{P}] \) as a linear combination of \( \mathbf{X}_\tilde{P} \) in each slice.

2.5 Implementation issues with SODA: tuning parameter and screening depth

Sections 3 characterizes asymptotic properties of the EBIC and SODA and provides some guidelines for choosing the tuning parameter \( \gamma \) of EBIC. However, these asymptotic results are not directly usable. In practice, we propose to use a 10-fold cross-validation (CV) procedure for selecting \( \gamma \) from \( \{0, 0.5, 1.0\} \). For simulation studies and real data analyses in Sections 4 and 5, to make SODA more easily comparable with Lasso-EBIC studied in Chen and Chen (2012), we fixed \( \gamma = 0.5 \) as suggested in Chen and Chen (2012).

The forward variable addition stage terminates if EBICs of all candidate models are larger than the EBIC of the current model. Therefore, the screening depth of the forward stage is determined by the EBIC. In Theorem 3, we show that this procedure is asymptotically screening consistent; namely, the truly relevant terms will be all included by the end of the forward stage. Nevertheless, SODA is not sensitive to adding more terms in the forward stage since those unrelated terms will be eventually eliminated in the backward stage. Missing one relevant term is usually more harmful than including one noise term. Therefore, to optimize the empirical performance, we let SODA continue the forward variable addition for \( p_f \) steps after the step that fails to decrease EBIC (default \( p_f = 3 \)).
3 Theoretical Properties of SODA

To study theoretical properties of SODA procedure, we assume the following conditions:

(C1) The divergence speed of $p$ is bounded above by $p \leq n^\kappa$ for some $\kappa > 0$, and the size of the true predictor set $P$ is bounded as $|P| \leq p_0$ for a fixed integer $p_0$.

(C2) Magnitudes of true coefficients in $\theta_A$ are bounded above and below by constants, namely there exist positive constants $\theta_{\text{max}} > \theta_{\text{min}} > 0$ such that

$$\theta_{\text{min}} \leq \min \{|\theta_j| : j \in A\} \leq \max \{|\theta_j| : j \in A\} \leq \theta_{\text{max}}.$$

(C3) Let $Z$ be the augmented version of $X$, containing intercept 1, as well as all first-order and second-order terms of $X$. Each $Z_j \in Z$ is sub-exponential, i.e. there are positive constants $C_1$ and $C_2$ such that,

$$\Pr (|Z_j - \mathbb{E}[Z_j]| > t) \leq C_1 \exp (-C_2 t) \quad \text{for all } t > 0.$$

(C4) Let $\text{Cov} (Z)$ denote the covariance matrix of $Z$. There exist constants $0 < \tau_1 < \tau_2 < \infty$ such that

$$\tau_1 \leq \lambda_{\text{min}} (\text{Cov} (Z)) < \lambda_{\text{max}} (\text{Cov} (Z)) \leq \tau_2,$$

where $\lambda_{\text{min}} (\cdot)$ and $\lambda_{\text{max}} (\cdot)$ denote the smallest and largest eigenvalues of a matrix.

We show that the forward variable addition stage (Stage 2 of SODA) is already screening consistent. To proceed, we need to define the following concept to study the stepwise detectability of true predictors in $P$. Let $\theta^*_S$ denote the population version of the risk minimizer,

$$\theta^*_S = \arg \min_\theta \mathbb{E} [-\log p (Y \mid X, \theta_S)],$$

where the expectation is over the joint distribution of $(Y, X)$. Let vector $\theta^*_S$ be parameters in $\theta^*_S$ associated with predictor $X_j$. The stepwise detectable condition is necessary for the screening consistency of the forward variable addition stage.

Definition 1. (Stepwise detectable condition) A set of predictors $C_1$ is stepwise detectable given $C_2$ if $C_1 \cap C_2 = \emptyset$, and for any set $C$ satisfying $C \supset C_2$ and $C \not\supset C_1$, there exist constants $\theta_{\text{max}} > \theta_{\text{min}} > 0$, such that

$$\theta_{\text{min}} \leq \max_{j \in C \cap C_1} \left\| \theta^*_S |_{S_{C \cup \{j\}}} \right\|_\infty \leq \theta_{\text{max}},$$

where $S_{C \cup \{j\}} = \mathcal{M}_j \cup \mathcal{I}_j$ with $\mathcal{M}_j = C \cup \{j\}$ and $\mathcal{I}_j = \mathcal{M}_j \times \mathcal{M}_j$, and $\|\cdot\|_\infty$ denotes the $L_\infty$ norm. Let $T_m = \left\{ j : \text{predictor } j \text{ is stepwise detectable given } \bigcup_{i=0}^{m-1} T_i \right\}$ and $T_0 = \emptyset$. The set of true predictors $P$ is said to be stepwise detectable if $j \in \bigcup_{i=1}^{\infty} T_i$ for all $j \in P$. 

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In other words, if the current selection $C$ contains $C_2$, then there always exist detectable predictors conditioning on currently selected variables until we include all the predictors indexed by $C_1$. A true predictor $j \in P$ is not stepwise detectable either because it perfectly correlates with some other terms, or its effects can only be detected conditioning on some other stepwise undetectable terms.

We give an example to illustrate the scenarios when stepwise detectable condition may or may not hold. Suppose there are two true jointly normal relevant predictors $X_1$ and $X_2$ with means $\mu_1$ and $\mu_2$, and there is only one interaction term $X_1X_2$ in model (2), i.e. $A = \{(1, 2)\}$. $P$ is not stepwise detectable if both $\mu_1 = 0$ and $\mu_2 = 0$. Starting from empty set $\emptyset$, the forward procedure will not add $X_1$ or $X_2$ into the model, because there is no main effect for $X_1$ and $X_2$ and the interaction term $X_1X_2$ does not correlate with marginal terms $X_1$ and $X_2$ ($\text{Cov} (X_1, X_1X_2) = 0$ and $\text{Cov} (X_2, X_1X_2) = 0$). However, if either $\mu_1 \neq 0$ or $\mu_2 \neq 0$, $P = \{1, 2\}$ is stepwise detectable.

Let $\tilde{S}_F = \tilde{M}_F \cup \tilde{C}_F \cup (\tilde{C}_F \times \tilde{C}_F)$ denote the selected set of terms at the end of forward variable addition stage. It is unrealistic to require $\tilde{S}_F = A$. However, it should be demanded that $\tilde{S}_F \supseteq A$, i.e. $\tilde{S}_F$ contains all relevant terms. We define the forward stage to be screening consistent if $p(\tilde{S}_F \supseteq A) \to 1$. We also do not want the size of $\tilde{S}_F$ to be too large, otherwise forward variable addition loses its purpose. The screening consistency of forward stage is established by the following theorem.

**Theorem 3. (Forward stage screening consistency)** If conditions C1 $\sim$ C4 hold, and all predictors in $P$ are stepwise detectable, then the forward variable addition stage finishes in finite number of steps and is screening consistent. In particular, as $n \to \infty$,

$$Pr \left( \left| \tilde{C}_F \right| \leq Q \right) \to 1, \text{ and } Pr \left( \tilde{C}_F \supseteq P \right) \to 1,$$

where $Q = \left\lceil 8\lambda_1^{-1}\theta_{\min}^{-2} \log K \right\rceil$, $\lambda_1$ is a positive constant defined in Lemma 2 in appendix, $K$ is the number of classes, and $\theta_{\min}$ is a positive constant defined in condition C2.

In other words, asymptotically $\tilde{C}_F$ contains all predictors in $P$, which implies $\tilde{S}_F \supseteq A$, and the forward stage stops in finite number of steps. We show in the following theorem two uniform bounds guaranteeing that all unrelated terms will be eliminated and all related terms will be kept in the backward stage.

**Theorem 4. (Uniform bound of EBIC in backward stage)** Fix any positive constant $Q > 0$. Under conditions C1 $\sim$ C4, as $n \to \infty$,

$$Pr \left( \max_{S \supseteq A; |S| \leq Q} \min_{j \in S \setminus A} \{EBIC_\gamma (S \setminus \{j\}) - EBIC_\gamma (S)\} < 0 \right) \to 1,$$

and

$$Pr \left( \min_{S \supseteq A; |S| \leq Q} \min_{j \in A} \{EBIC_\gamma (S \setminus \{j\}) - EBIC_\gamma (S)\} < 0 \right) \to 0,$$

for any constant $\gamma > Q - |A| - (2\kappa)^{-1}$.
Eq (11) implies that if $\mathcal{S} \supseteq \mathcal{A}$ and $|\mathcal{S}| \leq Q$, there will be at least one unrelated term $j \in \mathcal{S} \setminus \mathcal{A}^c$ such that removing $j$ from $\mathcal{S}$ leads to lower EBIC. Eq (12) implies that if $\mathcal{S} \supset \mathcal{A}$ and $|\mathcal{S}| \leq Q$, there is no related term $j \in \mathcal{A}$ such that removing $j$ from $\mathcal{S}$ leads to lower EBIC. As a summary, as $n \to \infty$, with probability tending to 1, no related term will be eliminated, and all unrelated terms will be eliminated in the backward stage until $\tilde{\mathcal{S}} = \mathcal{A}$. Theorem 4 requires candidate sets have finite size ($|\mathcal{S}| \leq Q$), which is proved by Theorem 3 to hold asymptotically for the starting set of the backward stage $\tilde{\mathcal{S}}_F$. Hence, combining Theorem 3 and 4 establishes the model selection consistency of SODA. Proofs of the theorems are in the on-line Supplemental Materials.

4 Simulation Results

4.1 Discriminant analysis with interactions

We first evaluate performances of a few methods on main and interaction effects selection under the discriminant analysis framework. Besides SODA, we consider the backward procedure in Zhang and Wang (2011) (denoted as ZW), the forward-backward method in Murphy et al. (2010) (denoted as MDR), hierNet in Bien et al. (2013) and IIS-SQDA in Fan et al. (2015). Both ZW and MDR require the joint normality between $\mathbf{X}_P$ and $\mathbf{X}_{P^c}$. HierNet is a Lasso-like procedure to detect multiplicative interactions between predictors under hierarchical constraints. For hierNet, we select the regularization parameter with the lowest CV error. We have also reported in the Supplemental Materials a comparison between SODA and Lasso-logistic for variable selections when the underlying model has only linear main effects, and found that SODA was competitive with Lasso in all cases we tested and out-performed Lasso significantly when the “incoherence” (Ravikumar et al. 2010) or the “irrepresentable” (Zhao and Yu 2006) condition was violated.

We first considered four simulation settings in Examples 1.1~1.4 for the classification example introduced in Section 1 (see Figure 1 for more details), and then examined two more simulation scenarios (Examples 1.5 and 1.6) in which the interaction effects and main effects are from different predictors. For Examples 1.1~1.4, there are two classes ($K = 2$) and $p$ predictors, among which $X_1, X_2$ and $X_3$ are relevant ones, i.e., $\mathcal{P} = \{1, 2, 3\}$, and are simulated as multivariate Gaussian conditional on the class label. Other $p - 3$ predictors are irrelevant but correlated with the three relevant ones. The oracle Bayes classification rule for these four examples is to label an observation class 1 if $Q(\mathbf{x}) > 0$, and 0 otherwise, where

$$Q(\mathbf{x}) = 1.627 + X_1 - 0.6X_1^2 - 0.6X_3^2 - 0.7X_1X_2 - 0.7X_2X_3,$$

indicating that $\mathcal{A} = \{1, (1, 1), (3, 3), (1, 2), (2, 3)\}$, representing one linear effect and four interaction effects without the hierarchy restriction. The setting of Example 1.1 follows the multivariate normal model while the other three do not. Examples 1.1~1.3 are of moderate dimension with $p=50$, and Example 1.4 simulates a high-dimensional scenario with $p=1000$.

For each simulation setting, we generated 100 datasets with 10 different sample sizes for each
class, ranging linearly in log-scale from 100 to 1000: $n = 100, [100 \times 10^{1/9}], \ldots, 1000$. For SODA, hierNet, and IIS-SQDA, the set of selected predictor variables is defined as the union of all predictors appearing in the selected linear and interaction terms. We calculated the average number of false negatives and false positives for variable selection (VFN and VFP), main effect term selection (MFN and MFP), and interaction term selection (IFN and IFP).

To benchmark the classification accuracy, we also include the full model of LDA and QDA with all predictors, and the Oracle model that contains exactly the five true terms. The average classification test error rate (TE) of each method is estimated by applying the trained model to 10,000 extra observations simulated from the true model. Results for Examples 1.1∼1.4 are shown in Figure 2. For SODA, hierNet and IIS-SQDA, we also counted the numbers of FNs and FPs for the selection of main effect and interaction terms, respectively, and show them in Table 2.

**Example 1.1.** *Multivariate Gaussian.* Irrelevant predictors were simulated as linear combinations of relevant ones as follows:

$$X_j = b_{j,0} + b_{j,1}X_l + b_{j,2}X_k + \varepsilon_j, \ j = 3, \ldots, 50,$$

where $X_k$ and $X_l$ were randomly selected from $\{X_1, X_2, X_3\}$, coefficients $b_{j,0}, b_{j,1}$ and $b_{j,2}$ were drawn from uniform distribution $U[-1, 1]$, and $\varepsilon_j \sim N(0,2)$.

As shown in Figure 2, for this example ZW, MDR, and SODA were all able to detect all relevant predictors as $n$ increases, with both VFN and VFP being very low. They achieved almost the Oracle classification accuracy. In contrast, IIS-SQDA and hierNet selected too many false positives, which resulted in high test error rates, and the number VFP+VFN increased with $n$. This strange phenomenon has also been observed by other researchers (Fan et al. 2015; Yu and Feng 2014). The performances of IIS-SQDA, hierNet and SODA on individual term selection are shown in Table 2. SODA selected individual terms nearly perfectly. HierNet is based on Lasso and IIS-SQDA uses elastic net. The variable selection consistency of Lasso and elastic net require the *Irrepresentable Condition* (Zhao and Yu 2006) and the *Elastic Irrepresentable Condition* (Jia and Yu 2010), which may not hold here. Moreover, it was observed that the cross-validation is too liberal for Lasso, leading to a large number of false positives (Yu and Feng 2014). As expected, LDA and QDA without variable selection performed the worst.

**Example 1.2.** *Non-Gaussian irrelevant predictors.* Irrelevant variables were simulated to be quadratically dependent of relevant ones:

$$X_j = b_{j,0} + b_{j,1}X_k + b_{j,2}X_l + b_{j,3}X_k^2 + b_{j,4}X_l^2 + \varepsilon_j, \ j = 3, \ldots, 50,$$

where $X_k$ and $X_l$ were randomly selected from $\{X_1, X_2, X_3\}$, coefficients $b_{j,0}, \ldots, b_{j,4}$ were drawn from $U[-1, 1]$, and $\varepsilon_j \sim N(0,5)$. As shown in Figure 2, ZW and MDR selected 4 to 10 FP and FN predictors on average. IIS-SQDA and hierNet selected a large number of FP terms, as shown in Table 2, due to the correlation between relevant and irrelevant predictors as well as correlations...
between main and interaction terms.

**Example 1.3. Heteroskedastic covariates.** Irrelevant we simulated as follows:

\[
X_j = b_{j,1}X_k + b_{j,2}X_l + |X_k| \epsilon_j, \ j = 3, \ldots, 50,
\]  

(14)

where \(X_k\) and \(X_l\) were randomly selected from \(\{X_1, X_2, X_3\}\), coefficients \(b_{j,1}\) and \(b_{j,3}\) were drawn from \(U[-1, 1]\), and \(\epsilon_j \sim N(0, 1)\). It violates the constant variance assumption of ZW and MDR.

Thus, ZW, MDR, IIS-SQDA and hierNet all performed sub-optimally. In contrast, SODA selected almost no VFP and VFN, and achieved near-Oracle prediction accuracy when \(n \geq 200\).

**Example 1.4. High-dimensional and non-Gaussian.** Irrelevant predictors were simulated as follows. For \(j \in \{4, \ldots, 100\}\), we drew 60% of the \(X_j\)'s at random and simulated them from \(N(m_j, 1)\), \(m_j \sim U[0, 1]\). The remaining 40% of the \(X_j\)'s were simulated as non-linearly related to \((X_k, X_l)\) similarly as (13) or (14), where \(k\) and \(l\) were randomly chosen from \(\{1, 2, 3\}\). For \(j \in \{101, \ldots, 1000\}\), we first drew all predictors from \(N(m_j, 1)\), and then randomly selected 40% of them and re-simulated each of the selected \(X_j\) as (13) or (14), where \(k\) and \(l\) are indexes uniformly drawn from \(\{101, \ldots, 1000\}\). We changed ZW to a forward procedure since the backward procedure is not feasible when \(p > n\). Results are shown in Figure 2 and Table 2. MDR results are not shown because it is unstable for highly correlated \(X\) matrices and usually keeps on adding new predictors until the estimation of covariance matrices become singular. Overall, SODA performed much better than ZW and IIS-SQDA, and achieved near-oracle the classification accuracy for \(n > 100\). Figure 3 shows the running times in log-scale versus \(n\) for IIS-SQDA, ZW, and SODA, On average, IIS-SQDA took 800 minutes, ZW took 22 minutes, and SODA took 4 minutes to analyze one simulated dataset with \(p = 1000\) and \(n = 1000\). In contrast, hierNet did not finish the simulation experiments in 24 hours and is thus not included in the comparison.

**Example 1.5. Interactions only.** We simulated the scenario in which there are only interaction effects. In particular, we removed the main effect term \(X_1\) from the previous classification rule so that the new classification function becomes

\[
Q(x) = 1.777 - 0.6X_1^2 - 0.6X_3^2 - 0.7X_1X_2 - 0.7X_2X_3.
\]

**Example 1.6. Anti-hierarchical interactions.** We adopt the terminology “anti-hierarchical” from Bien et al. (2013), which refers to the scenario that the main effects and interaction effects are from different set of predictors. In this example, the classification function \(Q(x)\) is

\[
Q(x) = 1.777 + X_4 - X_5 - 0.6X_1^2 - 0.6X_3^2 - 0.7X_1X_2 - 0.7X_2X_3.
\]

For both Examples 1.5 and 1.6, we let \(p = 50\) and let irrelevant predictors be simulated in the same way as Example 1.2. The results are shown in Figure 4. Overall, the results are similar to
| Example | $n$ | SODA | IIS-SQDA | hierNet |
|---------|-----|------|----------|---------|
|         |     | MFN  | MFP      | IFN     | IFP     | MFN  | MFP  | IFN  | IFP |
| 1.1     | 100 | 0.05 | 0.16     | 1.01    | 0.30    | 0.27 | 2.39 | 0.90 | 48.5 |
|         | 215 | 0    | 0.01     | 0.04    | 0.02    | 0.08 | 2.90 | 0.25 | 63.2 |
|         | 1000| 0    | 0        | 0       | 0       | 0    | 6.39 | 0    | 112  |
|         |     | 100  | 0.26     | 0.58    | 1.74    | 0.28 | 12.9 | 0.40 | 7.42 |
| 1.2     | 215 | 0    | 0.13     | 0.27    | 0.03    | 0    | 19.7 | 0.02 | 11.1 |
|         | 1000| 0    | 0        | 0       | 0       | 0    | 28.5 | 0    | 24.3 |
|         |     | 100  | 0.12     | 0.13    | 1.50    | 0.70 | 0.09 | 5.59 | 0.13 | 44.9 |
| 1.3     | 215 | 0    | 0.02     | 0.03    | 0.17    | 0.07 | 0    | 8.96 | 0    | 61.1 |
|         | 1000| 0    | 0        | 0       | 0       | 0    | 14.71| 0    | 99.8 |
|         |     | 100  | 0.20     | 0.22    | 1.58    | 0.30 | 0.68 | 1.58 | 0.42 | 6.08 |
| 1.4     | 215 | 0    | 0        | 0       | 0.14    | 0    | 0    | 1.74 | 0.10 | 8.84 |
|         | 1000| 0    | 0        | 0       | 0       | 0    | 3.68 | 0    | 40.7 |

Table 2: Variable Selection Results for Examples 1.1 ∼ 1.4. MFP / MFN: Average number of main effect false positives and negatives. IFP / IFN: Average number of interaction effect false positives and negatives. The number of observations for each class is denoted by $n$.

previous examples that SODA had fewer VFPs and VFNs, and also lower TE rates compared with other methods. In all cases we found that ZW and MDR performed very similarly when $n$ is large.

4.2 Continuous-response index models

We examine here variable selection methods for nonlinear models with continuous responses. Besides S-SODA, we considered all the five methods studied in Jiang and Liu (2014): Lasso, DC-SIS, hierNet, COP, and SIRI. DC-SIS (Li et al. 2012) is a sure independence screening procedure based on distance correlation, which has been shown to be capable of detecting relevant variables when interactions are present. HierNet (Bien et al. 2013) is a Lasso-like procedure to detect multiplicative interactions between predictors under hierarchical constraints. For SIRI and S-SODA, we equally partition $\{y_i\}_{i=1}^n$ into $H = 5$ slices. In order to improve SIRI’s robustness, we consider a modified version of SIRI, termed as N-SIRI, which pre-processes $X$ by marginally quantile-normalizing each predictor to the standard normal distribution.

We considered the following five simulation examples:

Example 2.1 : $Y = 3X_1 + 1.5X_2 + 2X_3 + 2X_4 + 2X_5 + \sigma\epsilon,$
Example 2.2 : $Y = X_1 + X_1X_2 + X_1X_3 + \sigma\epsilon,$
Example 2.3 : $Y = X_1^2X_2/X_3^2 + \sigma\epsilon,$
Example 2.4 : $Y = X_1/\exp(X_2 + X_3) + \sigma\epsilon,$
Example 2.5 : $Y = X_1 + X_2 + (1 + X_3)^2\epsilon,$
where $\sigma = 0.2$ and $\varepsilon \sim N(0,1)$ independent of $X$. In each example, we simulated the predictors $X$ with dimension $p = 1000$. In order to test robustness of the methods, we simulated $X$ under three scenarios.

- Scenario (a): $X$ is simulated from multivariate Gaussian with correlation $0.5^{|i-j|}$. In this scenario the linearity and constant variance conditions hold.

- Scenario (b): Each predictor $X_j$, $j = 1, \ldots, p$, is simulated from the $\chi^2_1$ distribution independently. In this scenario the linearity and constant variance conditions hold, but the distribution of $X$ is non-normal.

- Scenario (c): $X_1, \ldots, X_{125}$ were simulated from multivariate Gaussian with correlation $0.5^{|i-j|}$. For $X_{126}, \ldots, X_{1000}$, we simulated according to the following schemes:

\[
\begin{align*}
X_j &= X_{j-125}^2 + \varepsilon_j, \quad j = 126, \ldots, 250, \\
X_j &= \sqrt{\lvert X_{j-250} \rvert} + \varepsilon_j, \quad j = 251, \ldots, 375, \\
X_j &= \sin (X_{j-375}) + \varepsilon_j, \quad j = 376, \ldots, 500, \\
X_j &= \log (\lvert X_{j-500} \rvert) + \varepsilon_j, \quad j = 501, \ldots, 625, \\
X_j &= \exp (X_{j-625}) + \varepsilon_j, \quad j = 626, \ldots, 750, \\
X_j &= \exp (\lvert X_{j-750} \rvert) + \varepsilon_j, \quad j = 751, \ldots, 875, \\
X_j &= X_{j-875}^2 \varepsilon_j, \quad j = 876, \ldots, 1000.
\end{align*}
\]

For each simulation setting, we generated 100 datasets with sample size $n = 200$, and applied the aforementioned seven methods to each simulated dataset. For each method, the average number of false positives (FPs) and false negatives (FNs) were calculated over the 100 datasets. The results for the five examples are shown in Figure 5.

As expected, all the seven methods worked well for Example 2.1 in scenario (a), with low FPs and FNs, since the underlying structure is indeed linear Gaussian. For scenarios (b) and (c) with non-Gaussian predictors, DC-SCAD, hierNet, and SIRI generated more FPs and/or FNs than other methods. In general, SIRI performed the worst for this example. But with quantile-normalization, N-SIRI performed very competitively. S-SODA worked well for all the three scenarios, almost as good as Lasso.

In Examples 2.2~2.5 the relationships between $Y$ and $X$ is non-linear. Thus, as expected Lasso and DC-SCAD tended to miss important predictors, resulting in high number of FNs. HierNet can only detect second-order interactions, such as $X_1 X_2$, but fails to identify more complicated relationships such as $Y = X_1^2 X_2 / X_3^3$ and $Y = X_1 / \exp (X_2 + X_3)$. COP only identifies the information from the first conditional moment $\mathbb{E}(X \mid Y)$, and misses important variables with interaction or other second-order effects.

As expected, SIRI usually worked well for scenario (a). N-SIRI worked well for both scenarios (a) and (b) since the joint distribution of the predictors become multivariate Gaussian after quantile-normalization. For scenario (c), SIRI performed very poorly, while N-SIRI performed very
respectfully, although it still had more FPs and FNs than S-SODA. In contrast, S-SODA worked well for all three scenarios. All these examples demonstrated the efficiency and robustness of S-SODA for variable selection in semi-parametric nonlinear regression models.

4.3 Prediction of continuous surface

We consider three examples to test the performance of using formula (10) to predict $Y$, with $p = 1000$ predictors simulated in the same way as scenario (a) in the previous section. In order to visualize $\mathbb{E}[Y \mid X_P]$ and $\mathbb{E}[Y \mid X_{\tilde{P}}]$ surface in a three-dimensional plot, we only had 2 relevant predictors, i.e., $X_P = (X_1, X_2)$:

Example 3.1: $Y = X_1 + X_2 + \sigma \epsilon$,  
Example 3.2: $Y = X_1 / \exp(X_2) + \sigma \epsilon$,  
Example 3.3: $Y = \left(1 + X_1^2 + X_2^2\right)^{-1} + \sigma \epsilon$,

where $\sigma = 0.2$ and $\epsilon \sim N(0, 1)$. For each example we simulated $n = 500$ samples, and applied S-SODA to the simulated data. S-SODA correctly identified $\tilde{P} = \{1, 2\}$. We further used formula (10) with $\hat{\mu}$ and $\hat{\Sigma}$ being the MLEs to predict $\mathbb{E}[Y \mid X_P]$ with $H = 25$ slices for each example. The results are shown in Figure 6. Encouragingly, it is observed that even though we do not know the true functional form of $\mathbb{E}[Y \mid X_P]$, our prediction $\mathbb{E}[Y \mid X_{\tilde{P}}]$ well captures the landscape of $\mathbb{E}[Y \mid X_P]$ in these examples.

5 Real Data Applications

We applied SODA, Lasso-Logistic, MDR and IIS-SQDA on real datasets to compare their performances. We did not include the ZW method due to its similarity with MDR. The classification accuracy of the selected models were evaluated by 10-fold cross-validation after the variable selection. For Lasso-Logistic and SODA, we used EBIC$_{0.5}$ as model selection criterion. We consider three datasets: (1) a Michigan lung cancer dataset analyzed in Efron (2009) with large $p > 5000$; (2) the Ionosphere dataset, with $p = 33$; and (3) the dataset Pumadyn, with $p = 32$ and a continuous response. The Ionosphere dataset was downloaded from UCI Machine Learning Repository$^1$, and the Pumadyn dataset was downloaded from DELVE (Data for Evaluating Learning in Valid Experiments)$^2$.

5.1 Michigan lung cancer dataset

This dataset was published in Beer et al. (2002), in which researchers measured mRNA expression levels of $p = 5,217$ genes in tumor tissues of 86 lung cancer patients. Among the 86 patients, 62 are labeled as in “good status”, and 26 in “bad status”. The goal is to classify new patients into

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$^1$https://archive.ics.uci.edu/ml/datasets/Concrete+Compressive+Strength  
$^2$http://www.cs.toronto.edu/~delve/data/pumadyn/desc.html
one of two statuses. Results on this dataset are summarized in Table 3. IIS-SQDA did not finish in 48 hours for this dataset, so we omitted its result.

In the solution path of Lasso-Logistic, the lowest $EBIC_{0.5}$ was achieved at 112.2 with 1 gene, and the corresponding CV error rate was 29%. SODA selected 2 main effects and 2 interaction effects with the $EBIC_{0.5}$ score at 69.8 and the CV error rate at 11%. Similar to the prostate cancer dataset (see Supplemental Materials), SODA worked much better than Lasso-Logistic for finding the minimum of $EBIC_{0.5}$ (69.8 vs 112.2). Comparing results of Lasso-Logistic and SODA selected models, it is obvious that interaction effects selected by SODA contribute substantially to the classification accuracy.

MDR failed to converge on this dataset. MDR selected as many genes as possible until the number of selected genes was the same as the number of samples in the smaller class (26) and achieved a CV error rate of 28%. The observation that MDR failed to converge for both of these two large $p$ datasets illustrates the fact that the QDA variable selection methods with joint normality assumption work poorly for high-dimensional real datasets.

| Shrunken centroid | Empirical Bayes | MDR | Lasso-Logistic | SODA |
|-------------------|----------------|-----|----------------|------|
| CVE               | CVE            | #BIC| CVE            | CVE  |
| #P                | #P             | #P  | #P             | #P   |
| 0.28              | 0.41           | -353| 1              | 0.27 |
| 5                 | 0.43           | -177| 2              | 0.26 |
| 11                | 0.39           | -178| 3              | 0.25 |
| 21                | 0.41           | -165| 4              | 0.24 |
| 55                | 0.40           | -156| 5              | 0.25 |
| 109               | 0.39           | -134| 8              | 0.24 |
| 260               | 0.40           | -132| 11             | 0.29 |
| 567               | 0.40           | -131| 14             | 0.28 |
| 1,173             | 0.42           | -143| 17             | 0.30 |
| 2,532             | 0.38           | -146| 20             | 0.27 |
| 5,217             | 0.38           | -151| 25             | 0.28 |

Table 3: Analysis results of the Michigan lung cancer dataset by five methods. For Lasso-Logistic, MDR and SODA, the selected set with the lowest BIC score is highlighted in bold font. $\Delta BIC$: For MDR method, the difference of BIC between two adjacent steps. CVE: prediction error rate estimated by 10-fold cross-validation. #P: number of selected predictors. #M / #I: number of selected main effect and interaction terms by SODA.

5.2 Ionosphere dataset

This dataset is a two-class classification problem with 351 samples and 32 predictors. Targets are “Good” and “Bad” radar returns from the ionosphere. “Good” radar returns are those showing evidence of some type of structure in the ionosphere, while “Bad” returns do not.

We applied Lasso-Logistic, MDR, IIS-SQDA and SODA to this dataset. Since the number of candidate predictors is not large, we also ran Lasso-Logistic with all main effect terms and $32 \times (32 + 1) / 2 = 528$ interaction terms, which is referred to as Lasso-Logistic-2. Results are
summarized in Table 4. In the solution path of Lasso-Logistic, the lowest EBIC\(_{0.5}\) was achieved at 302.9 with 6 predictors, and the corresponding CV error rate was 14%. Lasso-Logistic-2 selected 2 main effect terms and 5 interaction terms with EBIC\(_{0.5}=248.7\) and CV error rate 8%. SODA selected 4 main effect and 4 interaction effect terms with EBIC\(_{0.5}=204.2\) and CV error rate 6%. Again, SODA found a smaller EBIC\(_{0.5}\) value than both Lasso methods.

MDR method selected all 32 predictors and achieves CV error rate 28%. IIS-SQDA selected 10 main effect and 96 interaction terms and achieved CV error rate 16%. Since MDR selected all 32 predictors, by definition MDR selected model is the full QDA model. Comparing this full QDA model with the SODA selected model, we see that EBIC-based variable selection resulted in a much more interpretable model with a substantially reduced classification error rate.

|          | MDR | Lasso-Logistic | Lasso-Logistic-2 | IIS-SQDA | SODA |
|----------|-----|----------------|-----------------|----------|------|
| \(\Delta\text{BIC}\) | #P  | CVE            | EBIC\(_{0.5}\)  | #P / #I  | CVE  |
| -326     | 1   | 0.20           | 343.5           | 2 / 1    | 0.19 |
| -221     | 3   | 0.26           | 329.9           | 4 / 1    | 0.19 |
| -338     | 5   | 0.25           | \textbf{302.9}  | 6 / 0    | \textbf{0.14} |
| -298     | 7   | 0.24           | 313.5           | 8 / 1    | 0.16 |
| -242     | 9   | 0.25           | 312.5           | 10 / 1   | 0.15 |
| -200     | 11  | 0.24           | 321.7           | 12 / 1   | 0.15 |
| -278     | 15  | 0.29           | 345.3           | 15 / 1   | 0.15 |
| -361     | 20  | 0.28           | 363.8           | 18 / 1   | 0.15 |
| -434     | 25  | 0.30           | 383.1           | 22 / 1   | 0.15 |
| \textbf{-130} | \textbf{32} | \textbf{0.28} | 445.4 | 30 / 1 | 0.16 |

Table 4: The summary of results on the Ionosphere dataset by the five methods. \(\Delta\text{BIC}\): For MDR method, the difference of BIC\(_G\) between two adjacent steps. CVE: prediction error rate estimated by 10-fold cross-validation. #P: number of selected predictors. #M / #I: number of selected main effect and interaction terms by SODA.

### 5.3 Pumadyn dataset

This dataset was synthesized from a realistic simulation of the dynamics of a robotic arm. It has \(n=8192\) samples, \(p=32\) predictors, and a continuous response. The predictor set includes angular positions, velocities and torques of the robot arm. The goal is to predict the angular acceleration of the robot arm’s links. The samples are split into 4500 in-samples for modeling training, and 3692 out-samples for model evaluation.

We trained the S-SODA model with \(H=20\) for this dataset, and made the predictions using formula (10). We also applied linear regression with Lasso selection with/without interaction terms, denoted as Lasso-Linear and Lasso-Linear-2, respectively. The results are summarized in Table 5. Lasso’s highest out-sample correlation \(r=0.477\) were achieved when selecting only 1 predictor (named tau4). S-SODA selected two predictors (tau4 and theta5) and achieved an out-sample correlation \(r=0.707\). The predicted surfaces of \(\hat{E}[Y \mid X_{(\text{tau4,theta5})}]\) from the linear model and
S-SODA, respectively, are shown in Figure 7. The interaction between predictors tau4 and theta5 are captured by S-SODA but not the linear model. From Table 5 we can also see that the interaction between tau4 and theta5 cannot be simply captured by the multiplication term $X_{\text{tau4}} \cdot X_{\text{theta5}}$.

| # Predictors | Lasso-Linear | Lasso-Linear-2 | S-SODA |
|--------------|--------------|---------------|--------|
| # M / # I    | Out-$r$      | Out-$r$       | Out-$r$|
| 1            | 0.477        | 1 / 0         | 0.477  | 1 | 0.469 |
| 2            | 0.477        | 1 / 1         | 0.476  | 2 | 0.707 |
| 3            | 0.476        | 1 / 2         | 0.474  |    |        |
| 4            | 0.476        | 1 / 3         | 0.473  |    |        |
| 5            | 0.476        | 1 / 4         | 0.473  |    |        |
| 10           | 0.474        | 1 / 10        | 0.469  |    |        |
| 20           | 0.472        | 1 / 20        | 0.464  |    |        |
| 30           | 0.472        | 1 / 30        | 0.459  |    |        |

Table 5: Analysis results of the Pumadyn dataset by the three methods. #P: the number of selected predictors. #M / # I: the number of selected main effect and interaction terms by Lasso on linear model with interaction terms. Out-$r$: the out-sample correlation $r$.

6 Concluding Remarks

A somewhat striking observation in this article is that the proposed stepwise selection algorithm SODA, which is guided by EBIC and based on the classic stepwise regression idea with a twist for efficiently searching for interaction terms, out-performed all known advanced methods, such as those based on $L_1$ regularizations, in terms of variable selection accuracy, prediction accuracy, and robustness in a variety of settings when the joint distribution of the predictors do not "behave nicely." In contrast to Murphy et al. (2010), Zhang and Wang (2011), and Maugis et al. (2011), the consistency of SODA does not require the joint normality assumption of relevant and irrelevant predictors. Compared to IIS in Fan et al. (2015), SODA's forward variable addition does not need the normal assumption and does not need to estimate large precision matrices.

It is worth noting that even for logistic regression models with only main effects, we consistently observed that SODA performed better than or similarly to Lasso-logistic in terms of both the EBIC$_{0.5}$ score and the CV error rate under various settings, especially when the predictors are highly correlated or the joint distribution of the predictors is long-tailed. In Supplemental Materials, we also observed that Lasso-logistic failed miserably when the “incoherence condition” (Ravikumar et al. 2010) was violated in linear logistic models, whereas SODA still performed robustly. These indicate that EBIC is a good criterion to follow and SODA is a better optimizer of EBIC than Lasso. Indeed, when one moves away from the $L_1$ regularization realm but adopts the $L_0$ regularization framework (such as AIC, BIC, EBIC), Lasso can no longer guarantee to find the optimal solution and is more ad hoc than stepwise approaches.

LDA and QDA complement each other in terms of the bias-variance trade-off. Given finite observations, LDA is simpler and more robust when the response $Y$ can be explained well by
the linear effects of $X$. QDA has the ability to exploit interaction effects, which may contribute dramatically to the classification accuracy, but also has many more parameters to estimate and is more vulnerable to including noise predictors. SODA is designed to be adaptive in the sense that it automatically chooses between LDA and QDA models and takes advantage of both sides. Instead of selecting predictors, SODA selects individual main and interaction terms, which enables SODA to simultaneously utilize interaction terms and avoid including a large number of unnecessary terms.

An interesting and also somewhat surprising twist of SODA is its extension S-SODA for dealing with the variable selection problem for semi-parametric models with continuous responses. Our simulation results demonstrated that the simple idea of slicing (aka discretizing) the response variable can bring a lot to the table, especially coupled with stepwise variable selection tools such as N-SIRI (Jiang and Liu 2014) and S-SODA. Even for linear models, S-SODA performed competitively with Lasso, and outperformed other linear or near-linear methods such as hierNet and DC-SCAD when the joint distribution of the covariates is long-tailed. Compared with existing SIR-based methods, SODA does not require the linearity and constant variance conditions and enjoys a much improved robustness.

A main limitation of SODA is that the stepwise detectable condition might not hold when main effects are very weak or nonexistent but the interaction effects are strong. This is a generic issue that troubles almost all methods unless we put all interaction terms into the set of candidate variables subject to selection. In empirical studies we found that SODA worked well and had better performances compared to other methods for both simulated and real-data examples, which suggests that this may not be a serious issue in many real applications. Indeed, even for QDA models it is quite unusual and nearly pathological to construct mean vectors and covariance matrices that result in a discriminant function with no main effects but only interaction terms.

The Implementation of SODA and S-SODA procedures is available in the R package sodavis on CRAN (http://cran.us.r-project.org).

References

Anderson, T. W. (1958). An introduction to multivariate statistical analysis. Wiley, New York.

Beer, D. G., Kardia, S. L., Huang, C.-C., Giordano, T. J., Levin, A. M., Misek, D. E., Lin, L., Chen, G., Gharib, T. G., Thomas, D. G., et al. (2002). Gene-expression profiles predict survival of patients with lung adenocarcinoma. Nature medicine, 8(8):816–824.

Bien, J., Taylor, J., Tibshirani, R., et al. (2013). A lasso for hierarchical interactions. The Annals of Statistics, 41(3):1111–1141.

Boser, B. E., Guyon, I. M., and Vapnik, V. N. (1992). A training algorithm for optimal margin classifiers. In Proceedings of the fifth annual workshop on Computational learning theory, pages 144–152. ACM.
Breiman, L. (2001). Random forests. Machine learning, 45(1):5–32.

Broman, K. W. and Speed, T. P. (2002). A model selection approach for the identification of quantitative trait loci in experimental crosses. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 64(4):641–656.

Cai, T. and Liu, W. (2011). A direct estimation approach to sparse linear discriminant analysis. Journal of the American Statistical Association, 106(496):1566–1577.

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, 22(2):555.

Chowdhary, R., Zhang, J., and Liu, J. S. (2009). Bayesian inference of protein–protein interactions from biological literature. Bioinformatics, 25(12):1536–1542.

Clemmensen, L., Hastie, T., Witten, D., and Ersbøll, B. (2011). Sparse discriminant analysis. Technometrics, 53(4):406–413.

Cook, R. D. (2007). Fisher lecture: Dimension reduction in regression. Statistical Science, pages 1–26.

Efron, B. (2009). Empirical bayes estimates for large-scale prediction problems. Journal of the American Statistical Association, 104(487):1015–1028.

Efron, B. (2010). Large-scale inference: empirical Bayes methods for estimation, testing, and prediction, volume 1. Cambridge University Press.

Fan, J. and Fan, Y. (2008). High dimensional classification using features annealed independence rules. Annals of statistics, 36(6):2605.

Fan, Y., Jin, J., Yao, Z., et al. (2013). Optimal classification in sparse gaussian graphic model. The Annals of Statistics, 41(5):2537–2571.

Fan, Y., Kong, Y., Li, D., Zheng, Z., et al. (2015). Innovated interaction screening for high-dimensional nonlinear classification. The Annals of Statistics, 43(3):1243–1272.

Foygel, R. and Drton, M. (2011). Bayesian model choice and information criteria in sparse generalized linear models. arXiv preprint arXiv:1112.5635.

Guo, Y., Hastie, T., and Tibshirani, R. (2007). Regularized linear discriminant analysis and its application in microarrays. Biostatistics, 8(1):86–100.

Han, F., Zhao, T., and Liu, H. (2013). Coda: High dimensional copula discriminant analysis. The Journal of Machine Learning Research, 14(1):629–671.
Jia, J. and Yu, B. (2010). On model selection consistency of the elastic net when \( p \gg n \). *Statistica Sinica*, 20(2):595–611.

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.

Joachims, T. (1998). *Text categorization with support vector machines: Learning with many relevant features*. Springer.

Li, K.-C. (1991). Sliced inverse regression for dimension reduction. *Journal of the American Statistical Association*, 86(414):316–327.

Li, L. (2007). Sparse sufficient dimension reduction. *Biometrika*, 94(3):603–613.

Li, L., Dennis Cook, R., and Nachtsheim, C. J. (2005). Model-free variable selection. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 67(2):285–299.

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

Lin, Q., Zhao, Z., and Liu, J. S. (2015). On consistency and sparsity for sliced inverse regression in high dimensions. *arXiv preprint arXiv:1507.03895*.

Lin, Q., Zhao, Z., and Liu, J. S. (2016). Sparse sliced inverse regression for high dimensional data. *arXiv preprint arXiv:1611.06655*.

Mai, Q., Zou, H., and Yuan, M. (2012). A direct approach to sparse discriminant analysis in ultra-high dimensions. *Biometrika*, 99(1):29–42.

Maugis, C., Celeux, G., and Martin-Magniette, M.-L. (2011). Variable selection in model-based discriminant analysis. *Journal of Multivariate Analysis*, 102(10):1374–1387.

Murphy, T. B., Dean, N., and Raftery, A. E. (2010). Variable selection and updating in model-based discriminant analysis for high dimensional data with food authenticity applications. *The Annals of Applied Statistics*, 4(1):396.

Phillips, P. J. (1998). *Support vector machines applied to face recognition*, volume 285. Citeseer.

Ravikumar, P., Wainwright, M. J., Lafferty, J. D., et al. (2010). High-dimensional ising model selection using l1-regularized logistic regression. *The Annals of Statistics*, 38(3):1287–1319.

Schwarz, G. et al. (1978). Estimating the dimension of a model. *The annals of statistics*, 6(2):461–464.

Shao, J., Wang, Y., Deng, X., Wang, S., et al. (2011). Sparse linear discriminant analysis by thresholding for high dimensional data. *The Annals of Statistics*, 39(2):1241–1265.
Simon, N. and Tibshirani, R. (2012). A permutation approach to testing interactions in many dimensions. *arXiv preprint arXiv:1206.6519*.

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

Tibshirani, R., Hastie, T., Narasimhan, B., and Chu, G. (2002). Diagnosis of multiple cancer types by shrunken centroids of gene expression. *Proceedings of the National Academy of Sciences*, 99(10):6567–6572.

Waldmann, P., Mészáros, G., Gredler, B., Fuerst, C., and Sölkner, J. (2013). Evaluation of the lasso and the elastic net in genome-wide association studies. *Frontiers in genetics*, 4.

Wang, H. (2009). Forward regression for ultra-high dimensional variable screening. *Journal of the American Statistical Association*, 104(488):1512–1524.

Wasserman, L. and Roeder, K. (2009). High dimensional variable selection. *Annals of statistics*, 37(5A):2178.

Witten, D. M. and Tibshirani, R. (2011). Penalized classification using fisher’s linear discriminant. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 73(5):753–772.

Yu, Y. and Feng, Y. (2014). Modified cross-validation for penalized high-dimensional linear regression models. *Journal of Computational and Graphical Statistics*, 23(4):1009–1027.

Zhang, Q. and Wang, H. (2011). On BIC’s selection consistency for discriminant analysis. *Statistica Sinica*, 21(2):731.

Zhao, P. and Yu, B. (2006). On model selection consistency of lasso. *The Journal of Machine Learning Research*, 7:2541–2563.

Zhong, W., Zhang, T., Zhu, Y., and Liu, J. S. (2012). Correlation pursuit: forward stepwise variable selection for index models. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 74(5):849–870.

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.
Figure 2: Results for Example 1.1–1.4. VFP: average number of variable selection false positives. VFN: average number of variable selection false negatives. LDA and QDA used all the variables without any selection, so they do not appear in the left panel and their TEs were high. MDR and hierNet all broke down for Example 1.4. LDA and QDA also did not work due to large $p$.  

[Figure 2 showing graphs for different examples with VFP and VFN on the left and estimated test error rate on the right.]
Example 2.4 (Time in seconds)

Figure 3: Mean running time in seconds for ZW, IIS-SQDA, and SODA for Example 1.4; and hierNet did not finish the job within 24 hours.

Example 1.5 (VFP + VFN)
Example 1.5 (Test error rate)
Example 1.6 (VFP + VFN)
Example 1.6 (Test error rate)

Figure 4: Results for Example 1.5 ~ 1.6. VFP: average number of variable selection false positives. VFN: average number of variable selection false negatives.
Figure 5: Simulation study results for Examples 2.1~2.5.
Figure 6: Results for the simulation Examples 3.1-3.3. Left panel: theoretical surface $\mathbb{E}[Y \mid X]$; Right panel: surface $\hat{\mathbb{E}}[Y \mid X]$ predicted by S-SODA.
Figure 7: The predicted $\hat{E}[Y \mid X_{(\tau_{4}, \theta_{5})}]$ surface from linear model (left) and S-SODA (right).