SLLD - Module 2

Feature Screening

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Libraries

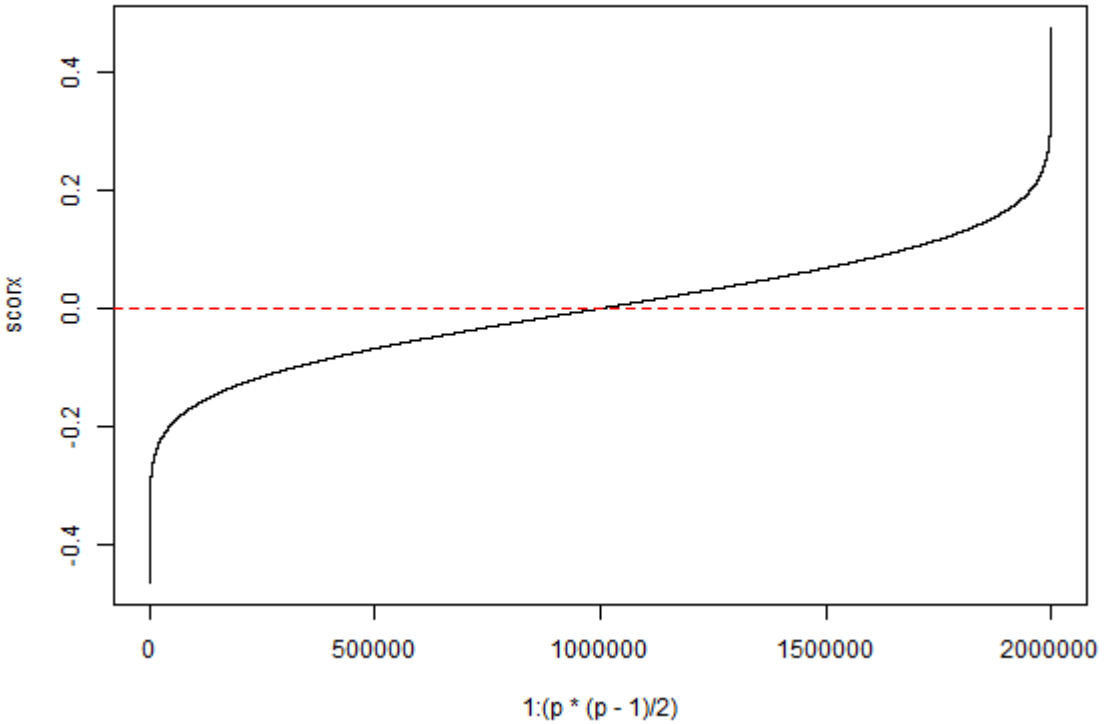
```
if(!require(SIS)){install.packages("SIS", dep=T); library(SIS)}
library(glmnet) # elastic net for GLMs
library(mvtnorm) # to generate multivariate normal distributions
library(corrplot) # correlation plot
```

Data: “Ideal” scenario

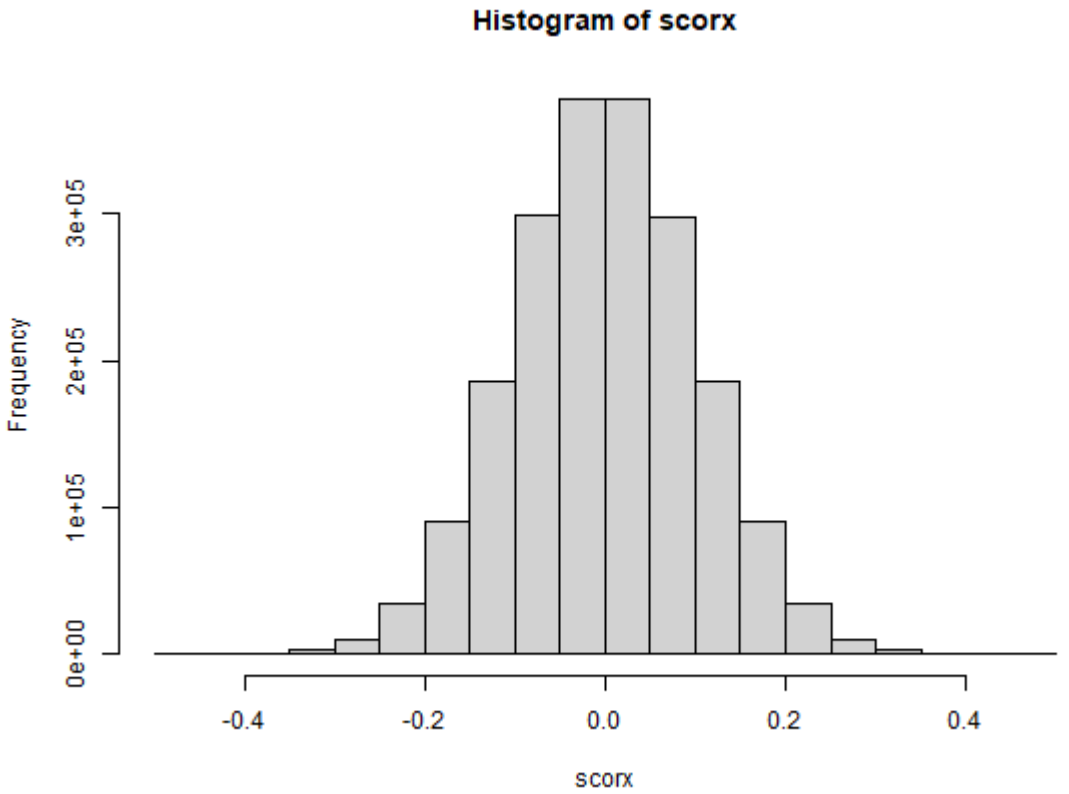
Let’s generate some data with strong signals and low collinearity:

```
set.seed(1)
n <- 100 # obs
p <- 2000 # predictors
pnot <- 5 # relevant predictors
SNR <- 3 # => R^2 approx 0.8
b <- rep(0, p)
b[1:pnot] <- 0.5
mu <- rep(0, p) # create a random matrix X (mean zero and
# uncorrelated predictors with unit variance)
sigma <- diag(p)
X <- rmvnorm(n, mu, sigma)
# strongest (spurious) correlations
corx <- cor(X)
corxtri <- corx[upper.tri(cor(X))]
scorx <- sort(corxtri)
```

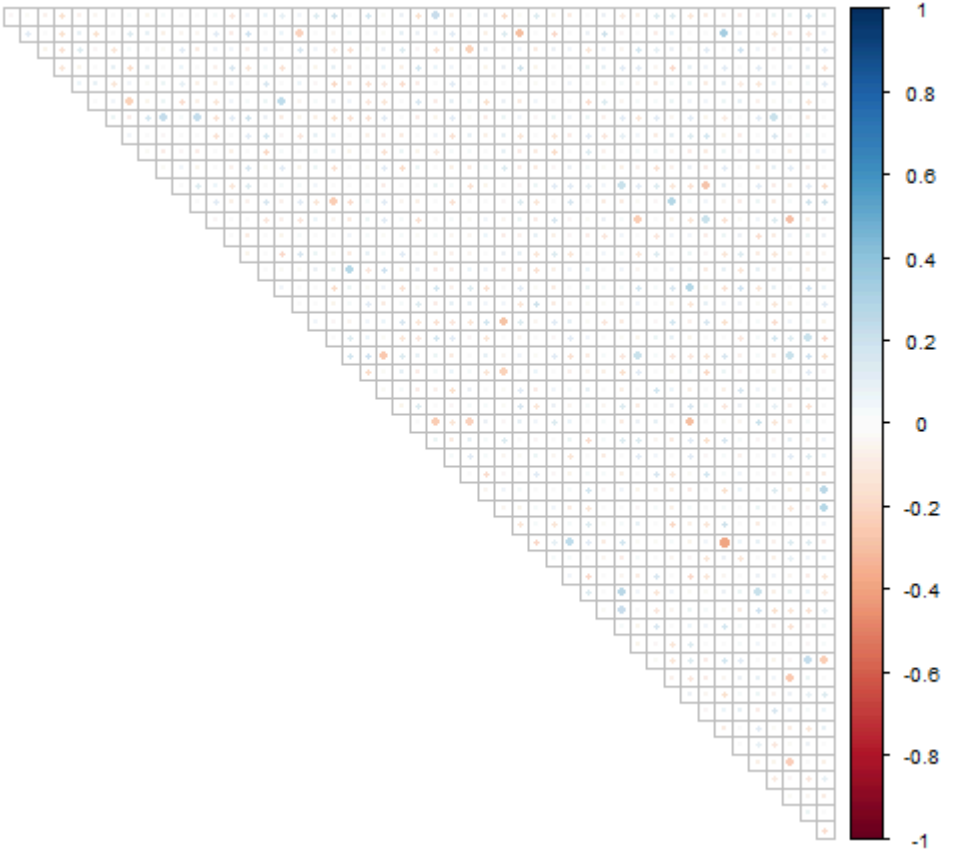
```
plot(1:(p*(p-1)/2), scorx, type="l")
abline(h=0, col="red", lty=2)
```



```
hist(scorx)
```


Histogram of scorx
Frequency
0e+00
1e+05
2e+05
3e+05
-0.4
-0.2
0.0
0.2
0.4
scorx

```
# plot correlations in X (just take 50 predictors at random)
randp <- sample(1:p, 50)
corrplot(corx[randp,randp], tl.pos='n', type="upper", diag=F)
```



```r
# true predictions
truepred <- X %*% b
# variance of the error term according to the SNR
varerr <- var(truepred)/SNR
# generate the error
err <- rnorm(n)*sqrt(varerr)
# create the response
y <- truepred + err
# sanity check
var(truepred)/var(err)
```

```
##          [,1]
## [1,] 3.754791
```

Let’s check the **SIS** function. It first implements the Iterative Sure Independence Screening for different variants of (I)SIS, and then fits the final regression model using the R packages **ncvreg** and **glmnet** for the SCAD/MCP/LASSO regularized loglikelihood for the variables picked by (I)SIS. The main arguments are:

- **x:** The design matrix
- **y:** The response vector
- **penalty:** The penalty to be applied in the regularized likelihood subproblems. 'SCAD' (the default), 'MCP', or 'lasso' are provided.
- **varISIS:** Specifies whether to perform any of the two ISIS variants based on randomly splitting the sample into two groups. The variant varISIS='aggr' is an aggressive variable screening procedure, while varISIS='cons' is a more conservative approach. The default is varISIS='vanilla', which performs the traditional vanilla version of ISIS.
- **iter:** Specifies whether to perform iterative SIS. The default is iter=TRUE.
- **iter.max:** Maximum number of iterations for (I)SIS and its variants.
- **tune:** Method for tuning the regularization parameter of the penalized likelihood subproblems and of the final model selected by (I)SIS. Options include tune='bic', tune='ebic', tune='aic', and tune='cv'.
- **nfolds:** Number of folds used in cross-validation. The default is 10.
- **nsis:** Number of pedictors recuited by (I)SIS.
- **standardize:** Logical flag for x variable standardization
- **seed:** Random seed used for sample splitting, random permutation, and cross-validation sampling of training and test sets.

We now perform variable selection using: - SIS: in its vanilla version - ISIS: the iterated version of SIS These are paired with the LASSO penalty and the ten-fold cross-validation method for choosing the regularization parameter.

```
# num of features retained by SIS/ISIS
# q <- n-1
q <- round(n / log(n))
q
```

```
## [1] 22
```

```
# maximum num of iterations for ISIS
maxit <- 10
# vanilla SIS
model1 = SIS(X, y, penalty = "lasso",
varISIS = "vanilla", iter=F, tune = "cv", nfolds = 10,
nsis=q, standardize = FALSE, seed = 1)
```

```
options(width = 60)
# SIS selected features: 22
model1$sis.ix0
```

```
##  [1]    1    2    3    4    5   24  240  288  332  343  717
## [12]  721  759  788  927  979 1302 1607 1635 1816 1868 1893
```

```
# SIS+LASSO selected features: 14
model1$ix
```

```
##  [1]    1    2    3    4    5  240  288  721  788  979 1607
## [12] 1635 1868 1893
```

```r
options(width = 60)
# vanilla ISIS
model2 = SIS(X, y,
penalty = "lasso",
varISIS = "vanilla", iter=T, iter.max=maxit,
tune = "cv", nfolds = 10, nsis=q,
standardize = FALSE, seed = 1)
```

```
## Iter 1 , screening:  1 2 3 4 5 240 717 721 788 979 1302 1607 1635 1893
## Iter 1 , selection:  1 2 3 4 5 240 721 788 979 1607 1635 1893
## Iter 1 , conditional-screening:  341 389 565 610 1073 1082 1113 1173 1338 1342
## Iter 2 , screening:  1 2 3 4 5 240 341 389 565 610 721 788 979 1073 1082 1113 117
## Iter 2 , selection:  1 2 3 4 5 240 341 389 565 610 721 788 979 1073 1082 1113 117
## Iter 2 , conditional-screening:  938
## Iter 3 , screening:  1 2 3 4 5 240 341 389 565 610 721 788 938 979 1073 1082 1113
## Iter 3 , selection:  1 2 3 4 5 240 341 389 565 610 721 788 938 979 1073 1082 1113
## Maximum number of variables selected
```

```
options(width = 60)
# ISIS selected features: 22
model2$ix0
```

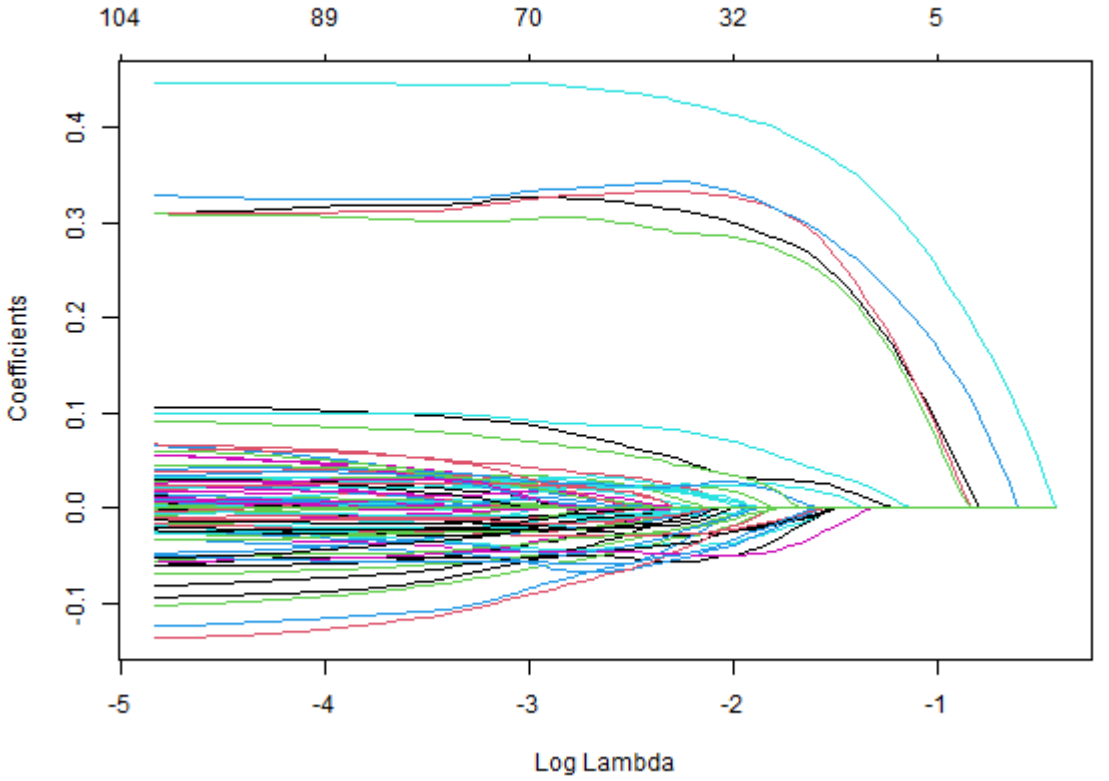
```
##  [1]    1    2    3    4    5  240  341  389  565  610  721
## [12]  788  938  979 1073 1082 1113 1173 1338 1342 1607 1635
```

```
# ISIS+Lasso selected features: 22
model2$ix
```

```
##  [1]    1    2    3    4    5  240  341  389  565  610  721
## [12]  788  938  979 1073 1082 1113 1173 1338 1342 1607 1635
```

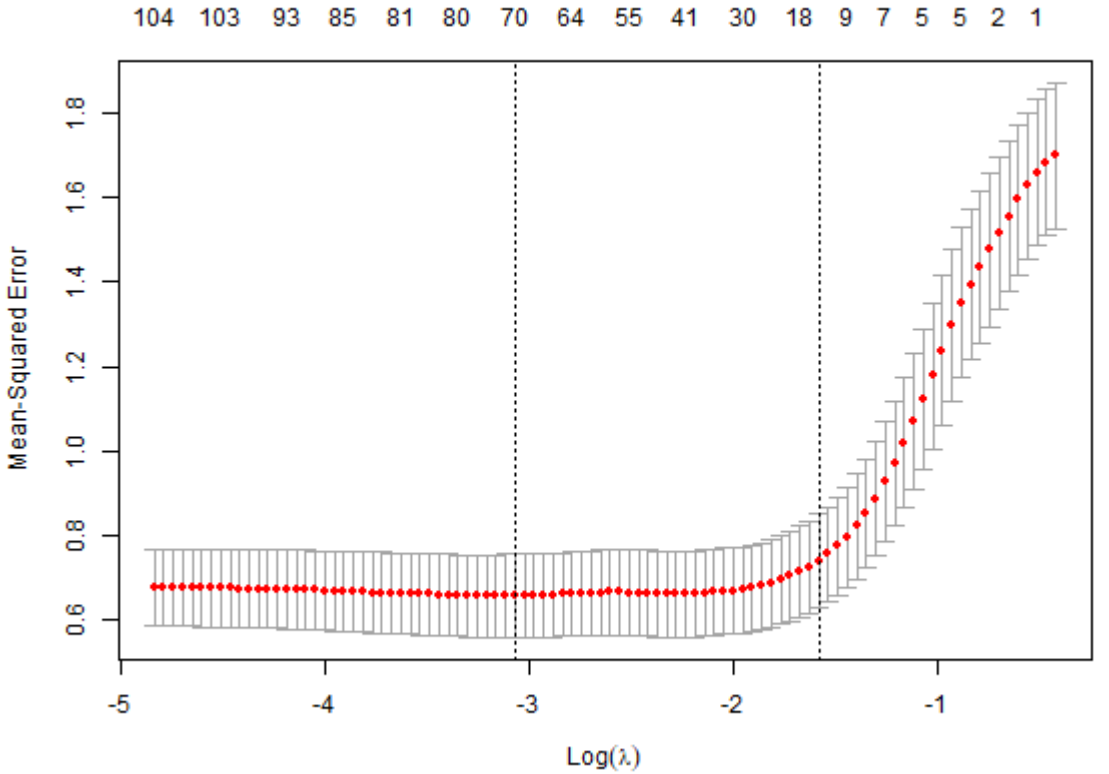
Compare it with a Lasso fit. Here is the overall path:

```
modelLasso = glmnet(X, y, standardize = F)
plot(modelLasso, xvar="lambda")
```



Let’s select the tuning parameter:

```
set.seed(1)
modelLassoCV = cv.glmnet(X, y, standardize = F)
plot(modelLassoCV)
```



Extract the associated features

```
modelLasso = glmnet(X, y, standardize = F,
lambda=modelLassoCV$lambda.1se)
Lassocoef <- which(coef(modelLasso) != 0)
Lassocoef
```

```
##  [1]    1    2    3    4    5    6   30  144  289  454  613
## [12]  722  789  980 1010 1608
```

```
# compare them with SIS
Lassocoef %in% model1$ix
```

```
##  [1]  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE
## [10] FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
# compare them with ISIS
Lassocoef %in% model2$ix
```

```
##  [1]  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE
## [10] FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

Now it's your turn!!!