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MODEL-FREE FEATURE SCREENING FOR ULTRAHIGH DIMENSIONAL DATATHROUGH A MODIFIED BLUM-KIEFER-ROSENBLATT CORRELATION

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Abstract: In this paper we introduce a modified Blum-Kiefer-Rosenblatt correlation (MBKR for short) to rank the relative importance of each predictor in ultrahigh-dimensional regressions. We advocate using the MBKR for two reasons. First, it is nonnegative and is zero if and only if two random variables are independent, indicating that the MBKR can detect nonlinear dependence. We illustrate that the sure independence screening procedure based on the MBKR (MBKR-SIS for short) is effective in detecting nonlinear effects, including interactions and heterogeneity, particularly when both continuous and discrete predictors are involved. Second, the MBKR is conceptually simple, easy to implement, and affine-invariant. It is free of tuning parameters and no iteration is required in estimation. It remains unchanged when order-preserving transformations are applied to the response or predictors, indicating that the MBKR-SIS is robust to the presence of extreme values and outliers in the observations. We show that, under mild conditions, the MBKR-SIS procedure has the sure screening and ranking consistency properties, guaranteeing that all important predictors can be retained after screening with probability approaching one. We also propose an iterative screening procedure to detect the important predictors that are marginally independent of the response variable. We demonstrate the merits of the MBKR-SIS procedure through simulations and an application to a dataset.

Key words and phrases: Blum-Kiefer-Rosenblatt correlation, feature screening, independence test, ranking consistency property, sure screening property.

1. Introduction

Ultrahigh-dimensional data arise in many scientific fields. For instance, in order to identify gene mutations which probably cause a disease, medical scientists typically collect thousands of gene expression levels or genetic markers from a relatively small number of subjects, borrowing the strength of microarray technology. To analyze such datasets effectively, it is often assumed that the disease depends upon only a few among thousands of gene expression levels or genetic markers. Such an assumption, usually referred to as sparsity, illuminates extensive research on feature selection over the past two decades.

To identify important features in regressions, many penalized least squares and penalized likelihood algorithms have been proposed, such as bridge regression (Frank and Friedman (1993)), LASSO (Tibshirani (1996)), SCAD (Fan and Li (2001)), adaptive Lasso (Zou (2006)), Dantzig selector (Candes and Tao (2007)), nonnegative garrote (Yuan and Lin (2006)). These algorithms are effective in mean regressions and parametric models, yet lack computational expediency, statistical accuracy, and algorithmic stability when the predictors are ultrahigh-dimensional and the sample size is relatively small (Fan, Samworth and Wu (2009)).

To analyze ultrahigh-dimensional data, marginal screening procedures are typically regarded as acceptable preludes to penalized regressions. Marginal screening breaks an ultrahigh-dimensional regression into many low-dimensional problems, hence dramatically reducing overall computational complexity.

There are two classes of marginal screening procedures in the literature. One is concerned with the conditional mean regression, the other is with the conditional distribution function. Let $Y \in \mathbb{R}^1$ be the response variable and $\mathbf{x} = (X_1, \ldots, X_p)^{\mathrm{T}} \in \mathbb{R}^p$ be the predictor vector. The first class of screening procedures aims to identify important features indexed by

$$\mathcal{I} = \{k : E(Y|\mathbf{x}) \text{ varies with } X_k\}. \tag{1.1}$$

In this area, Fan and Lv (2008) proposed a sure independence screening (SIS for short) procedure based on the Pearson correlation coefficient, assuming that $E(Y|\mathbf{x})$ is a linear function of $\mathbf{x}$. Pearson correlation-based screening was later generalized from many different perspectives. For example, Hall and Miller (2009) suggested using polynomial transformations of the predictors in SIS. Li et al. (2012) recommended Kendall's rank correlation, and Shao and Zhang (2014) proposed martingale difference correlation in place of Pearson correlation to perform marginal screening. Fan and Song (2010) and Fan, Feng and Song (2011) extended the linear model assumption to the generalized linear model and nonparametric additive model, respectively. The second class of screening procedures aims to identify important features indexed by

$$\mathcal{A} = \{k : F(y|\mathbf{x}) \text{ varies with } X_k \text{ for some } y \in \mathbb{R}^1\}, \tag{1.2}$$

where $F(y|\mathbf{x})$ is the conditional distribution function of Y given $\mathbf{x}$. In this area, Zhu et al. (2011) proposed a sure independent ranking and screening procedure

(SIRS for short), and Li, Zhong and Zhu (2012) suggested a distance correlation-based sure independence screening procedure (DC-SIS for short). Mai and Zou (2013) and Mai and Zou (2015) suggested a nonparametric Kolmogorov filter when the response variable is binary, as then $\mathcal{A} = \mathcal{I}$. Though all the aforementioned marginal screening procedures assumed the marginal distribution functions of either $\mathbf{x}$ or Y, or both, have exponential tails, they all have the desirable sure screening property, a terminology introduced by Fan and Lv (2008). In this, all important predictors, possibly together with a few unimportant ones, are retained after screening, with an overwhelming probability.

In addition to main effects which are of our interests, interactions and heterogeneity are common phenomena in ultrahigh-dimensional data. Detecting interactions through mean regressions indexed by $\mathcal{I}$ hinges upon either a utility that can measure a possibly nonlinear relation between X_k and Y, or a correctly specified mean model for $E(Y|\mathbf{x})$. In analysis of ultrahigh-dimensional data, we often lack prior information on the regression structure (Zhu et al. (2011)). Modelling interactions in $E(Y|\mathbf{x})$ will increase the model size from $O(p)$ to $O(p^2)$ if two-way interactions are concerned and to $O(p^3)$ if three-way interactions are concerned, precluding computation even for marginal screening. The Pearson correlation-based screening procedures, such as Fan and Lv (2008) and Li et al. (2012), may fail to detect interactions even in linear models. Heterogeneity is another important issue, characterized by $\text{var}(Y|\mathbf{x})$. Those mean regression-based screening procedures cannot detect important features that merely describe the heterogeneity of the data. We demonstrate these issues through simulations in Sections 2 and 3.

The overarching goal of regression analysis is to characterize how the conditional distribution function of Y varies with the realizations of $\mathbf{x}$. As a prelude to subsequent regression analysis, an ideal screening procedure is expected to retain the important predictors indexed by $\mathcal{A}$ rather $\mathcal{I}$. In effect, identifying $\mathcal{A}$ rather $\mathcal{I}$ is sufficient to capture both the interactions and heterogeneity, in addition to main effects. Important covariates involved in interactions and heterogeneity are generally nonlinear effects. A prerequisite to identify $\mathcal{A}$ is to design a utility that can measure the possibly nonlinear relations between X_k and Y without requiring information on the underlying regression structure. Our goal in this paper is to design a utility that can detect the main effects, the interactions and the heterogeneity simultaneously or, more precisely, the important predictors indexed by $\mathcal{A}$. Following Blum, Kiefer and Rosenblatt (1961), we introduce a modified Blum-Kiefer-Rosenblatt correlation (MBKR for short) to rank the relative importance of the predictors. The MBKR correlation measures the relation between X_k and Y through

$$\begin{aligned} &MBKR(X_k, Y) \\ &= \int_{\mathbb{R}^1}\int_{\mathbb{R}^1} \frac{\{F_{X_k,Y}(x_k, y) - F_{X_k}(x_k)F_Y(y)\}^2}{F_{X_k}(x_k)\{1 - F_{X_k}(x_k)\}F_Y(y)\{1 - F_Y(y)\}} dF_{X_k}(x_k)dF_Y(y), \qquad (1.3) \end{aligned}$$

where F_{X_k} and F_Y are the respective marginal distribution functions of X_k and Y, and $F_{X_k,Y}(x_k, y)$ is the joint distribution of (X_k, Y). We advocate using the MBKR for at least two reasons.

First, the MBKR is nonnegative and is zero if and only if two random variables are independent, indicating that the MBKR can detect nonlinear dependence. We illustrate through simulations that the sure independence screening procedure based on the MBKR (MBKR-SIS for short) is effective to detect nonlinear effects including interactions and heterogeneity, particularly when both continuous and discrete predictors are involved.

As well, the MBKR is conceptually simple, easy to implement, and affine invariant. The MBKR is free of tuning parameters and no iteration is required in estimation. It remains unchanged when order-preserving transformations are applied to either the response or the predictors, indicating that the MBKR-SIS is robust to the presence of extreme values and outliers in the observations.

We study the asymptotic properties of the sample MBKR. We show that the sample MBKR is n consistent if X_k and Y are independent, and root n consistent otherwise. If X_k and Y are independent and both are continuous random variables, the asymptotic distribution of the sample MBKR does not depend on the marginal distribution of X_k or that of Y. This is appealing in that the critical value can be easily determined when applying the sample MBKR to test independence between X_k and Y. We also show that, under mild conditions, the MBKR-SIS procedure has desirable sure screening and ranking consistency properties, which guarantee that all important predictors can be retained after screening with an overwhelming probability.

The rest of this paper is organized as follows. In Section 2, we introduce the MBKR correlation and consider two applications. One is to test independence between two random variables and the other is to screen out irrelevant features for ultrahigh-dimensional data. We investigate the theoretical properties of our proposals. In Section 3, we evaluate the finite sample performance of our proposals through Monte Carlo simulations and an application to a rat eye dataset consisting of gene expression levels and genetic markers. We also propose an iterative approach to detect the important predictors that are marginally independent of the response. We conclude with a brief discussion in Section 4. The technical details are relegated to the supplement.

2. A Modified Blum-Kiefer-Rosenblatt Correlation

2.1. Two relevant utilities

The MBKR defined in (1.3) originates from the Blum-Kiefer-Rosenblatt correlation (BKR for short) introduced in 1961.

$$BKR(X_k, Y) = \int_{\mathbb{R}^1}\int_{\mathbb{R}^1} \{F_{X_k,Y}(x_k, y) - F_{X_k}(x_k)F_Y(y)\}^2 dF_{X_k}(x_k)dF_Y(y). \quad (2.1)$$

By definition, $F_{X_k,Y}(x_k, y) - F_{X_k}(x_k)F_Y(y) = \text{cov}\{I(X_k \leq x_k), I(Y \leq y)\}$. Throughout, the indicator function $I(A)$ is one if the event A is true, and zero otherwise. The difference between the MBKR and the BKR is that the integrand of the former is $\text{corr}^2\{I(X_k \leq x_k), I(Y \leq y)\}$ while that of the latter is $\text{cov}^2\{I(X_k \leq x_k), I(Y \leq y)\}$. Here the notation $\text{corr}(\cdot, \cdot)$ stands for the Pearson correlation coefficient. If both Y and X_k are continuous, using correlation or covariance does not make significant difference because $F_Y(Y)$ and all $F_{X_k}(X_k)$s, $k = 1, \ldots, p$, follow uniform distributions. If some of the predictors are continuous while others are discrete or categorical, then the difference between using correlation and covariance to rank the relative importance of X_k may not be negligible. We illustrate this issue by a simple example.

Another relevant measure is the Hoeffding's index (Hoeffding (1948)).

$$H(X_k, Y) = \int_{\mathbb{R}^1}\int_{\mathbb{R}^1} \{F_{X_k,Y}(x_k, y) - F_{X_k}(x_k)F_Y(y)\}^2 dF_{X_k,Y}(x_k, y). \quad (2.2)$$

The Hoeffding's index is similar to the BKR and the MBKR correlations in the sense that all are nonnegative, and zero under independence between X_k and Y. However, the Hoeffding's index may be zero if there exists an association between X_k and Y. And so, it does not lead to a consistent test of independence.

We use a toy example to show why we prefer using the MBKR to rank the relative importance of predictors.

Example 1. Let $\mathbf{z} = (Z_1, Z_2, Z_3)^{\mathrm{T}}$ be multivariate normal with mean zero and covariance matrix $\boldsymbol{\Sigma} = (\sigma_{kl})_{3\times 3}$, where $\sigma_{kl} = 0.9^{|k-l|}$, and let ε, independently, be standard normal. Consider the predictors $\mathbf{x} = (X_1, X_2, X_3)^{\mathrm{T}} = \{Z_1, Z_2, I(Z_3 \geq 0)\}^{\mathrm{T}}$ and the response $Y = \kappa X_1 + X_3 + \varepsilon$, for $\kappa = 1, \sqrt{3}$, and 3. Here, X_1 and X_3 are important predictors while X_2 is not predictive for Y when X_1 and X_3 are given. Thus, $\mathcal{A} = \{1, 3\}$ and $\mathcal{A}^c = \{2\}$. For sample size $n = 100$ and

Table 1. The empirical probabilities of $\mathrm{pr}(\min_{k\in\mathcal{A}} \omega_k \geq \max_{k\in\mathcal{A}^c} \omega_k)$ based on 1,000 repetitions for Example 1.

Measure	n=100			n=200		
	$\kappa = 1$	$\kappa = \sqrt{3}$	$\kappa = 3$	$\kappa = 1$	$\kappa = \sqrt{3}$	$\kappa = 3$
Hoeffding's index	0.513	0.380	0.142	0.645	0.349	0.074
BKR correlation	0.513	0.380	0.142	0.645	0.349	0.074
MBKR correlation	0.845	0.984	0.960	0.911	1.000	0.995

200, we applied the MBKR, the BKR, and the Hoeffding's index to rank the relative importance of the predictors. The larger a measure between each predictor and the response, the more important the predictor is, accordingly. To compare performances, we report the probability of ranking important predictors above the unimportant ones, namely, $\mathrm{pr}(\min_{k\in\mathcal{A}} \omega_k \geq \max_{k\in\mathcal{A}^c} \omega_k)$, where ω_k can be $MBKR(X_k, Y)$, $BKR(X_k, Y)$ or $H(X_k, Y)$. This criterion is stringent in quantifying the capability of a measure to rank the important predictors prior to those unimportant ones. The closer to one this probability is, the better the measure.

We repeated each scenario 1,000 times and chart the simulation results in Table 1.

In Table 1 the MBKR ranks X_1 and X_3 above X_2 with high probabilities across all scenarios, while the BKR and the Hoeffding's index yield lesser, even identical results. For the MBKR method, $\mathrm{pr}(\min_{k\in\mathcal{A}} \omega_k \geq \max_{k\in\mathcal{A}^c} \omega_k) \geq 0.845$ when $n = 100$ and $\mathrm{pr}(\min_{k\in\mathcal{A}} \omega_k \geq \max_{k\in\mathcal{A}^c} \omega_k) \geq 0.911$ when $n = 200$, and this performance is relatively stable for different κ values, which the BKR and the Hoeffding's index deteriorate sharply as κ, the coefficient of X_1 in this example, increases.

The MBKR has some further appealing properties. For example, $MBKR(X_k, Y)$ is always nonnegative and is zero if and only if X_k and Y are independent; $MBKR(X_k, Y) = MBKR\{m_k(X_k), m(Y)\}$ for monotone functions m_k and m , and $MBKR(X_k, Y) = MBKR(Y, X_k)$, indicating that the MBKR correlation is affine invariant. We work with the MBKR correlation in what follows, unless stated otherwise.

2.2. An estimation

Suppose $\{(\mathbf{x}_i, Y_i), i = 1, \ldots, n\}$ is a random sample from the population $(\mathbf{x}, Y)$. In this section, we propose an estimation for the MBKR correlation. Let F_{n,X_k}, $F_{n,Y}$ and $F_{n,X_k,Y}$ be the respective empirical versions of F_{X_k}, F_Y and

$F_{X_k,Y}$:

$$F_{n,X_k}(x_k) = n^{-1}\sum_{i=1}^{n} I(X_{i,k} \leq x_k), \quad F_{n,Y}(y) = n^{-1}\sum_{i=1}^{n} I(Y_i \leq y) \text{ and}$$

$$F_{n,X_k,Y}(x_k, y) = n^{-1}\sum_{i=1}^{n} I(X_{i,k} \leq x_k, Y_i \leq y).$$

Define $0/0 = 0$. A natural estimator of $MBKR(X_k, Y)$ is

$$\widehat{MBKR}(X_k, Y) = n^{-2}\sum_{i=1}^{n}\sum_{j=1}^{n} \frac{\{F_{n,X_k,Y}(X_{i,k}, Y_j) - F_{n,X_k}(X_{i,k})F_{n,Y}(Y_j)\}^2}{F_{n,X_k}(X_{i,k})\{1 - F_{n,X_k}(X_{i,k})\}F_{n,Y}(Y_j)\{1 - F_{n,Y}(Y_j)\}}. \tag{2.3}$$

A remarkable property of this estimator is that it depends on the ranks of X_k and Y only, remaining unchanged if order-preserving transformations are applied to either X_k or Y. This indicates that the MBKR is resilient to the presence of outliers and extreme values.

Theorem 1. ***(Convergence in Distribution)***

1. *If X_k and Y are not independent, then $MBKR(X_k, Y) > 0$ and*

$$n^{1/2}\left\{\widehat{MBKR}(X_k, Y) - MBKR(X_k, Y)\right\} \xrightarrow{d} \mathcal{N}(0, \sigma^2), \text{ as } n \to \infty,$$

where σ^2 is given in the Supplement.

2. *If X_k and Y are independent, then $MBKR(X_k, Y) = 0$ and*

$$n\ \widehat{MBKR}(X_k, Y) \xrightarrow{d} \sum_{l=1}^{\infty}\sum_{m=1}^{\infty} \lambda_{lm}\chi^2_{lm}(1), \text{ as } n \to \infty,$$

where the $\chi^2_{lm}(1)$ are independent chi-square random variables with one degree of freedom and the λ_{lm}'s may depend on the distributions of X_k and Y. If X_k and Y are continuous random variables, then $\lambda_{lm} = 1/\{l(l+1)m(m+1)\}$.

Thus, if X_k and Y are continuous, the MBKR offers a distribution-free test of independence. One can reject the independence of X_k and Y if $n\ \widehat{MBKR}(X_k, Y) \geq c_\alpha$, where c_α is the upper $\alpha \times 100\%$ quantile of its limiting distribution. The power of the test tends to one as $n \to \infty$.

Next we give another example to show that the MBKR is effective in detecting the interactions and the heterogeneity of the data.

Example 2. Consider simulating:

$$Y = (5\kappa)(X_1 X_2) + \varepsilon; \tag{2.4}$$

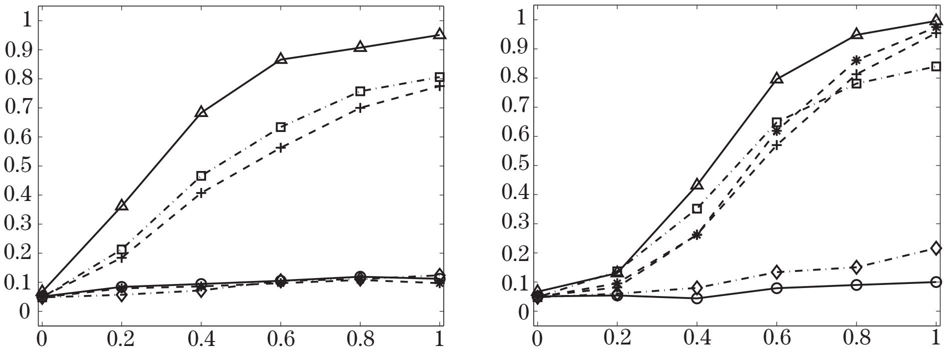
$$Y = \exp\{\kappa(X_1 + X_2)\}\varepsilon. \tag{2.5}$$

In the interaction model (2.4) and the heterogeneity model (2.5), we drew $\mathbf{x} = (X_1, X_2)^{\mathrm{T}}$ from a multivariate normal with mean zero and covariance matrix $\boldsymbol{\Sigma} = (\sigma_{kl})_{2\times 2}$, where $\sigma_{kl} = 0.8^{|k-l|}$. We drew ε from a standard Cauchy distribution. We set $\kappa = 0, 0.2, 0.4, \ldots, 1$ in both (2.4) and (2.5). We test the independence of X_1 and Y; independence holds if $\kappa = 0$, and fails otherwise.

We compared the performances of six tests of independence. The first four are based on Pearson correlation, Kendall's rank correlation, the distance correlation (Székely, Rizzo and Bakirov (2007))and the rank-based distance correlation (Székely and Rizzo (2009)). The distance correlation and rank-based distance correlation are also nonnegative with equality to zero if and only if the random variables are independent. The fifth is based on the utility used in the SIRS procedure (Zhu et al. (2011)), $\omega_k = E\{\Omega_k^2(Y)\}/\mathrm{var}(X_k)$ and $\Omega_k(y) = \mathrm{cov}\{X_k, I(Y \leq y)\}$. The sixth is based on the MBKR correlation $\omega_k = MBKR(X_k, Y)$. The Pearson correlation was used in the SIS procedure (Fan and Lv (2008)); the Kendall's rank correlation was suggested by (Li et al. (2012)) for screening out irrelevant predictors; the distance correlation was used in the DC-SIS procedure (Li, Zhong and Zhu (2012)). For fair comparison, we include rank-based distance correlation to test independence between X_k and Y.

We fixed the sample size $n = 50$ and the significance level $\alpha = 0.05$. We repeated the simulations 1,000 times, and report the sizes and the power curves in Figure 1(A) for model (2.4), and in Figure 1(B) for model (2.5).

From Figure 1, when $\kappa = 0$, the sizes of all six tests are close to the significance level 0.05. The power curves of the distance correlation, the rank-based distance correlation and the MBKR increase gradually as the κ values increase in both models. The MBKR is apparently the most powerful to detect interactions and heterogeneity, followed by distance correlation, rank-based distance correlation in model (2.4) and SIRS, rank-based distance correlation and distance correlation in model (2.5). In both models, the performances of distance correlation are slightly influenced by the heavily-tailed distribution of the unobservable error term and the asymptotic distribution of its sample estimate is not tractable. The Pearson correlation and the Kendall's rank correlation lose power to detect interactions and heterogeneity. The example suggests that the MBKR, among the six aforemetioned correlation measures, is the most powerful utility to detect



(A): model (2.4) (B): model (2.5)

Figure 1. The empirical power curves based on the Pearson correlation test (dashdot line marked with diamond), Kendall's rank correlation test(solid line marked with circle), the distance covariance test(dashdot line marked with square), the rank-based distance covariance test(dashed line marked with plus), the marginal utility in SIRS test(dashed line marked with star) and the MBKR test(solid line marked with up triangle). The horizontal axis: the κ value varies from 0 to 1 in models (2.4) and (2.5). The vertical axis: the size and power curves increase from 0 to 1.

interactions and heterogeneity, even when all the predictors are continuous.

2.3. A screening procedure

In this section we present a sure independence screening procedure based on the MBKR correlation (MBKR-SIS for short) for ultrahigh-dimensional data. Suppose Y is the response variable and $\mathbf{x} = (X_1, \ldots, X_p)^{\mathrm{T}}$ is the associated predictor vector with large dimension p, and the available sample size n is small. With a sample of size n, we aim to screen out as many unimportant predictors, indexed by $\mathcal{A}^c$, as possible. These are predictors, upon which the response variable Y does not depend when the important predictors $\mathcal{A}$ are given. In mathematical symbols, $Y \perp\!\!\!\perp \mathbf{x}_{\mathcal{A}^c} | \mathbf{x}_{\mathcal{A}}$.

Because the conditional distribution of Y given $\mathbf{x}$ varies with $\mathbf{x}_{\mathcal{A}}$ only, one expects that Y depends on X_k nonlinearly for $k \in \mathcal{A}$. In using the $MBKR(X_k, Y)$ to measure the relation between X_k and Y, one expects $MBKR(X_k, Y)$, for $k \in \mathcal{A}$, to not be small. We spell out this assumption below.

(A1) The important predictors satisfy

$$\min_{k \in \mathcal{A}} MBKR(X_k, Y) \geq 2dn^{-\gamma}, \text{ for some constants } d > 0,\ 0 \leq \gamma < \frac{1}{4}.$$

Similar conditions are widely assumed in the marginal screening literature. See, for example, Condition 3 in Fan and Lv (2008) and Condition (C2) in Li, Zhong and Zhu (2012).

If (A1) holds, we suggest the MBKR-SIS procedure that retains the predictors indexed by

$$\widehat{\mathcal{A}} = \{k : \widehat{MBKR}(X_k, Y) \geq dn^{-\gamma}\ ,\ k = 1, \ldots, p\}. \tag{2.6}$$

Theorem 2. ***(Sure Screening Property)*** *If p satisfies $np\exp(-d_1 n^{1-4\gamma}) \to 0$ for a positive constant d_1, then under (A1), we have*

$$pr\big(\mathcal{A} \subseteq \widehat{\mathcal{A}}\big) \geq 1 - O\left\{n|\mathcal{A}|\exp(-d_1 n^{1-4\gamma})\right\},$$

where $|\mathcal{A}|$ denotes the cardinality of $\mathcal{A}$.

We can characterize the size of the reduced model after screening.

Theorem 3. ***(Minimum Model Size)*** *Under the conditions of Theorem 2, there exists a positive constant d_2, such that,*

$$pr\left\{|\widehat{\mathcal{A}}| \leq O(n^{\gamma}\sum_{k=1}^{p}|MBKR(X_k, Y)|)\right\} \geq 1 - O\left\{np\exp(-d_2 n^{1-4\gamma})\right\}.$$

We further notice that, the relation of conditional independence, that is $Y \perp\!\!\!\perp \mathbf{x}_{\mathcal{A}^c}|\mathbf{x}_{\mathcal{A}}$, indicates that the conditional distribution of Y give $\mathbf{x}_{\mathcal{A}}$ is independent of $\mathbf{x}_{\mathcal{A}^c}$. We expect that Y depends more upon $\mathbf{x}_{\mathcal{A}}$ than upon $\mathbf{x}_{\mathcal{A}^c}$, that $MBKR(X_k, Y)$, for $k \in \mathcal{A}$, is larger than $MBKR(X_k, Y)$, for $k \in \mathcal{A}^c$. This is formulated as follows.

(A2) $\liminf_{p\longrightarrow\infty}\{\min_{k\in\mathcal{A}}\ MBKR(X_k, Y) - \max_{k\in\mathcal{A}^c}\ MBKR(X_k, Y)\} \geq d_3$, where d_3 is a positive constant.

With (A2), we have the ranking consistency property for the MBKR-SIS procedure.

Theorem 4. ***(Rank Consistency Property)*** *Suppose* (A2) *holds in addition to the conditions of Theorem* 2*. Then*

$$\liminf_{n\longrightarrow\infty}\left\{\min_{k\in\mathcal{A}}\widehat{MBKR}(X_k, Y) - \max_{k\in\mathcal{A}^c}\widehat{MBKR}(X_k, Y)\right\} > 0 \textit{ almost surely.}$$

To ensure these sure screening and ranking consistency properties, we do not impose any moment conditions on either $\mathbf{x}$ or Y. We merely use the ranks of the observations to achieve the consistency.

3. Numerical Studies

3.1. Some additional simulations

We conducted some Monte Carlo simulations to evaluate the finite sample performance of our proposed MBKR-SIS method in comparison to such existing screening methods as the SIS (Fan and Lv (2008)), SIRS (Zhu et al. (2011)), Kendall's rank correlation-based sure independent screening procedure (Li et al. (2012), RRCS for short), distance correlation based on SIS (Li, Zhong and Zhu (2012), DC-SIS for short) and the sure independent screening procedure using rank-based distance correlation (Székely and Rizzo (2009), RDC-SIS for short).

Following Li, Zhong and Zhu (2012), we use three criteria to assess their performances.

1. $\mathcal{S}$: The minimum model size to ensure that all important predictors are retained after screening. We report the 5%, 25%, 50%, 75% and 95% quantiles of $\mathcal{S}$ out of 1,000 replications.

2. $\mathcal{P}_a$: The proportion of including all the important predictors for a given model size $[n/\log n] \approx 37$ out of 1,000 replications.

3. $\mathcal{P}_s$: The proportion of including each single important predictor for a given model size $[n/\log n] \approx 37$ out of 1,000 replications.

Example 3. We took sample size $n = 200$ and the predictor dimension $p = 2,000$ throughout. We generated the predictor vector $\mathbf{x} = (X_1, X_2, \cdots, X_p)^{\mathrm{T}}$ from a multivariate t distribution $T(\mathbf{0}, \mathbf{\Sigma}, v)$ with $v = 1$ and $\mathbf{\Sigma} = (\sigma_{kl})_{p\times p}$ for $\sigma_{kl} = 0.9^{|k-l|}$. The error term was independently drawn from a standard Cauchy distribution. We considered five models for generating Y.

$$Y = 0.5X_1 + 0.4X_2 + 0.3X_3 + 0.2X_4 + 0.1X_5 + \varepsilon; \tag{3.1}$$

$$Y = 0.5X_1 + 0.4X_2 + 0.3X_3 + 0.2X_4 + 0.1X_5 + \exp\{3I(X_{20} \le 4)X_{20}\}\varepsilon; \tag{3.2}$$

$$Y = 2X_1X_2 + 2X_{20}X_{21} + \varepsilon; \tag{3.3}$$

$$Y = 2X_1X_2X_3X_4 + 6X_{21}X_{22} + \varepsilon; \tag{3.4}$$

$$Y = 4X_1X_2 + 3X_3^2 + \exp\{5I(X_{20} \le 3)X_{20}\}\varepsilon. \tag{3.5}$$

Model (3.1) is a homoscedastic linear model, and models (3.2)-(3.5) contain either interactions or heterogeneity or both. Note that model (3.4) contains a four-way interaction term. Such complicated interactions are rarely considered in the literature.

Table 2. Simulation results for Example 3. The 5%, 25%, 50%, 75% and 95% quantiles of the minimum model size $\mathcal{S}$ such that all the truly important predictors are retained after screening, out of 1,000 replications.

Model	Quantiles	SIS	SIRS	RRCS	DC-SIS	RDC-SIS	MBKR-SIS
(3.1)	5%	5	5	5	5	5	5
	25%	12	6	5	5	5	5
	50%	155	16	5	10	5	5
	75%	930	137	5	352	5	5
	95%	1,896	1,638	6	1,660	6	6
(3.2)	5%	678	73	26	376	6	6
	25%	1,325	392	187	879	7	6
	50%	1,699	931	603	1,337	9	7
	75%	1,889	1,538	1,282	1,674	12	9
	95%	1,982	1,926	1,822	1,950	17	13
(3.3)	5%	444	625	557	271	5	4
	25%	978	1,252	1,234	744	9	5
	50%	1,458	1,655	1,632	1,201	15	7
	75%	1,791	1,908	1,840	1,627	27	12
	95%	1,959	1,992	1,971	1,923	70	31
(3.4)	5%	547	725	730	477	8	6
	25%	1,129	1,422	1,445	1,012	15	8
	50%	1,569	1,759	1,744	1,467	26	13
	75%	1,831	1,909	1,898	1,775	47	20
	95%	1,971	1,991	1,984	1,964	122	49
(3.5)	5%	423	597	437	206	5	4
	25%	1,020	1,178	1,043	646	9	5
	50%	1,466	1,596	1,533	1,088	16	8
	75%	1,791	1,871	1,817	1,509	30	13
	95%	1,966	1,987	1,967	1,888	83	41

Each experiment was repeated 1,000 times. The simulation results are given in Table 2 for $\mathcal{S}$ and in Table 3 for both $\mathcal{P}_a$ and $\mathcal{P}_s$.

The MBKR-SIS performs the best in most scenarios, followed by the RDC-SIS method. The MBKR-SIS retains all interactions and heterogeneity terms with a high probability. The medians of the minimum model size $\mathcal{S}$ are very close to the number of important predictors across all scenarios, and the interquartiles of the minimum model size $\mathcal{S}$ are also small, indicating that the MBKR ranks the important predictors above the unimportant ones with an overwhelming probability, and the performances of the MBKR-SIS are very stable. In terms of the 95% quantile of the minimum model size $\mathcal{S}$, the RDC-SIS method is slightly worse than it.

The SIS method is designed for homoscedastic linear models. In model (3.1),

Table 3. Simulation results for Example 3. For a given model size $S = [n/\log(n)]$, the proportion $\mathcal{P}_s$ of each single important predictor is retained after screening and the proportion $\mathcal{P}_a$ of all truly important predictors are retained after screening.

Model			SIS	SIRS	RRCS	DC-SIS	RDC-SIS	MBKR-SIS
(3.1)	$\mathcal{P}_s$	X_1	0.738	0.788	1.000	0.879	1.000	1.000
		X_2	0.845	0.825	1.000	0.952	1.000	1.000
		X_3	0.778	0.816	1.000	0.902	1.000	1.000
		X_4	0.640	0.774	1.000	0.809	1.000	1.000
		X_5	0.506	0.727	1.000	0.685	1.000	1.000
	$\mathcal{P}_a$	ALL	0.348	0.607	1.000	0.597	1.000	1.000
(3.2)	$\mathcal{P}_s$	X_1	0.021	0.758	1.000	0.026	1.000	1.000
		X_2	0.011	0.806	1.000	0.024	1.000	1.000
		X_3	0.029	0.778	1.000	0.039	1.000	1.000
		X_4	0.016	0.740	0.999	0.025	1.000	1.000
		X_5	0.021	0.660	0.993	0.022	0.998	0.999
		X_{20}	0.026	0.036	0.077	0.327	1.000	1.000
	$\mathcal{P}_a$	ALL	0.000	0.024	0.077	0.002	0.998	0.999
(3.3)	$\mathcal{P}_s$	X_1	0.068	0.027	0.028	0.104	0.957	0.996
		X_2	0.073	0.023	0.025	0.122	0.955	0.992
		X_{20}	0.060	0.028	0.033	0.095	0.957	0.991
		X_{21}	0.061	0.021	0.038	0.090	0.948	0.987
	$\mathcal{P}_a$	ALL	0.001	0.000	0.000	0.006	0.841	0.969
(3.4)	$\mathcal{P}_s$	X_1	0.089	0.030	0.036	0.089	0.861	0.982
		X_2	0.087	0.030	0.040	0.104	0.918	0.991
		X_3	0.083	0.029	0.046	0.105	0.938	0.998
		X_4	0.079	0.031	0.032	0.097	0.860	0.979
		X_{21}	0.020	0.019	0.021	0.019	0.985	0.979
		X_{22}	0.017	0.026	0.025	0.018	0.983	0.980
	$\mathcal{P}_a$	ALL	0.001	0.000	0.000	0.000	0.676	0.922
(3.5)	$\mathcal{P}_s$	X_1	0.056	0.029	0.039	0.090	0.912	0.962
		X_2	0.056	0.031	0.044	0.091	0.974	0.989
		X_3	0.049	0.029	0.040	0.095	0.988	0.998
		X_{20}	0.015	0.024	0.082	0.145	0.927	0.991
	$\mathcal{P}_a$	ALL	0.000	0.000	0.002	0.008	0.829	0.946

the median of the minimum model size $\mathcal{S}$ is as large as 155 and close to the sample size $n = 200$. The SIS procedure is not very effective in detecting some weak signals, especially when the error distribution is heavily tailed. Given the retained model size $S = [n/\log n]$, the SIS has only a chance of 50.6% of detecting X_5. The SIRS, RRCS and DC-SIS perform satisfactorily in model (3.1) while none of them is capable of detecting either heterogeneity terms or interactions in the other four models. These observations are in line with what we observed from Example 2 The performance of DC-SIS is not satisfactory, partly because the distribution functions of $\mathbf{x}$ and Y are heavily tailed in these examples.

3.2. An application

In this section we illustrate the performance of MBKR-SIS through an empirical analysis of a rat eye microarray expression dataset collected by Scheetz et al. (2006). They experimented on 120 twelve-week-old male rats, obtained 31,042 different probe sets, and conducted genome-wide linkage analysis with 399 genetic markers. The dataset is available at Gene Expression Omnibus `http://www.ncbi.nlm.nih.gov/geo` with GEO accession number GSE5680. To gain insight into genetic variation involved in human eye disease, Scheetz et al. (2006) applied the expression quantitative trait locus (eQTL) mapping method to 18,976 probes that are considered sufficiently expressed and exhibit at least two-fold variation. Following Scheetz et al. (2006) and Huang, Ma and Zhang (2008), our analysis focuses on these 18,976 probes and 399 genetic markers, where genes expression levels are continuous and genetic markers are categorical with 3 classes. Chiang et al. (2006) found that the gene TRIM32 at probe 1389163_at is a critical gene to the Bardet-Biedl syndrome, a genetic human disease concerning the retina. Our goal is to find out which gene expression levels and genetic markers are the most predictive for the expression level of the gene TRIM32. Because the number of predictors is extremely large while the sample size is relatively small, a screening approach ie needed to screen out most of irrelevant genes before an elaborative second-stage analysis. For our analysis, all 18,976 probes were scaled to have zero mean and unit variance.

We implemented the SIS, the SIRS, the DC-SIS, the RDC-SIS, the RRCS, and the MBKR-SIS, on the whole dataset to reduce the dimensionality of the involved genes to $[n/\log(n)] = 25$. We then conducted a second-stage selection based on the retained predictors to obtain a more interpretable model. Following Huang, Horowitz and Wei (2010), we applied the elaborative variable selection by using group SCAD (GS) for a nonparametric additive model. The additive components were approximated by cubic splines. The tuning parameters were selected via generalized cross-validation. To evaluate the performances of different methods, we report the number of probes selected by each method, together with the median of the absolute values of residuals, denoted by "Size" and "MAR", respectively, in the the second and third columns of Table 4.

Our proposed screening procedure followed by group SCAD selection, the MBKR-SIS-GS, appears superior to other methods in terms of MAR. The boxplot and the histogram of gene TRIM32 are given in Figure 2 (A) and (B). The

Table 4. Results for analyzing the rat eye data.

Method	All Data		Test Data	
	Size	MAR	Med. Size	Med. PE
SIS-GS	10	0.0463	8(2.42)	0.2131(0.1128)
SIRS-GS	7	0.0526	7(2.72)	0.1829(0.1008)
RRCS-GS	9	0.0507	7(3.27)	0.1851(0.0991)
DC-SIS-GS	11	0.0425	8(2.72)	0.2095(0.1110)
RDC-SIS-GS	8	0.0530	7(3.35)	0.1854(0.1073)
MBKR-SIS-GS	8	**0.0406**	7(3.29)	**0.1824(0.0981)**

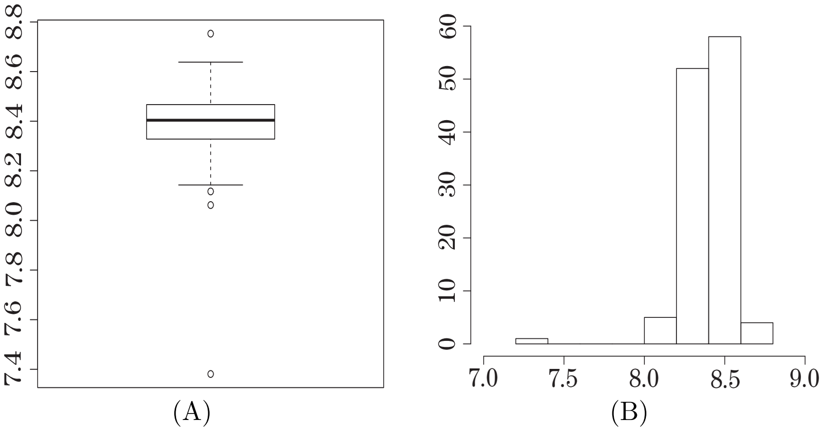


Figure 2. (A) is the boxplot of gene TRIM32 at probe 1389163_at, and (B) is the histogram of gene TRIM32 at probe 1389163_at.

response contains some obvious outliers and its distribution is negative skewed. This may explain the SIS-GS and DC-SIS-GS appear conservative in terms of model size.

We studied the eight genes selected by the MBKR-SIS-GS procedure, at probes 1373534_at, 1372453_at, 1372710_at, 1399134_at, 1393510_at, 1378590_at 1380583_s_at and 1373165_at. Six of them were also detected by DC-SIS-GS while five were identified by RRCS-GS and RDC-SIS-GS, separately. The genes at probes 1399134_at, 1372453_at, 1373534_at, and 1393510_at are also regarded as important ones by SIRS-GS. SIS-GS only selects the two same genes as MBKR-SIS-GS. The gene at probe 1380583_s_at was missed by all other five competitors.

We randomly split the data into a training set of size 100 and a test set of size 20. Subsequent analyses on the training set were identical to our previous analyses on the whole dataset. We selected the tuning parameter for the training set again through generalized cross-validation and evaluated the performance of different methods. We repeat this random partition step 200 times. The median of the model size (Med. Size) selected by each method with its standard deviation is summarized in the fourth column of Table 4. In the fifth column of Table 4, we also report the medians of the absolute values of prediction errors (Med. PE) based on the test data set. Their standard deviations are reported in the parentheses of the fifth column. The smaller the Med. Size and Med. PE are, the better the procedure performs. Our analyses indicate that, compared to the other five methods, our proposed approach selects a relatively small number of genes with smallest prediction errors.

3.3. An iterative procedure

Our simulations found that the MBKR-SIS procedure is effective in retaining the important predictors that satisfy Assumption (A1), but some important predictors may be marginally independent of the response variable and hence have weak signals. To retain these signals in the screening stage, we follow Zhu et al. (2011) and introduce an iterative procedure.

We describe the iterative MBKR-SIS procedure (MBKR-ISIS for short). Let $\mathbf{y} = (Y_1, \ldots, Y_n)^{\mathrm{T}}$ and $\mathbf{X} = (\mathbf{x}_1, \ldots, \mathbf{x}_n)^{\mathrm{T}}$.

1. We apply the MBKR-SIS procedure to the observations $(\mathbf{X}, \mathbf{y})$. Denote by $\mathbf{x}_{\mathcal{A}_1} = \big(X_1^{(1)}, \ldots, X_{p_1}^{(1)}\big)^{\mathrm{T}}$ the predictors selected in this step, where p_1 is a user-specified number. Throughout our simulations, we follow Zhu et al. (2011) and set $p_1 = 5$.
2. Let $\mathbf{X}_1 = (\mathbf{x}_{1,\mathcal{A}_1}, \ldots, \mathbf{x}_{n,\mathcal{A}_1})^{\mathrm{T}}$, $\mathbf{X}_1^c = (\mathbf{x}_{1,\mathcal{A}_1^c}, \ldots, \mathbf{x}_{n,\mathcal{A}_1^c})^{\mathrm{T}}$ and $\mathbf{X}_{\mathrm{new}} = \big\{\mathbf{I}_{n\times n} - \mathbf{X}_1(\mathbf{X}_1^{\mathrm{T}}\mathbf{X}_1)^{-1}\mathbf{X}_1^{\mathrm{T}}\big\}\mathbf{X}_1^c$. Here, $\mathbf{X}_1$ is an $n \times |\mathcal{A}_1|$ matrix and $\mathbf{X}_1^c$ is an $n \times (p - |\mathcal{A}_1|)$ matrix. We apply the MBKR-SIS procedure to $(\mathbf{X}_{\mathrm{new}}, \mathbf{y})$ to select p_2 additional predictors. Denote by $\mathbf{x}_{\mathcal{A}_2} = \big(X_1^{(2)}, \ldots, X_{p_2}^{(2)}\big)^{\mathrm{T}}$ the predictors selected in this step.
3. Update $\mathcal{A}_1$ with $\mathcal{A}_1 \cup \mathcal{A}_2$ and p_1 with $p_1 + p_2$. Repeat the second step until the total number of selected predictors reaches a pre-specified number. The final model selected by MBKR-ISIS is indexed by $\mathcal{A}_1$.

This MBKR-ISIS procedure differs from the ISIS procedure proposed by Fan and Lv (2008). Instead of working with $(\mathbf{X}_{\mathrm{new}}, \mathbf{y})$ in the second step, the ISIS procedure works with $(\mathbf{X}_1^c, \mathbf{y}_{\mathrm{new}})$, where $\mathbf{y}_{\mathrm{new}} = \big\{\mathbf{I}_{n\times n} - \mathbf{X}_1(\mathbf{X}_1^{\mathrm{T}}\mathbf{X}_1)^{-1}\mathbf{X}_1^{\mathrm{T}}\big\}\mathbf{y}$. The ISIS uses Pearson correlation while MBKR-ISIS uses the modified BKR correlation defined in (1.3). The ISIS assumes implicitly that Y depends linearly on $\mathbf{x}$. In the present context, we hope to retain the model-free nature of the MBKR-SIS procedure and hence are reluctant to impose any dependence structure between Y and $\mathbf{x}$. The idea of regressing $\mathbf{X}_1^c$ onto $\mathbf{X}_1$ was first proposed by Zhu et al. (2011) and later elaborated upon by Zhong and Zhu (2015). The merit of this idea is that it does not assume the dependence of Y onto $\mathbf{x}$, though it imposes additional distributional assumptions on $\mathbf{x}$ to ensure its validity.

We demonstrated the performance of our proposed MBKR-ISIS approach through simulations. We compared both the non-iterative and the iterative versions of our MBKR-SIS and SIS (Fan and Lv (2008)). The simulation studies of SIS/ISIS (Fan and Lv (2008)) were conducted by the R packages (Fan, Samworth and Wu (2010)). The sample size n was 200 and the predictor dimension p was 2,000.

Example 4. We considered three models:

$$Y = 5X_1 + 5X_2 + 5X_3 - 15\sqrt{\rho}X_4 + \varepsilon; \tag{3.6}$$

$$Y = I(5X_1 + 5X_2 + 5X_3 - 15\sqrt{\rho}X_4 + \varepsilon > 0); \tag{3.7}$$

$$Y = \exp\left\{(5X_1 + 5X_2 + 5X_3 - 15\sqrt{\rho}X_4)\frac{1}{2} + \varepsilon\right\}. \tag{3.8}$$

Here, the predictors $\mathbf{x} = (X_1, X_2, \cdots, X_p)^{\mathrm{T}}$ were generated as multivariate normal $\mathcal{N}(\mathbf{0}, \mathbf{\Sigma})$, where $\mathbf{\Sigma} = (\sigma_{ij})_{p\times p}$ with $\sigma_{ii} = 1$ for $i = 1, \ldots, p$, $\sigma_{4i} = \sigma_{i4} = \sqrt{\rho}$ for $i = 1, \ldots, p$ and $i \neq 4$, $\sigma_{ij} = \rho$ for $i \neq j$, $j \neq 4$ and $i \neq 4$. We set $\rho = 0.5$. For model (3.6), we generated ε from the standard normal and the standard Cauchy distributions. For model (3.7) and (3.8), we drew ε from a standard normal distribution only. In all three models, the important predictor X_4 is marginally independent of Y. We repeated each experiment 1,000 times.

Table 5 gives the probabilities that each single active predictor and all four truly important predictors rank in the top $[n/\log(n)]$ in 1,000 repetitions. These results indicate that both SIS and MBKR-SIS fail to detect X_4 with high probabilities. The ISIS procedure performs satisfactorily when ε is normal in model (3.6), but its performance deteriorates dramatically if the error distribution is heavily-tailed or if the underlying true model is nonlinear. By contrast, our proposed MBKR-ISIS is robust to heavily tailed distribution and performs effectively with respective $\mathcal{P}_a = 0.992$ and $\mathcal{P}_a = 0.962$ corresponding to two different distributions of error terms in model (3.6), $\mathcal{P}_a = 0.949$ in model (3.7), and $\mathcal{P}_a = 0.989$ in model (3.8).

4. Discussion

In this paper we suggest a modified Blum-Kiefer-Rosenblart correlation to

Table 5. Simulation results for Example 4. For a given model size $S = [n/\log(n)]$, the proportion $\mathcal{P}_s$ of each single important predictor is retained after screening and the proportion $\mathcal{P}_a$ of all truly important predictors are retained after screening.

Model	ε			SIS	ISIS	MBKR-SIS	MBKR-ISIS
(3.6)	$N(0,1)$	$\mathcal{P}_s$	X_1	0.996	1.000	0.994	1.000
			X_2	0.996	1.000	0.997	1.000
			X_3	0.996	1.000	0.995	0.999
			X_4	0.000	1.000	0.000	0.993
		$\mathcal{P}_a$	ALL	0.000	1.000	0.000	0.992
(3.6)	$t(1)$	$\mathcal{P}_s$	X_1	0.491	0.557	0.981	0.996
			X_2	0.462	0.551	0.982	0.993
			X_3	0.494	0.567	0.986	0.999
			X_4	0.000	0.818	0.000	0.974
		$\mathcal{P}_a$	ALL	0.000	0.311	0.000	0.962
(3.7)	$N(0,1)$	$\mathcal{P}_s$	X_1	0.975	0.655	0.981	0.998
			X_2	0.981	0.652	0.980	0.993
			X_3	0.971	0.654	0.978	0.997
			X_4	0.000	0.656	0.000	0.961
		$\mathcal{P}_a$	ALL	0.000	0.648	0.000	0.949
(3.8)	$N(0,1)$	$\mathcal{P}_s$	X_1	0.542	0.641	0.993	0.999
			X_2	0.547	0.636	0.995	1.000
			X_3	0.534	0.660	0.994	1.000
			X_4	0.000	0.863	0.000	0.990
		$\mathcal{P}_a$	ALL	0.000	0.247	0.000	0.989

measure the possibly nonlinear relation between two random variables. Both the original and the modified Blum-Kiefer-Rosenblart correlations are nonnegative and equal zero if and only if two random variables are independent, indicating that they lead to a consistent test of independence. Compared with the original Blum-Kiefer-Rosenblart correlation, the modified correlation appears more useful when some of the predictors are categorical or discrete, while others are continuous. Our limited numerical experience indicates that, if all the predictors are continuous, the modified measure behaves similarly to its original version. We develop a model-free sure independence screening procedure based on a modified Blum-Kiefer-Rosenblatt correlation. Our proposed screening procedure is robust against heavy-tailed distributions, outliers, and extreme values. We also propose an iterative approach to detect the important predictors which are marginally independent of the response. In contrast to existing screening approaches, our proposals are effective in detecting important predictors that influence the response variable nonlinearly. Simulations suggest that our proposed screening approaches are superior to alternative ones in many scenarios. Still, our proposal are not very effective when the underlying true model is not very sparse or contains many weak signals. Research along this line is warranted.

Supplementary Materials

The proofs of Theorems 1-4 are included in the online supplemental materials.

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