

# Representative approach for big data dimension reduction with binary responses

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# Sufficient dimension reduction

## Fundamental assumption

Let random vector  $X \in \mathbb{R}^{p \times 1}$ ,  $Y \in \mathbb{R}$ ,  $B = (b_1, \dots, b_d) \in \mathbb{R}^{p \times d}$ , where  $d \ll p$  and  $A \in \mathbb{R}^{d \times d}$  is a non-singular matrix.

$$Y|X \stackrel{d}{=} Y|B^T X$$

$$Y \perp\!\!\!\perp X|B^T X \Rightarrow Y \perp\!\!\!\perp X|(BA)^T X,$$

So  $B$  is not identifiable, but  $\text{span}(B)$  is identifiable.

# Sufficient dimension reduction

## Dimension-reduction subspace (DRS)

$$Y \perp\!\!\!\perp X | P_S X, \quad P_S = B(B^T B)^{-1} B^T$$

$\mathcal{S}$  is called the dimension-reduction subspace.

However,  $\mathcal{S}$  is not unique. Actually if  $\mathcal{S} \subset \mathcal{S}_1$ , then  $\mathcal{S}_1$  is also a dimension-reduction space.

## Target: Central Subspace

$$S_{Y|X} = \cap S_{DRS}$$

Under mild conditions,  $S_{Y|X}$  is unique and a DRS subspace itself (Cook, 1996).

# Estimating the central subspace

## Inverse regression: Condition $X$ on $Y$

To Estimate a linear subspace  $\Rightarrow$  a Basis  $B$  of  $S_{Y|X}$   
Sliced Inverse Regression (SIR) (Li 1991)

$$E(X|Y) - E(X) \in \Sigma_X S_{Y|X} \Rightarrow \hat{B} = (\hat{b}_1, \dots, \hat{b}_d)$$

Sliced Average Variance Estimation (SAVE) (Cook et al. 1991)

$$\text{span}(\Sigma_X - \Sigma_{X|\tilde{Y}}) \subseteq S_{Y|X} \Rightarrow \hat{B} = (\hat{b}_1, \dots, \hat{b}_d)$$

# Slicing method

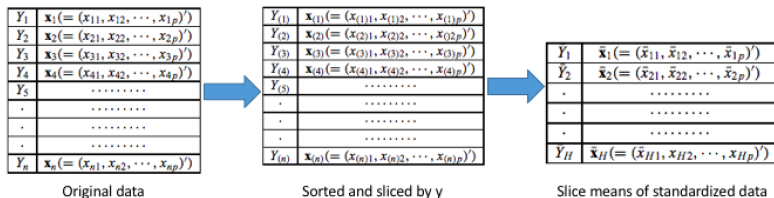


Figure 1:

- 1 Sort the data based on the response values.
- 2 Split data into the slices based on the sorted responses.

# Binary response

Binary response only has two levels, e.g. 0, 1.

## Limited number of slices

- Only two slices are available
- For SIR, it can only find one direction at most
- For SAVE, it also suffers from the limit number of slices

# Probability Enhanced (PRE) method (Shin et al. 2014)

## Main idea

- $S_{Y|X} = S_{P(X)}$ ,  $P(x) = \mathcal{P}(Y = 1|X = x)$  is the conditional probability
- $Y \Rightarrow P(X) \in [0, 1]$
- Weighted Support Vector Machine(WSVM) to estimate the  $\hat{P}(X)$

## Computational time

- SVM method is sensitive to the number of observation N



# Representative approach

## Representative

A Representative is a summary statistic of data points within a cluster: For  $(X_i, Y_i), i \in I_k$  and  $n_k$  is sample size of  $I_k$

$$X_k^* = R(X_1, \dots, X_{n_k}) = \frac{\sum_i X_i}{n_k}, \quad Y_k^* = R(Y_1, \dots, Y_{n_k}) = \frac{\sum_i Y_i}{n_k},$$

where  $R$  is the summarizing function.

## Steps

- 1 Cluster  $(X_1, \dots, X_N)$  into  $K$  groups  $I_1, \dots, I_K$ , e.g. K-means
- 2 Calculate the representatives for each cluster  $I_k$
- 3 Apply dimension reduction methods on the  $K$  representatives

# Additional value: Big data solution ( $N$ is large)

## Clustering step

Clustering step reduced the sample size from  $N$  to  $K$ .

- $(Y_1, X_1) \dots (Y_N, X_N) \rightarrow (Y_1^*, X_1^*) \dots (Y_K^*, X_K^*)$
- Note if the data set is too large, we could also use the online clustering method.

# Additional value: Big data solution (N is large)

## Parallel Algorithm for SIR and SAVE

- 1 Split the sliced data into  $b$  blocks,  $X_1, \dots, X_B$
- 2 Load each block  $X_b$  and calculate the statistics for each block such as  $\bar{X}_b, \bar{X}_{hb}, n_{hb}, X_{hb}^T X_{hb}$
- 3 Summary the statistics across the blocks and slices to get the candidate matrix  $M_{SIR}, M_{SAVE}$

# Simulation setup

## Data generation model: Latent model

$$Y = \begin{cases} 0 & f(b_1^T X, b_2^T X, b_3^T X, \epsilon) < 0 \\ 1 & \text{Otherwise} \end{cases}$$

where

- $X \in \mathbb{R}^6 \sim N(\mathbf{0}, \mathbf{I})$
- $b_i = e_i = (0, \dots, 1, 0, \dots, 0)^T$ , so  
 $b_1^T X = X_1, b_2^T X = X_2, b_3^T X = X_3$
- $\epsilon \sim N(0, 1)$

# Simulation result

## Performance evaluation

- 1 The number of directions of the central space: Hypothesis Test
- 2 Difference between a true bias  $B$  and an estimated  $\hat{B}$ :
  - Trace correlation and Frobenius distance

## Result summary

- The true basis is  $(e_1, e_2, e_3)$ .
- The proposed method is able to recover the whole true central space.
- Other methods can only find part of the central space.

# Simulation result of SAVE

Table 1: Simulation result of SAVE

		Original SAVE				Proposed SAVE			
		log n							
	$H_0$ vs $H_1$	3	4	5	6	3	4	5	6
Power	0D vs $\geq$ 1D	0.9	1	1	1	0	0.05	<b>1</b>	<b>1</b>
	1D vs $\geq$ 2D	0.08	0.52	0.52	0.5	0	0	<b>1</b>	<b>1</b>
	2D vs $\geq$ 3D	0	0.05	0.06	0.06	0	0	0.05	<b>1</b>
Type-I	3D vs $\geq$ 4D	0	0	0	0.01	0	0	0	0.01
	4D vs $\geq$ 5D	0	0	0	0	0	0	0	0
	5D vs $\geq$ 6D	0	0	0	0	0	0	0	0
Distance	F	1.33	1.2	1.21	1.19	1.71	1.03	<b>0.23</b>	<b>0.07</b>
	R	0.17	0.14	0.14	0.13	0.29	0.1	<b>0.01</b>	<b>0</b>

# Conclusion and Future work

## Conclusion

- Better recover the central space in binary responses
- Greatly shorten the running time in big data

## Future work

- Investigate optimal the choice of  $k$  to achieve the best performance of SDR methods.

# Reference

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