

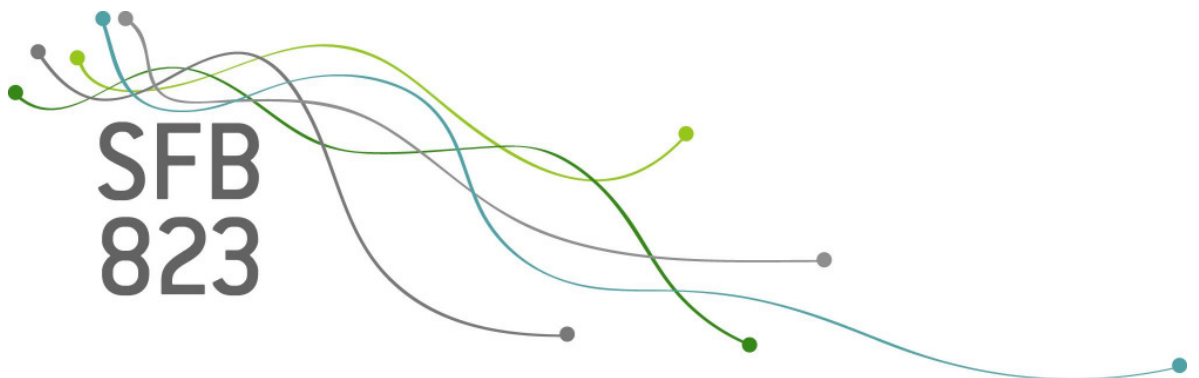
SFB
823

MCD-RoSIS – A robust procedure for variable selection

Charlotte Guddat, Ursula Gather,
Sonja Kuhnt

Nr. 4/2010

Discussion Paper



MCD-RoSIS — A Robust Procedure for Variable Selection

Charlotte Guddat, Ursula Gather and Sonja Kuhnt

Faculty of Statistics, TU Dortmund University, 44221 Dortmund,
Germany

Abstract

Consider the task of estimating a regression function for describing the relationship between a response and a vector of p predictors. Often only a small subset of all given candidate predictors actually effects the response, while the rest might inhibit the analysis. Procedures for variable selection aim to identify the *true* predictors. A method for variable selection when the dimension p of the regressor space is much larger than the sample size n is SIS — Sure Independence Screening — recently proposed by Fan and Lv (2008). The number of predictors is to be reduced to a value less than the number of observations *before* conducting the regression analysis. As SIS is based on nonrobust estimators, outliers in the data might lead to the elimination of true predictors. Hence, Gather and Guddat (2008) propose a *robustified* version of SIS called RoSIS which is based on robust estimators. Here, we give a modification of RoSIS by using the MCD estimator in the new algorithm. The new procedure MCD-RoSIS leads to better results, especially under collinearity. In a simulation study we compare the performance of SIS, RoSIS and MCD-RoSIS w.r.t. their robustness against different types of data contamination as well as different degrees of collinearity.

Keywords: Variable selection, dimension reduction, regression, outliers, robust estimation.

1 Introduction

In the analysis of high dimensional data the curse of dimensionality (Bellman, 1961) is a phenomenon which hinders an accurate modeling of the relation between a response variable $Y \in \mathbb{R}$ and a p -dimensional vector of predictors $\mathbf{X} = (X_1, \dots, X_p)^T \in \mathbb{R}^p$. There are essentially two ways to handle the problem: we either use a regression method that is able to cope with high dimensional data, or we apply a dimension reduction technique that projects the p -dimensional predictor onto a subspace of lower dimension $K \ll p$ followed by a *usual* regression procedure.

For the latter approach, Li (1991) proposed the model

$$Y = f(\mathbf{b}_1 \mathbf{X}, \dots, \mathbf{b}_K \mathbf{X}, \varepsilon), \quad (1.1)$$

where $f : \mathbb{R}^K \rightarrow \mathbb{R}$ is an unknown link function to be estimated from observations $(\mathbf{x}_i^T, y_i)^T$, $i = 1, \dots, n$, and ε is an error term that is independent from \mathbf{X} . The vectors \mathbf{b}_i , $i = 1, \dots, K$, are called effective dimension reduction (edr) directions which span a K -dimensional subspace $\mathcal{S}_{Y|\mathbf{X}}$ assumed to be the central subspace in the sense of Cook (1994, 1996). Under model (1.1) the projection of \mathbf{X} onto $\mathcal{S}_{Y|\mathbf{X}}$ captures all relevant information that is given by the original data.

Commonly, variable selection is conducted simultaneously to the regression analysis — it is part of the *model selection* (Li et al., 2005; Cox, Snell, 1974). Here, we focus on variable selection as a *prestep* to the regression and assume model (1.1). A special case of dimension reduction arises if all edr directions are projections onto one component of \mathbf{X} each. Hence, out of the p predictors at hand only K_{VS} canonical unit vectors $\mathbf{b}_i \in \mathbb{R}^p$, $i = 1, \dots, K_{VS}$, $K_{VS} \ll p$, are classified as being relevant and are solely used in the following regression analysis.

These days, we face a more difficult situation than the one described above more and more often: The sample size n can be much smaller than the dimension p of the regressor space. The accomplishment of this challenge is an important part of current research. Fan and Lv (2008) provide a procedure for variable selection especially for this situation. They can even show that

their method *Sure Independence Screening* (SIS) possesses the *sure screening property*. That is, after the selection of $n - 1$ or $n/\log(n)$ variables by SIS, all true predictors are in the chosen subset with a very high probability when some conditions are fulfilled. For more details see Fan and Lv (2008).

However, SIS is based on nonrobust estimators such that outliers in the data might influence the selection of predictors negatively, i.e. variables with an effect on Y are not extracted or noise variables are selected as being relevant. Hence, Gather and Guddat (2008) provide a robust version of SIS called *RoSIS* — *Robust Sure Independence Screening*. Here, we suggest a further modification which results in the new procedure *MCD-RoSIS* being in many situations even more robust than RoSIS and also working better under collinearity. We show this by a simulation study where we replace observations by outliers in the response as well as in the predictors and vary the sample size and the dimension of the regressor space. Also, we investigate different degrees of collinearity.

The paper is organized as follows. Section 2 provides an introduction into SIS, RoSIS and our new method MCD-RoSIS. In Section 3, we give a description of the design of the simulation study and proceed with our findings and conclusions. Figures with the results of the simulations are found in the appendix.

2 SIS and RoSIS

Sure Independence Screening (SIS; Fan, Lv, 2008) is a procedure for variable selection that is constructed for situations with $p \gg n$. Assuming the linear model, the method is based on the determination of the pairwise covariances of each standardized predictor Z_j , $j = 1, \dots, p$, with the response. Aim is to reduce the number of predictors to a value K_{SIS} which is smaller than the sample size n . Therefore, those variables whose pairwise covariance with Y belong to the absolutely largest, are selected for the following regression analysis.

The empirical version of $Z_j = (X_j - \mu_j)/\sigma_j$ results from the substitution of the expectation μ_j and the variance σ_j^2 of X_j by the corresponding arithmetic

mean \bar{X}_j and the empirical variance s_j^2 , $j = 1, \dots, p$, respectively. For the estimation of the covariance $\text{Cov}(Z_j, Y)$, $j = 1, \dots, p$, the empirical covariance is used. All these estimators are sensible against outliers as we know. Hence, it is possible that outliers lead to an underestimation of the relation between a true predictor and Y or to an overestimation of the relation between a noise variable and Y , respectively. In the case of a strong deviation between true and estimated covariance, the elimination of a true predictor results. To avoid this, Gather and Guddat (2008) introduce a robust version of SIS which is based on a robust standardization of the predictors and a robust estimation of the covariances using the Gnanadesikan-Kettenring estimator (Gnanadesikan, Kettenring, 1972) employing the robust tau-estimate for estimating the univariate scale (Maronna, Zamar, 2002). First comparisons of this new method *Robust Sure Independence Screening* (RoSIS) with SIS have shown promising results (Gather, Guddat, 2008).

However, as the Gnanadesikan-Kettenring estimator is not the best choice under collinearity for example, we suggest a version of RoSIS which employs the Minimum Covariance Determinant (MCD) estimator (Rousseeuw, 1984) coping with this situation much better. We call this version *MCD-RoSIS* and refer to RoSIS in the following as *GK-RoSIS* for a better distinction. After a robust standardization and the estimation of the pairwise covariances by the MCD estimator the resulting values are ordered by their absolute size. Those predictors belonging to the K_{SIS} largest results are selected for the following analysis. The number K_{SIS} is to be chosen smaller than the sample size, e.g. Fan and Lv (2008) suggest $K_{SIS} = n - 1$ or $K_{SIS} = n/\log(n)$.

Definition 2.1 MCD-RoSIS

Let $\{\mathbf{X}_1, \dots, \mathbf{X}_n\}$ be a sample of size n in \mathbb{R}^p , let $\{Y_1, \dots, Y_n\}$ be an associated sample of size n in \mathbb{R} , where $p \gg n$, and $K_{SIS} \in \{1, \dots, n\}$ given. *MCD-RoSIS* selects the variables in the following way:

- (i) Robust standardization of the observations of the predictors by Median und MAD.
- (ii) Robust estimation of the pairwise covariances $\text{Cov}(Z_j, Y)$ by

$\hat{\omega}_{rob,j} = C_{MCD}(\{z_{1,j}, \dots, z_{n,j}\}, \{y_1, \dots, y_n\})$, $j = 1, \dots, p$,
 by means of the MCD estimator.

(iii) Ordering of the estimated values by their absolute size:

$$|\hat{\omega}_{rob,j_1}|_{(1)} \leq |\hat{\omega}_{rob,j_2}|_{(2)} \leq \dots \leq |\hat{\omega}_{rob,j_p}|_{(p)}.$$

(iv) Selection of K_{SIS} variables:

$$\mathcal{U} = \left\{ Z_j : |\omega_{rob,j_{K_S}}|_{(K_S)} \leq |\omega_{rob,j}|, 1 \leq j \leq p \right\}.$$

In the following section we examine to which extent SIS, GK-RoSIS and MCD-RoSIS are robust against large aberrant data points by means of a simulation study and compare the performance of both methods in different situations regarding the dimension p , the sample size n , the types of outliers as well as the degree of collinearity.

3 Comparison of SIS and MCD-RoSIS

In order to examine the effect of outliers on the correct selection of predictors, we simulate different *outlier scenarios*. We look at the effect of outliers in predictor variables and in the response variable while we vary the dimension p , the sample size n as well as the degree of collinearity. The following subsection contains a detailed description of the data generating processes. All simulations are carried out using the free software R (2008).

We will look at three different models. The setup is the same as Fan and Lv (2008) chose for checking the performance of SIS. The n observations of the p predictors X_1, \dots, X_p are generated from a multivariate normal distribution $\mathcal{N}(0, \Sigma)$ with covariance matrix $\Sigma = (\sigma_{ij}) \in \mathbb{R}^{p \times p}$ having the entries $\sigma_{ii} = 1$, $i = 1, \dots, p$, and $\sigma_{ij} = \rho$, $i \neq j$. The observations of ε are drawn from an independent standard normal distribution. The response is assigned according to the model $Y = f(\mathbf{X}) + \varepsilon$ where $f(\mathbf{X})$ is the link function chosen as presented in Model 1 through Model 3.

Model 1: $Y = 5X_1 + 5X_2 + 5X_3 + \varepsilon,$

Model 2: $Y = 5X_1 + 5X_2 + 5X_3 - 15\rho^{1/2}X_4 + \varepsilon,$
 where $\text{Cov}(X_4, X_j) = \rho^{1/2}$, $j = 1, 2, 3, 5, \dots, p$

Model 3: $Y = 5X_1 + 5X_2 + 5X_3 - 15\rho^{1/2}X_4 + X_5 + \varepsilon$
 where $\text{Cov}(X_4, X_j) = \rho^{1/2}$, $j = 1, 2, 3, 5, \dots, p,$
 and $\text{Cov}(X_5, X_j) = 0$, $j = 1, 2, 3, 4, 6, \dots, p.$

The models are taken over from Fan and Lv's (2008) simulations. The link function in Model 1 is linear in three predictors and a noise term. The second testbed function includes a fourth predictor which has correlation $\rho^{1/2}$ with all the other $p - 1$ candidate predictors, but is uncorrelated with the response. Hence, SIS can pick all true predictors only by chance. In the third model a fifth variable is added that is uncorrelated with the other $p - 1$ predictors and that has the same correlation with Y as the noise has. Depending on ρ , X_5 has weaker marginal correlation with Y than X_6, \dots, X_p and hence has a lower priority of being selected by SIS.

We consider a dimension of $p = 100$ and 1000 ; the sample size is set to be $n = 50$ and 70 ; collinearity is varied by $\rho = 0, 0.1, 0.5, 0.9$. The number of repetitions is 200 . We apply SIS, GK-RoSIS and MCD-RoSIS to each generated data set for the selection of $n - 1$ variables.

For contaminating the data generated as described above, we use the concept of α -outliers introduced by Davies and Gather (1993). The level α depends on the sample size n and is given by $\alpha = 1 - (1 - \tilde{\alpha})^{1/n}$ for some $\tilde{\alpha} \in (0, 1)$. Response outliers are generated such that they fall into the α -outlier region of $P_{Y|\mathbf{X}=\mathbf{x}} = \mathcal{N}(f(\mathbf{X}), 1)$. Outliers in \mathbf{X} just fall in the α -outlier region of the predictor distribution $P_{\mathbf{X}} = \mathcal{N}(0, \Sigma)$. Concerning a contamination of \mathbf{X} we distinguish between two different direction. We place outliers in X_1 - or in $X_1 + X_2 + X_3$ -direction which is at least the direction of largest variability for link 1 and a one for large variability for links 2 and 3.

Here, an overview of the data contamination:

- **Positioning** of α -outliers in

Y: Replace y_i by $y_{i,out}$, keep \mathbf{x}_i .

Contamination by

$$y_{i,out} = f(\mathbf{x}) + z_{1-\alpha/2},$$

with $z_{1-\alpha/2}$ being the $(1 - \alpha/2)$ -quantile of the error distribution.

X: Replace \mathbf{x}_i by $\mathbf{x}_{i,out}$, keep y_i .

Contamination in

$$X_1\text{-direction by } \mathbf{x}_{i,out} = (x_{i,1,out}, x_{i,2}, \dots, x_{i,p})$$

with

$$x_{i,1,out} = \sum_{j=2}^p x_{i,j} \sigma_{j1} \pm \sqrt{\chi_{1-\alpha,p}^2 + (\sum_{j=2}^p x_{i,j} \sigma_{j1})^2 - \sum_{j=2}^p \sum_{k=2}^p x_{i,j} \sigma_{jk}}$$

$$(X_1 + X_2 + X_3)\text{-direction by } \mathbf{x}_{i,out} = (x_{i,1,out}, x_{i,2,out}, x_{i,3,out}, x_{i,4}, \dots, x_{i,p})$$

with

$$x_{i,1,out} = x_{i,2,out} = x_{i,3,out}$$

$$= \frac{\sum_{j=4}^p \sum_{k=1}^3 x_{i,j} \sigma_{jk}}{3+2(\sigma_{12}+\sigma_{13}+\sigma_{23})}$$

$$\pm \frac{\sqrt{(\sum_{j=4}^p \sum_{k=1}^3 x_{i,j} \sigma_{jk})^2 - [3+2(\sigma_{12}+\sigma_{13}+\sigma_{23})][\sum_{j=4}^p \sum_{k=4}^p x_{i,j} x_{i,k} \sigma_{jk} - \chi_{1-\alpha,p}^2]}}{3+2(\sigma_{12}+\sigma_{13}+\sigma_{23})}$$

with $\chi_{1-\alpha,p}^2$ being the $(1 - \alpha)$ -quantile of the χ^2 -distribution with p degrees of freedom.

- **Magnitude of outliers** assigned by

$$\alpha = 1 - (1 - \tilde{\alpha})^{1/n} \text{ with } \tilde{\alpha} = 0.001.$$

- **Fraction of outliers**

10%.

As the goal of a method for variable selection is to detect the predictors which have an influence on the response a natural measure of performance is the number of correctly selected as well as the number of falsely selected predictors. As we fix the number of variables to be selected as $K_{SIS} = n - 1$ it is sufficient to look at the number of correctly selected variables.

In the following we will summarize the performance of SIS, GK-RoSIS and MCD-RoSIS when outliers are present based on the results of our simulation study. All results are displayed in detail in tables 1 through 12. They show the percentage of 200 simulations in which one, two, ... (up to the possible number) predictors have been selected correctly. Hence, the more true predictors are revealed in as many cases as possible the better.

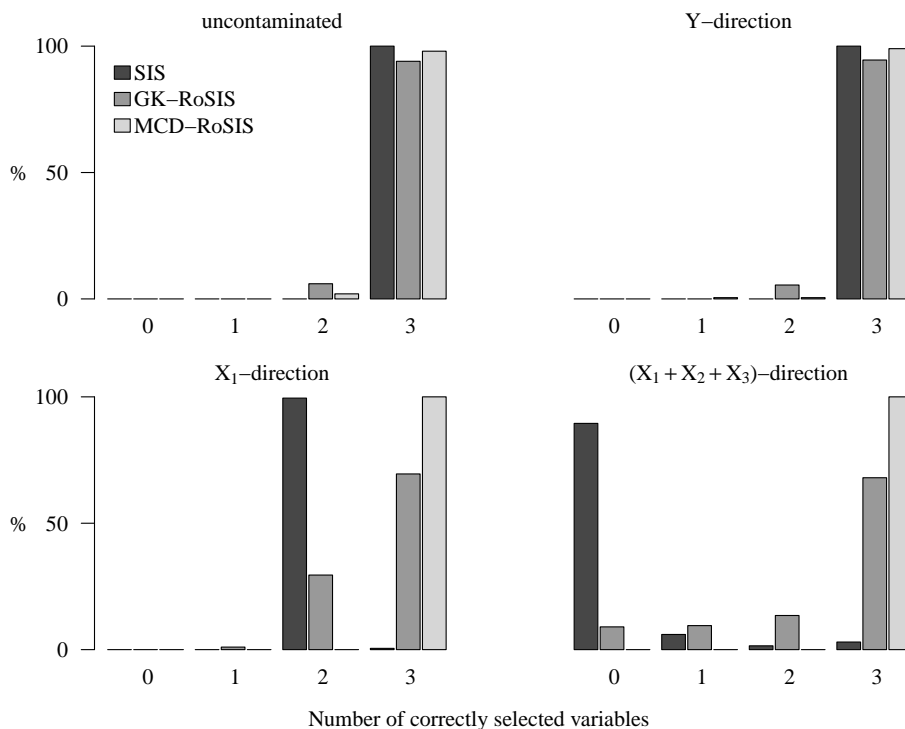


Figure 1: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 1 with $p = 100, n = 70, \rho = 0.5$

Generally, we observe that the new method MCD-RoSIS identifies all true predictors in almost 100% of the cases for all settings when the data are contaminated in one of the \mathbf{X} -directions while the classical procedure SIS fails here very often. Especially, under high collinearity or when the dimension p is large the performance of SIS is very bad. In these situations partly none of the predictors can be identified by SIS in many cases. GK-RoSIS works mostly

better than SIS, but not as good as MCD-RoSIS.

For a description of the comparison of both procedures when the data are uncontaminated or contaminated in Y -direction we have to distinguish between the models. While for Model 1 MCD-RoSIS is only almost as good as SIS, it is generally speaking the better choice for Model 2 and 3. GK-RoSIS is rather on the same level as SIS but suffers strongly from high collinearity. For a better overview, examine Figures 1 and 2. Figure 1 shows the performance

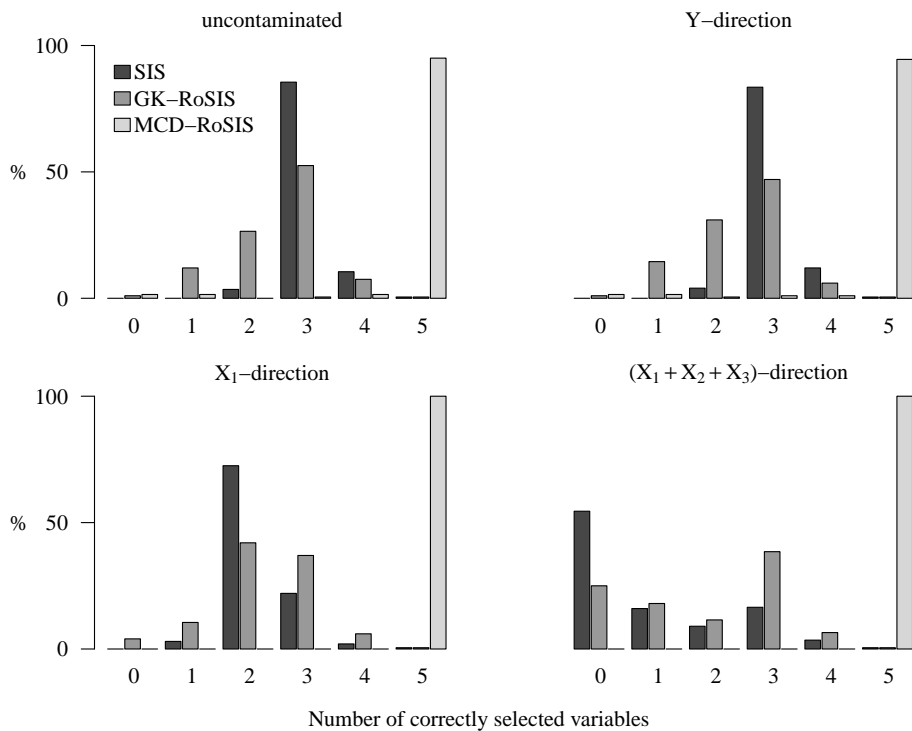


Figure 2: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 3 with $p = 1000, n = 50, \rho = 0.1$

of SIS GK- and MCD-RoSIS for Model 1 with parameters $p = 100, n = 70$ and $\rho = 0.5$. As described before, all three procedures perform similarly good for uncontaminated data and when outliers are given in the response. For the situations with outliers in \mathbf{X} the superiority of MCD-RoSIS is obvious.

In Figure 2 we find the results for Model 3 with parameters $p = 1000, n = 50$ and $\rho = 0.1$. This model includes a predictor that has only a very small corre-

lation with the response. That is why SIS is not able to identify this variable X_5 even when the data are generated from the assumed model. Clearly, MCD-RoSIS finds more true predictors.

We have seen that the MCD-RoSIS and GK-RoSIS are the better procedures for variable selection when outliers in \mathbf{X} are present while MCD-RoSIS is at least a little weaker in the uncontaminated situations but GK-RoSIS suffers from collinearity. We have also observed that MCD-RoSIS is more suitable even for uncontaminated data when true predictors have only a small or no correlation with the response.

At first sight it is a little bit unexpected that the robustified procedures do not perform generally better when there is a contamination in Y -direction. The reason is that the size of α -outliers is dependent on the dimension. As the response is one dimensional, the magnitude of outlying observations in this direction is comparatively small. Hence, the application of robust estimators in the algorithm for variable selection is not beneficial yet. But the superiority of MCD-RoSIS increases along with the magnitude of the outliers.

Altogether, we can conclude that MCD-RoSIS is a very good alternative for the variable selection in high dimensional settings.

4 Summary

We provide a robustified version of Sure Independence Screening (SIS) introduced by Fan and Lv (2008) which is a procedure for variable selection when the number of predictors is much larger than the sample size. Aim is the reduction of the dimension to a value which is smaller than the sample size such that *usual* regression methods are applicable. We modify the algorithm by using robust estimators. To be precise, we employ Median and MAD for standardization as well as the MCD covariance estimator for the identification of the important variables. This leads to the new procedure MCD Robust Sure Independence Screening (MCD-RoSIS).

In a simulation study we compare the performance of the classical procedure SIS and of the robustified versions GK- and MCD-RoSIS in different scenarios. We observe that MCD-RoSIS is the better choice for variable selection under strong contamination of the data. But we can also detect that MCD-RoSIS is at least almost as good as the classical procedure in the uncontaminated situations. GK-RoSIS is in many contaminated situations better than SIS, but it is also very sensible against collinearity. In case of predictors that have only small correlation with the response MCD-RoSIS always finds more often all true predictors even when the data are uncontaminated. Under comparatively small deviations the robustified procedure is not always the better choice. In these situations the behavior corresponds to that in the uncontaminated case. Obviously, as in other data situations the outliers must be of some size such that the use of robust estimators is profitable.

Acknowledgement

This work was partially supported by the German Science Foundation (Deutsche Forschungsgemeinschaft, Sonderforschungsbereich 475, "Reduction of complexity in multivariate data structures", and Sonderforschungsbereich 823, "Statistical modelling of nonlinear dynamic processes").

References

- Bellman, R. E. (1961), *Adaptive Control Processes*, Princeton University Press.
- Cook, R. D. (1994), On the Interpretation of Regression Plots, *J. Amer. Statist. Assoc.*, **89**, 177–189.
- Cook, R. D. (1998), *Regression Graphics: Ideas for Studying Regressions Through Graphics*, Wiley, New York.
- Cox, D. R., Snell, E. J. (1974), The Choice of Variables in Observational Studies, *Appl. Statist.*, **23**, 51–59.

- Davies, P. L., Gather, U. (1993), The Identification of Multiple Outliers (with discussion and rejoinder), *J. Amer. Statist. Assoc.*, **88**, 782–792.
- Fan, J. Q., Lv, J. (2008), Sure Independence Screening for Ultrahigh Dimensional Feature Space (with discussion and rejoinder), *J. Roy. Stat. Soc. B*, **70**, 849–911.
- Gather, U., Guddat, C. (2008), Comment on “Sure Independence Screening for Ultrahigh Dimensional Feature Space” by Fan, J.Q. and Lv, J., *J. Roy. Stat. Soc. B*, **70**, 893–895.
- Gnanadesikan, R., Kettenring, J. (1972), Robust Estimates, Residuals, and Outlier Detection With Multiresponse Data, *Biometrics*, **28**, 81–124.
- Li, K.-C. (1991), Sliced Inverse Regression for Dimension Reduction (with discussion), *J. Amer. Statist. Assoc.*, **86**, 316–342.
- Li, L., Cook, R. D., Nachtshiem, C. J. (2005), Model-free Variable Selection, *J. Roy. Stat. Soc. B*, **67**, 285–299.
- Maronna, R. A., Zamar, R. H. (2002), Robust Estimates of Location and Dispersion for High-dimensional Datasets, *J. Amer. Statist. Assoc.*, **44**, 307–317.
- R Development Core Team (2008), R: A Language and Environment for Statistical Computing, R Foundation for Statistical Computing, Vienna, Austria, ISBN 3-900051-07-0, URL <http://www.R-project.org>.
- Rousseeuw, P. J. (1984), Least Median of Squares Regression, *J. Amer. Statist. Assoc.*, **84**, 871–880.

Appendix

p	n	ρ	method	No. of correctly sel. predictors					
				0	1	2	3		
			uncontaminated						
$p = 100$	$n = 50$	0	SIS	0.000	0.000	0.000	1.000		
			GK-RoSIS	0.000	0.000	0.085	0.915		
			MCD-RoSIS	0.000	0.005	0.010	0.985		
			0.1	SIS	0.000	0.000	0.000	1.000	
				GK-RoSIS	0.000	0.000	0.035	0.965	
				MCD-RoSIS	0.000	0.000	0.000	1.000	
			0.5	SIS	0.000	0.000	0.000	1.000	
				GK-RoSIS	0.000	0.010	0.175	0.815	
				MCD-RoSIS	0.000	0.000	0.005	0.995	
			0.9	SIS	0.000	0.000	0.000	1.000	
				GK-RoSIS	0.070	0.270	0.435	0.225	
				MCD-RoSIS	0.000	0.000	0.015	0.985	
	$n = 70$	0	SIS	0.000	0.000	0.000	1.000		
			GK-RoSIS	0.000	0.000	0.020	0.980		
			MCD-RoSIS	0.000	0.005	0.020	0.975		
			0.1	SIS	0.000	0.000	0.000	1.000	
				GK-RoSIS	0.000	0.000	0.005	0.995	
				MCD-RoSIS	0.000	0.005	0.010	0.985	
		0.5	SIS	0.000	0.000	0.000	1.000		
			GK-RoSIS	0.000	0.000	0.060	0.940		
			MCD-RoSIS	0.000	0.000	0.020	0.980		
		0.9	SIS	0.000	0.000	0.000	1.000		
			GK-RoSIS	0.005	0.070	0.370	0.555		
			MCD-RoSIS	0.000	0.000	0.000	1.000		
$p = 1000$	$n = 50$	0	SIS	0.000	0.000	0.010	0.990		
			GK-RoSIS	0.020	0.130	0.225	0.625		
			MCD-RoSIS	0.025	0.020	0.005	0.950		
				0.1	SIS	0.000	0.000	0.020	0.980
					GK-RoSIS	0.010	0.195	0.300	0.495
					MCD-RoSIS	0.045	0.005	0.005	0.945
			0.5	SIS	0.000	0.005	0.085	0.910	
				GK-RoSIS	0.340	0.380	0.250	0.030	
				MCD-RoSIS	0.030	0.025	0.000	0.945	
			0.9	SIS	0.000	0.005	0.140	0.855	
				GK-RoSIS	0.815	0.165	0.020	0.000	
				MCD-RoSIS	0.020	0.010	0.000	0.970	
	$n = 70$	0	SIS	0.000	0.000	0.005	0.995		
			GK-RoSIS	0.005	0.015	0.140	0.840		
			MCD-RoSIS	0.000	0.015	0.010	0.975		
			0.1	SIS	0.000	0.000	0.005	0.995	
				GK-RoSIS	0.000	0.035	0.165	0.800	
				MCD-RoSIS	0.020	0.025	0.020	0.935	
		0.5	SIS	0.000	0.000	0.000	1.000		
			GK-RoSIS	0.120	0.295	0.435	0.150		
			MCD-RoSIS	0.040	0.025	0.010	0.925		
		0.9	SIS	0.000	0.000	0.025	0.975		
			GK-RoSIS	0.595	0.315	0.080	0.010		
			MCD-RoSIS	0.020	0.025	0.030	0.925		

Table 1: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 1

p	n	ρ	method	No. of correctly sel. predictors			
				0	1	2	3
			Y-direction				
p = 100	n = 50	0	SIS	0.000	0.000	0.000	1.000
			GK-RoSIS	0.000	0.000	0.075	0.925
			MCD-RoSIS	0.000	0.000	0.010	0.990
		0.1	SIS	0.000	0.000	0.000	1.000
			GK-RoSIS	0.000	0.000	0.030	0.970
			MCD-RoSIS	0.000	0.005	0.005	0.990
	0.5	SIS	0.000	0.000	0.000	1.000	
		GK-RoSIS	0.005	0.020	0.155	0.820	
		MCD-RoSIS	0.000	0.000	0.005	0.995	
	0.9	SIS	0.000	0.000	0.000	1.000	
		GK-RoSIS	0.065	0.265	0.425	0.245	
		MCD-RoSIS	0.000	0.000	0.000	1.000	
	n = 70	0	SIS	0.000	0.000	0.000	1.000
			GK-RoSIS	0.000	0.000	0.000	1.000
			MCD-RoSIS	0.000	0.000	0.015	0.985
		0.1	SIS	0.000	0.000	0.000	1.000
			GK-RoSIS	0.000	0.000	0.005	0.995
			MCD-RoSIS	0.000	0.000	0.005	0.995
	0.5	SIS	0.000	0.000	0.000	1.000	
		GK-RoSIS	0.000	0.000	0.055	0.945	
		MCD-RoSIS	0.000	0.005	0.005	0.990	
	0.9	SIS	0.000	0.000	0.000	1.000	
		GK-RoSIS	0.010	0.095	0.365	0.530	
		MCD-RoSIS	0.000	0.000	0.020	0.980	
p = 1000	n = 50	0	SIS	0.000	0.000	0.015	0.985
			GK-RoSIS	0.010	0.115	0.280	0.595
			MCD-RoSIS	0.030	0.030	0.005	0.935
		0.1	SIS	0.000	0.000	0.025	0.975
			GK-RoSIS	0.035	0.160	0.345	0.460
			MCD-RoSIS	0.020	0.020	0.010	0.950
	0.5	SIS	0.000	0.005	0.120	0.875	
		GK-RoSIS	0.355	0.365	0.240	0.040	
		MCD-RoSIS	0.040	0.010	0.025	0.925	
	0.9	SIS	0.000	0.020	0.210	0.770	
		GK-RoSIS	0.790	0.190	0.020	0.000	
		MCD-RoSIS	0.035	0.015	0.000	0.950	
	n = 70	0	SIS	0.000	0.000	0.005	0.995
			GK-RoSIS	0.005	0.030	0.095	0.870
			MCD-RoSIS	0.020	0.025	0.020	0.935
		0.1	SIS	0.000	0.000	0.005	0.995
			GK-RoSIS	0.000	0.015	0.205	0.780
			MCD-RoSIS	0.030	0.015	0.015	0.940
	0.5	SIS	0.000	0.000	0.010	0.990	
		GK-RoSIS	0.115	0.305	0.430	0.150	
		MCD-RoSIS	0.035	0.015	0.020	0.930	
	0.9	SIS	0.000	0.000	0.060	0.940	
		GK-RoSIS	0.615	0.305	0.080	0.000	
		MCD-RoSIS	0.035	0.015	0.005	0.945	

Table 2: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 1

p	n	ρ	method	No. of correctly sel. predictors				
				0	1	2	3	
			X_1 -direction					
$p = 100$	$n = 50$	0	SIS	0.000	0.000	0.235	0.765	
			GK-RoSIS	0.000	0.015	0.195	0.790	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.1	SIS	0.000	0.000	0.385	0.615	
			GK-RoSIS	0.000	0.010	0.170	0.820	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.000	1.000	0.000	
			GK-RoSIS	0.000	0.045	0.405	0.550	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.9	SIS	0.000	0.000	1.000	0.000	
			GK-RoSIS	0.035	0.265	0.430	0.270	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
	$n = 70$	0	SIS	0.000	0.000	0.095	0.905	
				GK-RoSIS	0.000	0.000	0.075	0.925
				MCD-RoSIS	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.195	0.805	
			GK-RoSIS	0.000	0.000	0.080	0.920	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.000	0.995	0.005	
			GK-RoSIS	0.000	0.010	0.295	0.695	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.9	SIS	0.000	0.000	1.000	0.000	
			GK-RoSIS	0.000	0.060	0.390	0.550	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
$p = 1000$	$n = 50$	0	SIS	0.000	0.005	0.865	0.130	
			GK-RoSIS	0.035	0.130	0.365	0.470	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.1	SIS	0.000	0.020	0.950	0.030	
			GK-RoSIS	0.050	0.190	0.435	0.325	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.060	0.940	0.000	
			GK-RoSIS	0.260	0.455	0.235	0.050	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.9	SIS	0.000	0.085	0.915	0.000	
			GK-RoSIS	0.410	0.505	0.075	0.010	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
	$n = 70$	0	SIS	0.000	0.000	0.830	0.170	
				GK-RoSIS	0.005	0.035	0.335	0.625
				MCD-RoSIS	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.950	0.050	
			GK-RoSIS	0.005	0.055	0.355	0.585	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.000	1.000	0.000	
			GK-RoSIS	0.135	0.355	0.360	0.150	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.9	SIS	0.000	0.015	0.985	0.000	
			GK-RoSIS	0.335	0.520	0.130	0.015	
			MCD-RoSIS	0.000	0.000	0.000	1.000	

Table 3: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 1

p	n	ρ	method	No. of correctly sel. predictors				
				0	1	2	3	
			$(X_1 + X_2 + X_3)$ -direction					
$p = 100$	$n = 50$	0	SIS	0.010	0.065	0.085	0.840	
			GK-RoSIS	0.015	0.065	0.150	0.770	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
			0.1	SIS	0.050	0.090	0.110	0.750
				GK-RoSIS	0.015	0.055	0.165	0.765
				MCD-RoSIS	0.000	0.000	0.000	1.000
			0.5	SIS	0.900	0.060	0.025	0.015
				GK-RoSIS	0.240	0.085	0.095	0.580
				MCD-RoSIS	0.000	0.000	0.005	0.995
			0.9	SIS	1.000	0.000	0.000	0.000
				GK-RoSIS	0.130	0.065	0.055	0.750
				MCD-RoSIS	0.000	0.000	0.000	1.000
	$n = 70$	0	SIS	0.000	0.010	0.015	0.975	
			GK-RoSIS	0.000	0.010	0.055	0.935	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
			0.1	SIS	0.010	0.010	0.035	0.945
				GK-RoSIS	0.000	0.020	0.050	0.930
				MCD-RoSIS	0.000	0.000	0.000	1.000
		0.5	SIS	0.895	0.060	0.015	0.030	
			GK-RoSIS	0.090	0.095	0.135	0.680	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.9	SIS	1.000	0.000	0.000	0.000	
			GK-RoSIS	0.050	0.025	0.030	0.895	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
$p = 1000$	$n = 50$	0	SIS	0.590	0.120	0.080	0.210	
			GK-RoSIS	0.245	0.175	0.115	0.465	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
			0.1	SIS	0.790	0.080	0.055	0.075
				GK-RoSIS	0.355	0.165	0.110	0.370
				MCD-RoSIS	0.000	0.000	0.000	1.000
			0.5	SIS	1.000	0.000	0.000	0.000
				GK-RoSIS	0.560	0.085	0.070	0.285
				MCD-RoSIS	0.000	0.000	0.000	1.000
			0.9	SIS	1.000	0.000	0.000	0.000
				GK-RoSIS	0.325	0.060	0.055	0.560
				MCD-RoSIS	0.000	0.000	0.000	1.000
	$n = 70$	0	SIS	0.445	0.150	0.125	0.280	
			GK-RoSIS	0.230	0.080	0.175	0.515	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
			0.1	SIS	0.715	0.125	0.035	0.125
				GK-RoSIS	0.240	0.085	0.135	0.540
				MCD-RoSIS	0.000	0.000	0.000	1.000
		0.5	SIS	1.000	0.000	0.000	0.000	
			GK-RoSIS	0.530	0.100	0.060	0.310	
			MCD-RoSIS	0.000	0.000	0.000	1.000	
		0.9	SIS	1.000	0.000	0.000	0.000	
			GK-RoSIS	0.320	0.050	0.060	0.570	
			MCD-RoSIS	0.000	0.000	0.000	1.000	

Table 4: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 1

p	n	ρ	method	No. of correctly sel. predictors				
				0	1	2	3	4
			uncontaminated					
p = 100	n = 50	0	SIS	0.000	0.000	0.000	0.530	0.470
			GK-RoSIS	0.000	0.000	0.060	0.485	0.455
			MCD-RoSIS	0.000	0.000	0.010	0.015	0.975
		0.1	SIS	0.000	0.000	0.000	0.545	0.455
			GK-RoSIS	0.000	0.000	0.080	0.535	0.385
			MCD-RoSIS	0.000	0.000	0.005	0.005	0.990
		0.5	SIS	0.000	0.010	0.010	0.520	0.460
			GK-RoSIS	0.000	0.010	0.085	0.555	0.350
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.995
		0.9	SIS	0.015	0.185	0.050	0.400	0.350
			GK-RoSIS	0.050	0.180	0.050	0.425	0.295
			MCD-RoSIS	0.000	0.000	0.005	0.010	0.985
	n = 70	0	SIS	0.000	0.000	0.000	0.305	0.695
			GK-RoSIS	0.000	0.000	0.010	0.280	0.710
			MCD-RoSIS	0.000	0.000	0.010	0.015	0.975
		0.1	SIS	0.000	0.000	0.000	0.390	0.610
			GK-RoSIS	0.000	0.000	0.000	0.305	0.695
			MCD-RoSIS	0.000	0.000	0.005	0.010	0.985
		0.5	SIS	0.000	0.000	0.005	0.300	0.695
			GK-RoSIS	0.000	0.005	0.020	0.285	0.690
			MCD-RoSIS	0.000	0.000	0.010	0.030	0.960
		0.9	SIS	0.000	0.140	0.030	0.155	0.675
			GK-RoSIS	0.010	0.185	0.055	0.195	0.555
			MCD-RoSIS	0.000	0.005	0.005	0.015	0.975
p = 1000	n = 50	0	SIS	0.000	0.000	0.010	0.940	0.050
			GK-RoSIS	0.015	0.130	0.230	0.605	0.020
			MCD-RoSIS	0.010	0.035	0.000	0.005	0.950
		0.1	SIS	0.000	0.000	0.035	0.945	0.020
			GK-RoSIS	0.025	0.140	0.280	0.545	0.010
			MCD-RoSIS	0.015	0.025	0.010	0.005	0.945
		0.5	SIS	0.040	0.065	0.100	0.795	0.000
			GK-RoSIS	0.115	0.165	0.280	0.440	0.000
			MCD-RoSIS	0.015	0.005	0.015	0.015	0.950
		0.9	SIS	0.265	0.030	0.065	0.640	0.000
			GK-RoSIS	0.320	0.125	0.170	0.385	0.000
			MCD-RoSIS	0.010	0.010	0.005	0.015	0.960
	n = 70	0	SIS	0.000	0.000	0.005	0.920	0.075
			GK-RoSIS	0.005	0.005	0.150	0.790	0.050
			MCD-RoSIS	0.000	0.010	0.005	0.010	0.975
		0.1	SIS	0.000	0.000	0.000	0.965	0.035
			GK-RoSIS	0.005	0.020	0.140	0.815	0.020
			MCD-RoSIS	0.015	0.035	0.025	0.020	0.905
		0.5	SIS	0.030	0.020	0.090	0.860	0.000
			GK-RoSIS	0.100	0.065	0.225	0.610	0.000
			MCD-RoSIS	0.030	0.025	0.010	0.005	0.930
		0.9	SIS	0.325	0.040	0.045	0.590	0.000
			GK-RoSIS	0.345	0.085	0.095	0.475	0.000
			MCD-RoSIS	0.025	0.025	0.020	0.010	0.920

Table 5: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 2

p	n	ρ	method	No. of correctly sel. predictors					
				0	1	2	3	4	
			Y-direction						
p = 100	n = 50	0	SIS	0.000	0.000	0.000	0.540	0.460	
			GK-RoSIS	0.000	0.000	0.035	0.495	0.470	
			MCD-RoSIS	0.000	0.000	0.005	0.005	0.990	
		0.1	SIS	0.000	0.000	0.000	0.530	0.470	
			GK-RoSIS	0.000	0.000	0.075	0.530	0.395	
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.010	0.015	0.530	0.445	
			GK-RoSIS	0.000	0.025	0.080	0.515	0.380	
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.995	
		0.9	SIS	0.010	0.215	0.045	0.425	0.305	
			GK-RoSIS	0.090	0.160	0.095	0.415	0.240	
			MCD-RoSIS	0.000	0.000	0.015	0.010	0.975	
	n = 70	0	SIS	0.000	0.000	0.000	0.320	0.680	
				GK-RoSIS	0.000	0.000	0.000	0.360	0.640
				MCD-RoSIS	0.000	0.000	0.010	0.005	0.985
		0.1	SIS	0.000	0.000	0.000	0.345	0.655	
			GK-RoSIS	0.000	0.000	0.005	0.300	0.695	
			MCD-RoSIS	0.000	0.000	0.005	0.015	0.980	
		0.5	SIS	0.000	0.005	0.005	0.250	0.740	
			GK-RoSIS	0.000	0.005	0.025	0.270	0.700	
			MCD-RoSIS	0.000	0.000	0.005	0.020	0.975	
		0.9	SIS	0.000	0.175	0.030	0.175	0.620	
			GK-RoSIS	0.005	0.175	0.080	0.215	0.525	
			MCD-RoSIS	0.000	0.005	0.005	0.010	0.980	
p = 1000	n = 50	0	SIS	0.000	0.000	0.015	0.940	0.045	
			GK-RoSIS	0.005	0.120	0.265	0.565	0.045	
			MCD-RoSIS	0.020	0.030	0.010	0.010	0.930	
		0.1	SIS	0.000	0.000	0.040	0.940	0.020	
			GK-RoSIS	0.020	0.135	0.310	0.530	0.005	
			MCD-RoSIS	0.030	0.030	0.015	0.005	0.920	
		0.5	SIS	0.040	0.060	0.100	0.800	0.000	
			GK-RoSIS	0.135	0.215	0.205	0.445	0.000	
			MCD-RoSIS	0.000	0.005	0.005	0.005	0.985	
		0.9	SIS	0.250	0.070	0.065	0.615	0.000	
			GK-RoSIS	0.365	0.135	0.190	0.310	0.000	
			MCD-RoSIS	0.025	0.005	0.010	0.000	0.960	
	n = 70	0	SIS	0.000	0.000	0.005	0.930	0.065	
				GK-RoSIS	0.005	0.025	0.100	0.825	0.045
				MCD-RoSIS	0.015	0.015	0.020	0.015	0.935
		0.1	SIS	0.000	0.000	0.000	0.965	0.035	
			GK-RoSIS	0.005	0.035	0.145	0.785	0.030	
			MCD-RoSIS	0.030	0.015	0.025	0.015	0.915	
		0.5	SIS	0.035	0.030	0.100	0.835	0.000	
			GK-RoSIS	0.110	0.090	0.215	0.585	0.000	
			MCD-RoSIS	0.030	0.015	0.030	0.010	0.915	
		0.9	SIS	0.320	0.045	0.055	0.580	0.000	
			GK-RoSIS	0.370	0.075	0.160	0.395	0.000	
			MCD-RoSIS	0.005	0.040	0.015	0.015	0.925	

Table 6: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 2

p	n	ρ	method	No. of correctly sel. predictors				
				0	1	2	3	4
			X_1 -direction					
p = 100	n = 50	0	SIS	0.000	0.000	0.110	0.545	0.345
			GK-RoSIS	0.000	0.015	0.120	0.460	0.405
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.125	0.535	0.340
			GK-RoSIS	0.000	0.010	0.115	0.540	0.335
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.000	0.010	0.175	0.550	0.265
			GK-RoSIS	0.000	0.025	0.150	0.545	0.280
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.9	SIS	0.015	0.150	0.165	0.545	0.125
			GK-RoSIS	0.045	0.145	0.165	0.355	0.290
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
	n = 70	0	SIS	0.000	0.000	0.035	0.330	0.635
			GK-RoSIS	0.000	0.000	0.030	0.295	0.675
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.055	0.400	0.545
			GK-RoSIS	0.000	0.000	0.010	0.335	0.655
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.000	0.000	0.045	0.435	0.520
			GK-RoSIS	0.000	0.005	0.010	0.360	0.625
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.9	SIS	0.000	0.110	0.080	0.365	0.445
			GK-RoSIS	0.005	0.145	0.115	0.210	0.525
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.990
p = 1000	n = 50	0	SIS	0.000	0.005	0.820	0.170	0.005
			GK-RoSIS	0.035	0.120	0.375	0.450	0.020
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.025	0.820	0.150	0.005
			GK-RoSIS	0.040	0.170	0.365	0.415	0.010
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.060	0.100	0.720	0.120	0.000
			GK-RoSIS	0.095	0.195	0.365	0.345	0.000
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.9	SIS	0.235	0.060	0.490	0.215	0.000
			GK-RoSIS	0.265	0.175	0.215	0.345	0.000
			MCD-RoSIS	0.000	0.010	0.005	0.005	0.980
	n = 70	0	SIS	0.000	0.000	0.755	0.240	0.005
			GK-RoSIS	0.005	0.025	0.330	0.605	0.035
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.780	0.220	0.000
			GK-RoSIS	0.005	0.040	0.355	0.585	0.015
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.035	0.065	0.735	0.165	0.000
			GK-RoSIS	0.050	0.135	0.320	0.495	0.000
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.9	SIS	0.300	0.075	0.425	0.200	0.000
			GK-RoSIS	0.260	0.165	0.180	0.395	0.000
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000

Table 7: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 2

p	n	ρ	method	No. of correctly sel. predictors				
				0	1	2	3	4
			$(X_1 + X_2 + X_3)$ -direction					
p = 100	n = 50	0	SIS	0.010	0.035	0.070	0.490	0.395
			GK-RoSIS	0.015	0.035	0.110	0.455	0.385
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.020	0.025	0.105	0.490	0.360
			GK-RoSIS	0.010	0.080	0.120	0.475	0.315
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.015	0.140	0.125	0.430	0.290
			GK-RoSIS	0.010	0.110	0.135	0.445	0.300
			MCD-RoSIS	0.000	0.000	0.005	0.005	0.990
		0.9	SIS	0.075	0.385	0.050	0.315	0.175
			GK-RoSIS	0.025	0.170	0.175	0.360	0.270
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.995
	n = 70	0	SIS	0.000	0.005	0.010	0.305	0.680
			GK-RoSIS	0.000	0.005	0.025	0.290	0.680
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.020	0.400	0.580
			GK-RoSIS	0.000	0.005	0.025	0.325	0.645
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.005	0.070	0.060	0.310	0.555
			GK-RoSIS	0.000	0.050	0.055	0.290	0.605
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.9	SIS	0.025	0.340	0.045	0.125	0.465
			GK-RoSIS	0.005	0.145	0.085	0.255	0.510
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.990
p = 1000	n = 50	0	SIS	0.560	0.145	0.085	0.195	0.015
			GK-RoSIS	0.245	0.175	0.115	0.435	0.030
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.600	0.115	0.080	0.200	0.005
			GK-RoSIS	0.270	0.150	0.155	0.415	0.010
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.685	0.050	0.095	0.170	0.000
			GK-RoSIS	0.350	0.120	0.145	0.385	0.000
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.9	SIS	0.690	0.020	0.015	0.275	0.000
			GK-RoSIS	0.390	0.120	0.170	0.320	0.000
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.990
	n = 70	0	SIS	0.395	0.190	0.125	0.280	0.010
			GK-RoSIS	0.210	0.095	0.170	0.500	0.025
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.475	0.150	0.115	0.260	0.000
			GK-RoSIS	0.240	0.110	0.150	0.490	0.010
			MCD-RoSIS	0.000	0.000	0.000	0.000	1.000
		0.5	SIS	0.645	0.065	0.070	0.220	0.000
			GK-RoSIS	0.255	0.155	0.135	0.455	0.000
			MCD-RoSIS	0.005	0.000	0.000	0.000	0.995
		0.9	SIS	0.700	0.030	0.035	0.235	0.000
			GK-RoSIS	0.360	0.160	0.100	0.380	0.000
			MCD-RoSIS	0.005	0.005	0.000	0.005	0.985

Table 8: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 2

p	n	ρ	method	No. of correctly sel. predictors						
				0	1	2	3	4	5	
			uncontaminated							
p = 100	n = 50	0	SIS	0.000	0.000	0.000	0.195	0.545	0.260	
			GK-RoSIS	0.000	0.000	0.005	0.245	0.515	0.235	
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.005	0.985	
		0.1	SIS	0.000	0.000	0.000	0.210	0.480	0.310	
			GK-RoSIS	0.000	0.000	0.015	0.245	0.495	0.245	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.010	0.990	
		0.5	SIS	0.000	0.005	0.005	0.140	0.580	0.270	
			GK-RoSIS	0.000	0.005	0.045	0.195	0.515	0.240	
			MCD-RoSIS	0.000	0.000	0.010	0.000	0.015	0.975	
		0.9	SIS	0.005	0.025	0.190	0.080	0.470	0.230	
			GK-RoSIS	0.010	0.070	0.170	0.085	0.475	0.190	
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.000	0.990	
	n = 70	0	SIS	0.000	0.000	0.000	0.050	0.360	0.590	
				GK-RoSIS	0.000	0.000	0.000	0.075	0.430	0.495
				MCD-RoSIS	0.000	0.000	0.000	0.005	0.010	0.985
		0.1	SIS	0.000	0.000	0.000	0.075	0.380	0.545	
			GK-RoSIS	0.000	0.000	0.000	0.055	0.345	0.600	
			MCD-RoSIS	0.000	0.000	0.005	0.015	0.015	0.965	
		0.5	SIS	0.000	0.000	0.000	0.040	0.360	0.600	
			GK-RoSIS	0.000	0.000	0.010	0.075	0.360	0.555	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.020	0.980	
		0.9	SIS	0.000	0.010	0.125	0.030	0.220	0.615	
			GK-RoSIS	0.000	0.035	0.140	0.045	0.270	0.510	
			MCD-RoSIS	0.000	0.000	0.000	0.015	0.025	0.960	
p = 1000	n = 50	0	SIS	0.000	0.000	0.015	0.830	0.150	0.005	
			GK-RoSIS	0.015	0.100	0.260	0.545	0.080	0.000	
			MCD-RoSIS	0.020	0.010	0.005	0.000	0.010	0.955	
		0.1	SIS	0.000	0.000	0.035	0.855	0.105	0.005	
			GK-RoSIS	0.010	0.120	0.265	0.525	0.075	0.005	
			MCD-RoSIS	0.015	0.015	0.000	0.005	0.015	0.950	
		0.5	SIS	0.035	0.050	0.100	0.615	0.200	0.000	
			GK-RoSIS	0.100	0.170	0.240	0.385	0.105	0.000	
			MCD-RoSIS	0.035	0.000	0.005	0.005	0.010	0.945	
		0.9	SIS	0.080	0.210	0.055	0.130	0.525	0.000	
			GK-RoSIS	0.145	0.225	0.145	0.270	0.215	0.000	
			MCD-RoSIS	0.020	0.015	0.005	0.015	0.010	0.935	
	n = 70	0	SIS	0.000	0.000	0.005	0.730	0.250	0.015	
				GK-RoSIS	0.000	0.010	0.110	0.695	0.175	0.010
				MCD-RoSIS	0.015	0.030	0.005	0.010	0.020	0.920
		0.1	SIS	0.000	0.000	0.000	0.740	0.250	0.010	
			GK-RoSIS	0.000	0.045	0.130	0.700	0.120	0.005	
			MCD-RoSIS	0.045	0.000	0.020	0.000	0.010	0.925	
		0.5	SIS	0.025	0.020	0.095	0.550	0.310	0.000	
			GK-RoSIS	0.050	0.095	0.210	0.500	0.145	0.000	
			MCD-RoSIS	0.025	0.020	0.000	0.010	0.025	0.920	
		0.9	SIS	0.045	0.275	0.060	0.095	0.525	0.000	
			GK-RoSIS	0.130	0.270	0.075	0.155	0.370	0.000	
			MCD-RoSIS	0.030	0.030	0.010	0.025	0.020	0.885	

Table 9: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 3

p	n	ρ	method	No. of correctly sel. predictors						
				0	1	2	3	4	5	
			Y-direction							
p = 100	n = 50	0	SIS	0.000	0.000	0.000	0.195	0.530	0.275	
			GK-RoSIS	0.000	0.000	0.020	0.220	0.515	0.245	
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.000	0.990	
		0.1	SIS	0.000	0.000	0.000	0.200	0.445	0.355	
			GK-RoSIS	0.000	0.000	0.020	0.230	0.490	0.260	
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.000	0.995	
		0.5	SIS	0.000	0.005	0.015	0.135	0.545	0.300	
			GK-RoSIS	0.000	0.025	0.050	0.180	0.570	0.175	
			MCD-RoSIS	0.000	0.000	0.005	0.015	0.010	0.970	
		0.9	SIS	0.000	0.050	0.200	0.045	0.495	0.210	
			GK-RoSIS	0.020	0.110	0.135	0.115	0.455	0.165	
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.015	0.980	
	n = 70	0	SIS	0.000	0.000	0.000	0.035	0.390	0.575	
				GK-RoSIS	0.000	0.000	0.000	0.075	0.425	0.500
				MCD-RoSIS	0.000	0.000	0.000	0.005	0.020	0.975
		0.1	SIS	0.000	0.000	0.000	0.075	0.345	0.580	
			GK-RoSIS	0.000	0.000	0.000	0.050	0.400	0.550	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.015	0.985	
		0.5	SIS	0.000	0.000	0.005	0.040	0.345	0.610	
			GK-RoSIS	0.000	0.000	0.010	0.040	0.440	0.510	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.015	0.985	
		0.9	SIS	0.000	0.020	0.155	0.040	0.185	0.600	
			GK-RoSIS	0.000	0.045	0.175	0.060	0.250	0.470	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.035	0.965	
p = 1000	n = 50	0	SIS	0.000	0.000	0.025	0.825	0.145	0.005	
			GK-RoSIS	0.005	0.115	0.295	0.500	0.085	0.000	
			MCD-RoSIS	0.005	0.010	0.005	0.005	0.020	0.955	
		0.1	SIS	0.000	0.000	0.040	0.835	0.120	0.005	
			GK-RoSIS	0.010	0.145	0.310	0.470	0.060	0.005	
			MCD-RoSIS	0.015	0.015	0.005	0.010	0.010	0.945	
		0.5	SIS	0.030	0.055	0.110	0.575	0.230	0.000	
			GK-RoSIS	0.110	0.205	0.210	0.395	0.080	0.000	
			MCD-RoSIS	0.010	0.025	0.010	0.000	0.010	0.945	
		0.9	SIS	0.110	0.170	0.050	0.185	0.485	0.000	
			GK-RoSIS	0.195	0.215	0.190	0.260	0.140	0.000	
			MCD-RoSIS	0.030	0.005	0.025	0.005	0.005	0.930	
	n = 70	0	SIS	0.000	0.000	0.005	0.725	0.255	0.015	
				GK-RoSIS	0.005	0.015	0.085	0.730	0.160	0.005
				MCD-RoSIS	0.015	0.020	0.025	0.005	0.010	0.925
		0.1	SIS	0.000	0.000	0.000	0.760	0.230	0.010	
			GK-RoSIS	0.005	0.035	0.140	0.690	0.130	0.000	
			MCD-RoSIS	0.010	0.035	0.010	0.000	0.020	0.925	
		0.5	SIS	0.025	0.030	0.110	0.515	0.320	0.000	
			GK-RoSIS	0.075	0.120	0.180	0.465	0.160	0.000	
			MCD-RoSIS	0.020	0.010	0.020	0.015	0.035	0.900	
		0.9	SIS	0.050	0.255	0.045	0.095	0.555	0.000	
			GK-RoSIS	0.100	0.300	0.100	0.205	0.295	0.000	
			MCD-RoSIS	0.025	0.020	0.005	0.010	0.025	0.915	

Table 10: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 3

p	n	ρ	method	No. of correctly sel. predictors						
				0	1	2	3	4	5	
			X_1 -direction							
p = 100	n = 50	0	SIS	0.000	0.000	0.035	0.290	0.495	0.180	
			GK-RoSIS	0.000	0.000	0.030	0.305	0.445	0.220	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.1	SIS	0.000	0.000	0.035	0.315	0.430	0.220	
			GK-RoSIS	0.000	0.000	0.055	0.300	0.420	0.225	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.005	0.015	0.335	0.480	0.165	
			GK-RoSIS	0.000	0.020	0.050	0.245	0.505	0.180	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.9	SIS	0.000	0.030	0.145	0.245	0.465	0.115	
			GK-RoSIS	0.005	0.050	0.140	0.185	0.455	0.165	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
	n = 70	0	SIS	0.000	0.000	0.010	0.070	0.385	0.535	
				GK-RoSIS	0.000	0.000	0.010	0.085	0.425	0.480
				MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.015	0.090	0.415	0.480	
			GK-RoSIS	0.000	0.000	0.000	0.075	0.355	0.570	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.000	0.000	0.015	0.100	0.415	0.470	
			GK-RoSIS	0.000	0.000	0.005	0.105	0.385	0.505	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.9	SIS	0.000	0.010	0.100	0.125	0.380	0.385	
			GK-RoSIS	0.000	0.035	0.110	0.080	0.285	0.490	
			MCD-RoSIS	0.000	0.000	0.000	0.010	0.005	0.985	
p = 1000	n = 50	0	SIS	0.000	0.010	0.735	0.215	0.040	0.000	
			GK-RoSIS	0.050	0.075	0.430	0.385	0.060	0.000	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.1	SIS	0.000	0.030	0.725	0.220	0.020	0.005	
			GK-RoSIS	0.040	0.105	0.420	0.370	0.060	0.005	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.040	0.120	0.500	0.290	0.050	0.000	
			GK-RoSIS	0.090	0.170	0.330	0.335	0.075	0.000	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.9	SIS	0.070	0.210	0.120	0.450	0.150	0.000	
			GK-RoSIS	0.120	0.230	0.190	0.285	0.175	0.000	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
	n = 70	0	SIS	0.000	0.000	0.585	0.370	0.045	0.000	
				GK-RoSIS	0.000	0.020	0.290	0.575	0.105	0.010
				MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.585	0.370	0.045	0.000	
			GK-RoSIS	0.000	0.055	0.315	0.540	0.085	0.005	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.025	0.075	0.475	0.370	0.055	0.000	
			GK-RoSIS	0.040	0.110	0.310	0.425	0.115	0.000	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.9	SIS	0.045	0.240	0.150	0.370	0.195	0.000	
			GK-RoSIS	0.095	0.240	0.130	0.220	0.315	0.000	
			MCD-RoSIS	0.010	0.000	0.000	0.000	0.005	0.985	

Table 11: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 3

p	n	ρ	method	No. of correctly sel. predictors						
				0	1	2	3	4	5	
			$(X_1 + X_2 + X_3)$ -direction							
p = 100	n = 50	0	SIS	0.010	0.020	0.035	0.240	0.485	0.210	
			GK-RoSIS	0.005	0.030	0.060	0.270	0.425	0.210	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.1	SIS	0.005	0.025	0.055	0.235	0.445	0.235	
			GK-RoSIS	0.010	0.010	0.085	0.240	0.445	0.210	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.005	0.995	
		0.5	SIS	0.000	0.060	0.115	0.235	0.410	0.180	
			GK-RoSIS	0.005	0.030	0.135	0.215	0.430	0.185	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.005	0.995	
		0.9	SIS	0.000	0.110	0.305	0.090	0.320	0.175	
			GK-RoSIS	0.005	0.060	0.125	0.220	0.430	0.160	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.005	0.995	
	n = 70	0	SIS	0.000	0.000	0.005	0.060	0.355	0.580	
				GK-RoSIS	0.000	0.005	0.010	0.075	0.445	0.465
				MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.000	0.000	0.000	0.095	0.370	0.535	
			GK-RoSIS	0.000	0.000	0.000	0.075	0.365	0.560	
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.000	0.995	
		0.5	SIS	0.000	0.035	0.060	0.070	0.325	0.510	
			GK-RoSIS	0.000	0.010	0.040	0.110	0.350	0.490	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.005	0.995	
		0.9	SIS	0.000	0.020	0.345	0.055	0.155	0.425	
			GK-RoSIS	0.000	0.030	0.095	0.125	0.240	0.510	
			MCD-RoSIS	0.000	0.000	0.000	0.005	0.015	0.980	
p = 1000	n = 50	0	SIS	0.495	0.200	0.080	0.175	0.050	0.000	
			GK-RoSIS	0.205	0.190	0.160	0.380	0.065	0.000	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.1	SIS	0.545	0.160	0.090	0.165	0.035	0.005	
			GK-RoSIS	0.250	0.180	0.115	0.385	0.065	0.005	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.535	0.215	0.040	0.150	0.060	0.000	
			GK-RoSIS	0.230	0.210	0.120	0.340	0.100	0.000	
			MCD-RoSIS	0.000	0.000	0.005	0.000	0.000	0.995	
		0.9	SIS	0.125	0.585	0.025	0.040	0.225	0.000	
			GK-RoSIS	0.135	0.295	0.175	0.195	0.200	0.000	
			MCD-RoSIS	0.005	0.005	0.000	0.000	0.000	0.990	
	n = 70	0	SIS	0.290	0.260	0.160	0.240	0.050	0.000	
				GK-RoSIS	0.150	0.130	0.170	0.465	0.070	0.015
				MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000
		0.1	SIS	0.345	0.280	0.095	0.235	0.045	0.000	
			GK-RoSIS	0.170	0.150	0.150	0.450	0.075	0.005	
			MCD-RoSIS	0.000	0.000	0.000	0.000	0.000	1.000	
		0.5	SIS	0.410	0.275	0.060	0.200	0.055	0.000	
			GK-RoSIS	0.210	0.185	0.130	0.380	0.095	0.000	
			MCD-RoSIS	0.005	0.000	0.000	0.000	0.000	0.995	
		0.9	SIS	0.075	0.625	0.030	0.045	0.225	0.000	
			GK-RoSIS	0.060	0.330	0.130	0.175	0.305	0.000	
			MCD-RoSIS	0.015	0.000	0.000	0.000	0.010	0.975	

Table 12: Comparison of SIS, GK-RoSIS and MCD-RoSIS in Model 3

