# HW5 (Due Fr. Dec. 5 by 5pm in D2L)

Statistical Computing (STT 802, EPI 853b)

11/26/2024

In this Homework, we will develop models to predict a phenotype (wheat grain yield) using DNA markers. We will use a data set (included in the BGLR R-package) that has data for 599 inbred lines of wheat. For each inbred line the data set has four phenotypes (we will use just one of them) and 1279 DNA markers.

### Packages and data sets

To complete this HW you will need to install the BGData and BGLR R-packages.

```
install.packages(pkg=c('BGLR','BGData'),repos='https://cran.r-project.org/',type='binary')
```

Use the following code to load the data set into the environment. The X matrix has the DNA markers and the y vector will have the phenotypes.

```
suppressMessages(library(BGLR))
data(wheat)
X=wheat.X
y=wheat.Y[,2]
dim(X)
```

```
## [1] 599 1279
str(y)
```

```
## Named num [1:599] -1.7275 0.4095 -0.6486 0.0939 -0.2825 ...
## - attr(*, "names")= chr [1:599] "775" "2166" "2167" "2465" ...
```

In the HW, we will build prediction models using forward (FWD) regression and Lasso. We will compare these two methods based on their prediction accuracy in testing data.

For Questions 1 and 2 use this training-testing partition.

```
N<-nrow(X) ; p<-ncol(X)
set.seed(12345)
tst<-sample(1:N,size=150,replace=FALSE)
XTRN<-scale(X[-tst,],center=TRUE,scale=FALSE)
yTRN<-scale(y[-tst],center=TRUE,scale=FALSE)
XTST<-scale(X[tst,],center=TRUE,scale=FALSE)
yTST<-scale(y[tst],center=TRUE,scale=FALSE)</pre>
```

# $\mathbf{Q}\mathbf{1}$ ) Evaluating prediction performance of a Forward regression along the forward path

The following script shows how to fit a FWD regression over 30 steps (i.e., including up to 30 predictors).

```
 \begin{aligned} & \text{suppressMessages(library(BGData))} \\ & \text{FM=FWD(y=yTRN,X=XTRN,df=30,verbose=FALSE)} \end{aligned}  The object FM$B has the effects, rows are used for predictiors and each column gives the effects on the i^{th} step. Note that the first row corresponds to the intercept, rows 1279-1280 contain the effects of the DNA markers.  & \dim(\text{FM\$B}) \end{aligned}
```

```
## [1] 1280 31
head(rownames(FM$B))
```

```
## [1] "Int" "wPt.0538" "wPt.8463" "wPt.6348" "wPt.9992" "wPt.2838"
```

At the  $j^{th}$  step there are only j predictors in the model. Thus, in the first column, only the intercept is included

```
sum(FM$B[,1]!=0)

## [1] 1
which(FM$B[,1]!=0)

## Int
## 1
At the j<sup>th</sup> step there are j active predictors (counting the intercept).
j=4
sum(FM$B[,j]!=0)

## [1] 4
```

```
## [1] 4
which(FM$B[,j]!=0)
```

```
## Int wPt.2151 wPt.7160 c.305387
## 1 314 518 756
```

To derive predictions in the training data set using the model of the  $j^{th}$  step you can use

```
j=4
yHatTRN=cbind(1,XTRN)%*%FM$B[,j]
```

#### Tasks:

- Run the Forward regression for up to 100 steps (note, this may take a few minutes),
- For each step, evaluate the squared-correlation between predictions and observations in the training and testing data set.
- Report a plot with step number in the x-axis and the pprediction squared correlation in the training data in the y-axis.
- Report a similar plot for the prediction squared-correlation in testing data.
- What was the maximum squared correlation in testing data achieved by the Forward regression?
- How many steps do you recommend to use?

# Q2) Evaluating prediction performance of a Lasso regression along the regularization path.

The following code shows how to fit a Lasso regression, by default, glmnet() fits the model for a grid of 100 values of the regularization parameter  $\lambda$ .

```
library(glmnet)

## Loading required package: Matrix

## Loaded glmnet 4.1-6

fmL=glmnet(y=yTRN,x=XTRN,alpha=1)
```

The fitted object has the values of the regularization parameter used fmL\$lambda and the estiamted effects.

The object fmL\$beta has the estiamted effects for each of the value if  $\lambda$  and fmL\$aO has the estimated intercept for each value of lambda. fmL\$df tells you how many predictors were active for each value of  $\lambda$ 

```
str(fmL$lambda)
## num [1:100] 0.248 0.237 0.226 0.215 0.206 ...
str(fmL$a0)
## Named num [1:100] 5.98e-17 6.10e-17 6.23e-17 6.30e-17 6.09e-17 ...
## - attr(*, "names")= chr [1:100] "s0" "s1" "s2" "s3" ...
dim(fmL$beta)
```

## [1] 1279 100

The function predict() can be called on the fitted object.

### Tasks:

- Fit the Lasso regression using the training data
- Use the model to derive predictions for the training and testing data set.
- Report a plot with step number in the x-axis and the pprediction squared correlation in the training data in the y-axis.
- Report a similar plot for the prediction squared-correlation in testing data.
- What was the maximum squared correlation in testing data achieved by Lasso?
- What value of  $\lambda$  do you recommend to use?
- How many active predictors did Lasso have for that value of  $\lambda$ ?

## Q3: Conclussions and recommendations

Summarize, in no more than 200 words your findings and recommendations.