# Jin Kweon_3032235207_HW4

*Jin Kweon*

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## Problem 1 (10 points)

It is given in the problem that $r_{12} = r_{13} = r_{23} = 0$. So, for one example, $r_{12} = cor(X_1, X_2) = \frac{cov(X_1,X_2)}{sd(X_1)sd(X_2)} = 0$. Since denominator cannot be zero (also, the problem never says standard deviation or variance of four predictors are zero), it implies that $cov(X_1, X_2) = 0$.

So, $r_{13}$ and $r_{23}$ also imply $cov(X_1, X_3) = 0$ and $cov(X_2, X_3) = 0$.

So, now, I need to prove $r_{14} = r_{24} = r_{34} = 0.577$. (or, closed to 0.577) I will start with proving $r_{14} = 0.577$.

$$r_{14} = \frac{cov(X_1,X_4)}{sd(X_1)sd(X_4)} = \frac{cov(X_1,X_1+X_2+X_3)}{sd(X_1)\sqrt{var(X_4)}} = \frac{cov(X_1,X_1) + cov(X_1,X_2) + cov(X_1,X_3)}{sd(X_1)\sqrt{var(X_1 + X_2 + X_3)}} = \frac{cov(X_1,X_1)}{sd(X_1)\sqrt{var(X_1 + X_2 + X_3)}} =$$
$$\frac{var(X_1)}{sd(X_1)\sqrt{var(X_1) + var(X_2) + var(X_3) + 2cov(X_1,X_2) + 2cov(X_1,X_3) + 2cov(X_2,X_3)}} = \frac{var(X_1)}{sd(X_1)\sqrt{var(X_1) + var(X_2) + var(X_3)}}$$
$$= \frac{sd(X_1)}{\sqrt{var(X_1) + var(X_2) + var(X_3)}} = \frac{\sigma_1}{\sqrt{\sigma_1^2 + \sigma_2^2 + \sigma_3^2}} = \frac{\sigma_1}{\sqrt{3\sigma_1^2}} = \frac{1}{\sqrt{3}} \approx 0.577.$$

Also, $r_{24}$ and $r_{34}$ can be proved in a similar way.

$$r_{24} = \frac{cov(X_2,X_4)}{sd(X_2)sd(X_4)} = \frac{cov(X_2,X_1+X_2+X_3)}{sd(X_2)\sqrt{var(X_4)}} = \frac{var(X_2)}{sd(X_2)\sqrt{var(X_1) + var(X_2) + var(X_3)}} = \frac{sd(X_2)}{\sqrt{var(X_1) + var(X_2) + var(X_3)}}$$
$$= \frac{\sigma_2}{\sqrt{3\sigma_2^2}} = \frac{1}{\sqrt{3}} \approx 0.577.$$

And, $r_{34}$ will be eventually $\frac{\sigma_3}{\sqrt{3\sigma_3^2}} = \frac{1}{\sqrt{3}} \approx 0.577$.

The key point of this problem is that variance of $X_1$, $X_2$, and $X_3$ are the same.

# Problem 2 (10 points)

As it says on the hint of the problem, it can definitely be proved by recursivity of PLS algorithm we learned in the class.

Here is the proof below:

I am going to pick i where $1 \leq i \leq n$. And, what I need to do is prove i is orthogonal to any other PLS component.

1) $z_i^T z_{i+1} = z_i^T(\frac{X_i w_{i+1}}{w_{i+1}^T w_{i+1}}) = \frac{1}{w_{i+1}^T w_{i+1}} z_i^T(X_i w_{i+1})$. I only need to prove $z_i^T(X_i w_{i+1}) = 0$.

And, $z_i^T(X_i w_{i+1}) = z_i^T([x_{i-1} - z_i p_i^T] w_{i+1}) = z_i^T([x_{i-1} - z_i[\frac{x_{i-1}^T z_i}{z_i^T z_i}]^T] w_{i+1}) = (z_i^T x_{i-1} - z_i^T x_{i-1}) w_{i+1} = 0$.

2) After, I will prove it recursively.

$z_i^T z_{i+2} = z_i^T(X_{i+1} w_{i+2}) \frac{1}{w_{i+2}^T w_{i+2}} = z_i^T(X_i - z_{i+1} p_{i+1}^T) \frac{w_{i+2}}{w_{i+2}^T w_{i+2}} = (z_i^T X_i - z_i^T z_{i+1} p_{i+1}^T) \frac{w_{i+2}}{w_{i+2}^T w_{i+2}}$.

And, since $z_i^T z_{i+1} = 0$ as we proved in the last recursion proof, $(z_i^T X_i - z_i^T z_{i+1} p_{i+1}^T) \frac{w_{i+2}}{w_{i+2}^T w_{i+2}} = z_i^T X_i \frac{w_{i+2}}{w_{i+2}^T w_{i+2}}$.

So, I only need to prove $z_i^T X_i = 0$.

$z_i^T X_i = z_i^T(X_{i-1} - z_i p_i^T) = z_i^T(X_{i-1} - z_i[\frac{x_{i-1}^T z_i}{z_i^T z_i}]^T) = z_i^T X_{i-1} - z_i^T X_{i-1} = 0$.

So, $z_i^T z_{i+2} = 0$ is proved.

3) I will prove one more recursion.

$z_i^T z_{i+3} = z_i^T(X_{i+2} w_{i+3}) \frac{1}{w_{i+3}^T w_{i+3}} = z_i^T(X_{i+1} - z_{i+2} p_{i+2}^T) w_{i+3} \frac{1}{w_{i+3}^T w_{i+3}}$.

I need to prove $z_i^T(X_{i+1} - z_{i+2} p_{i+2}^T) = z_i^T(X_{i+1} - z_{i+2}[\frac{x_{i+1}^T z_{i+2}}{z_{i+2}^T z_{i+2}}]^T) = z_i^T X_{i+1} - z_i^T z_{i+2}[\frac{x_{i+1}^T z_{i+2}}{z_{i+2}^T z_{i+2}}]^T$.

And, since we proved $z_i^T z_{i+2} = 0$, $z_i^T X_{i+1} - z_i^T z_{i+2}[\frac{x_{i+1}^T z_{i+2}}{z_{i+2}^T z_{i+2}}]^T = z_i^T X_{i+1}$.

So, I need to prove $z_i^T X_{i+1} = 0$.

$z_i^T X_{i+1} = (z_i^T X_i - z_i^T z_{i+1} p_{i+1}^T) = z_i^T X_i$, as $z_i^T z_{i+1} = 0$.

So, I need to prove $z_i^T X_i = 0$.

$z_i^T X_i = z_i^T(X_{i-1} - z_i p_i^T) = z_i^T(X_{i-1} - z_i[\frac{x_{i-1}^T z_i}{z_i^T z_i}]^T) = z_i^T X_{i-1} - z_i^T X_{i-1} = 0$.

I can keep proving this recursion.

Thus, $z_h^T z_l = 0$, for $h \neq l$ where $1 \leq h \leq n$ and $1 \leq l \leq n$.

## Problem 3 (100 points)

- lcavol: log cancer volume
- lweight: log prostate weight
- age: age of patient
- lbph: log of the amount of benign prostatic hyperplasia
- svi: seminal vesicle invasion
- lcp: log of capsular penetration
- gleason: Gleason score
- pgg45: percent of Gleason scores 4 or 5
- lpsa: log of prostate-specific antigen (response variable)

```
prostate <- prostate
```

```
training <- prostate %>% filter(train == "TRUE")
testing <- prostate %>% filter(train == "FALSE")
training <- training[,-10]
testing <- testing[,-10]

dim(training)
```

```
## [1] 67  9
```

```
dim(testing)
```

```
## [1] 30  9
```

```
sum(is.na(prostate)) #check NA
```

```
## [1] 0
```

lpsa is the response variable. The rest are the predictors. I will select training set and standardize training set only! After, I will get correlation matrix.

**Correlations of predictors, and some preprocessing (10 pts)**

```
trainingscale <- scale(training, T, T)

summary(trainingscale[,1:3]) #summary for lcavol, lweight, and age
```

```
##      lcavol           lweight              age         
##  Min.   :-2.1411   Min.   :-2.62526   Min.   :-3.16524  
##  1st Qu.:-0.6641   1st Qu.:-0.62054   1st Qu.:-0.49935  
##  Median : 0.1242   Median :-0.05755   Median : 0.03382  
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.00000  
##  3rd Qu.: 0.8334   3rd Qu.: 0.54029   3rd Qu.: 0.56700  
##  Max.   : 2.0180   Max.   : 2.42189   Max.   : 1.89994
```

```
summary(trainingscale[,4:6]) #summary for lbph, svi, lcp
```

```
##       lbph               svi                lcp         
##  Min.   :-0.99595   Min.   :-0.5331   Min.   :-0.8368  
##  1st Qu.:-0.99595   1st Qu.:-0.5331   1st Qu.:-0.8368  
##  Median :-0.08385   Median :-0.5331   Median :-0.4171  
##  Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.0000  
##  3rd Qu.: 1.00848   3rd Qu.:-0.5331   3rd Qu.: 0.8631  
##  Max.   : 1.54057   Max.   : 1.8480   Max.   : 2.0496
```

```
summary(trainingscale[,7:8]) #summary for gleason and pgg45
```

```
##     gleason           pgg45        
##  Min.   :-1.032   Min.   :-0.8965  
##  1st Qu.:-1.032   1st Qu.:-0.8965  
##  Median : 0.379   Median :-0.3846  
##  Mean   : 0.000   Mean   : 0.0000  
##  3rd Qu.: 0.379   3rd Qu.: 0.8099  
##  Max.   : 3.200   Max.   : 2.5163
```

```
trainingscale_x <- trainingscale[,-9]

correlation <- cor(trainingscale_x)
correlation <- correlation[-1,-8]
round(correlation, 3)
```

```
##         lcavol lweight   age   lbph    svi    lcp gleason
## lweight  0.300   1.000 0.317  0.437  0.181  0.157   0.024
## age      0.286   0.317 1.000  0.287  0.129  0.173   0.366
## lbph     0.063   0.437 0.287  1.000 -0.139 -0.089   0.033
## svi      0.593   0.181 0.129 -0.139  1.000  0.671   0.307
## lcp      0.692   0.157 0.173 -0.089  0.671  1.000   0.476
## gleason  0.426   0.024 0.366  0.033  0.307  0.476   1.000
## pgg45    0.483   0.074 0.276 -0.030  0.481  0.663   0.757
```

### Least Squares Model (10 pts)

```
#response is not scaled, but predictors are.
trainxscale_only <- cbind(trainingscale_x, lpsa = training$lpsa)

ols <- lm(lpsa ~., data = as.data.frame(trainxscale_only))

table3.2 <- summary(ols)$coefficients[,-4]
colnames(table3.2) <- c("Coefficient", "Std.Error", "Z score")

round(table3.2, 2)
```

```
##             Coefficient Std.Error Z score
## (Intercept)        2.45      0.09   28.18
## lcavol             0.72      0.13    5.37
## lweight            0.29      0.11    2.75
## age               -0.14      0.10   -1.40
## lbph               0.21      0.10    2.06
## svi                0.31      0.13    2.47
## lcp               -0.29      0.15   -1.87
## gleason           -0.02      0.14   -0.15
## pgg45              0.28      0.16    1.74
```

*Comment:*

I agree with the points professor Sanchez made on the instruction. The first three coefficients (also, maybe the last one: pgg45) are slightly off.

And, actually, it should be t-test, not z-score, since we do not know actual standard deviation.

We can actually scale response variable as well.

1. When we did not scale response variable: When x variable goes up 1 unit, reponse variable changes coefficient of x (in y).

2. when we scale reponse variable: When x variable goes up 1 unit, response variable changes coefficient of x unit/quantile (in y).

### Best Subset Regression (10 pts)

Good reference: http://rstudio-pubs-static.s3.amazonaws.com/2897_9220b21cfc0c43a396ff9abf122bb351.html

```
subset <- regsubsets(lpsa ~., data = as.data.frame(trainxscale_only), nvmax = 8)
summary(subset)
```

```
## Subset selection object
## Call: regsubsets.formula(lpsa ~ ., data = as.data.frame(trainxscale_only),
##     nvmax = 8)
## 8 Variables  (and intercept)
```

```
##         Forced in Forced out
## lcavol      FALSE      FALSE
## lweight     FALSE      FALSE
## age         FALSE      FALSE
## lbph        FALSE      FALSE
## svi         FALSE      FALSE
## lcp         FALSE      FALSE
## gleason     FALSE      FALSE
## pgg45       FALSE      FALSE
## 1 subsets of each size up to 8
## Selection Algorithm: exhaustive
##          lcavol lweight age lbph svi lcp gleason pgg45
## 1  ( 1 ) "*"    " "     " " " "  " " " " " "     " "
## 2  ( 1 ) "*"    "*"     " " " "  " " " " " "     " "
## 3  ( 1 ) "*"    "*"     " " " "  "*" " " " "     " "
## 4  ( 1 ) "*"    "*"     " " "*"  "*" " " " "     " "
## 5  ( 1 ) "*"    "*"     " " "*"  "*" " " " "     "*"
## 6  ( 1 ) "*"    "*"     " " "*"  "*" "*" " "     "*"
## 7  ( 1 ) "*"    "*"     "*" "*"  "*" "*" " "     "*"
## 8  ( 1 ) "*"    "*"     "*" "*"  "*" "*" "*"     "*"
```

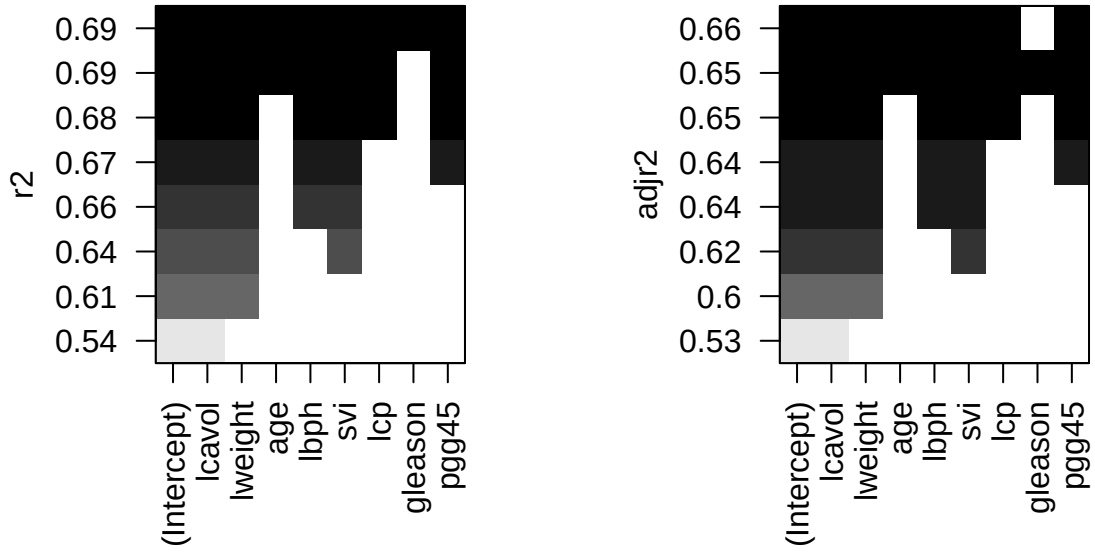
```
summary(subset)$bic
```

```
## [1] -43.25728 -51.29578 -51.15720 -51.09467 -48.42976 -47.49961 -45.75833
## [8] -41.57849
```

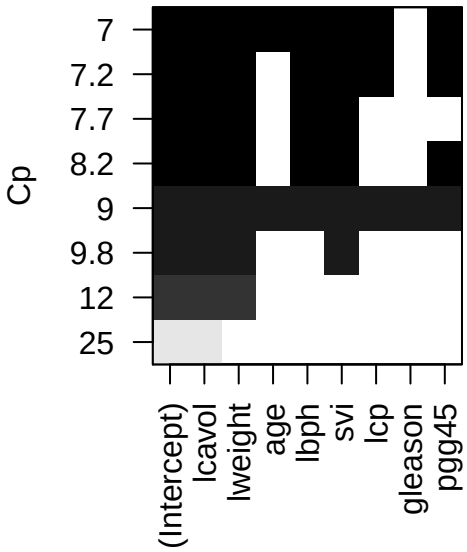
```
paste("So, I keep the", which.min(summary(subset)$bic), "variables.")
```

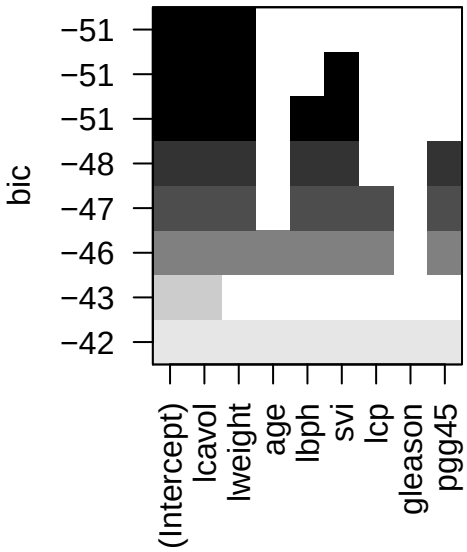
```
## [1] "So, I keep the 2 variables."
```

```
par(mfrow = c(1,2))
plot(subset, scale = "r2")
plot(subset, scale = "adjr2")
```




```
plot(subset, scale = "Cp")
plot(subset, scale = "bic")
```




```
subsetcoef <- lm(lpsa ~ lcavol + lweight, data = as.data.frame(trainxscale_only))$coefficients
# coef(subset, 2) - other way to get coefficients
```

*Comment:*

Using BIC, they tell me I should keep the best two variables. So, I output the minimum BIC for when each number of variables are kept. Actually, there are two steps.

First, since we have 8 variables, we need to find the minimum BIC when 1, 2, . . . , 8 variables are kept. So, I got -43.26 (miminimum BIC when 1 variable is kept), -51.30 (minimum BIC when 2 variables are kept), . . . , -41.58 (minimum BIC when 8 variables are kept). After that, I need to find how many variables to keep, by finding the mimimum from there. And, it is the second one.

Thus, the *BEST* two three variable model contains lcavol and lweight.

**PCR and PLSR (40 pts)**

Q. Is our regression coefficient already standardized coefficients? Q. What is X in summary(plsrfunc)? Is it kind of each cumulative of eigenvalue / 8? Q. Why do I have 8 variables for coef() function for plsr even though my tuning parameter is 6?

Use 10 fold cross validation.

```
set.seed(10)

#PLSR
plsrfunc <- plsr(formula = lpsa ~., data =as.data.frame(trainxscale_only), validation = "CV")
summary(plsrfunc)
```

```
## Data:    X dimension: 67 8
##  Y dimension: 67 1
## Fit method: kernelpls
## Number of components considered: 8
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           1.217   0.8546   0.8128   0.7945   0.7928   0.7853   0.7824
## adjCV        1.217   0.8518   0.8073   0.7891   0.7855   0.7787   0.7760
##        7 comps  8 comps
## CV      0.7833   0.7833
## adjCV   0.7768   0.7767
##
## TRAINING: % variance explained
##       1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X       41.64    58.29    71.13    79.75    86.08    90.21    94.70
## lpsa    55.79    64.60    67.51    69.12    69.37    69.43    69.44
##       8 comps
## X      100.00
## lpsa    69.44
```

```
paste("Tuning parameter is", which.min(plsrfunc$validation$PRESS))
```

```
## [1] "Tuning parameter is 6"
```

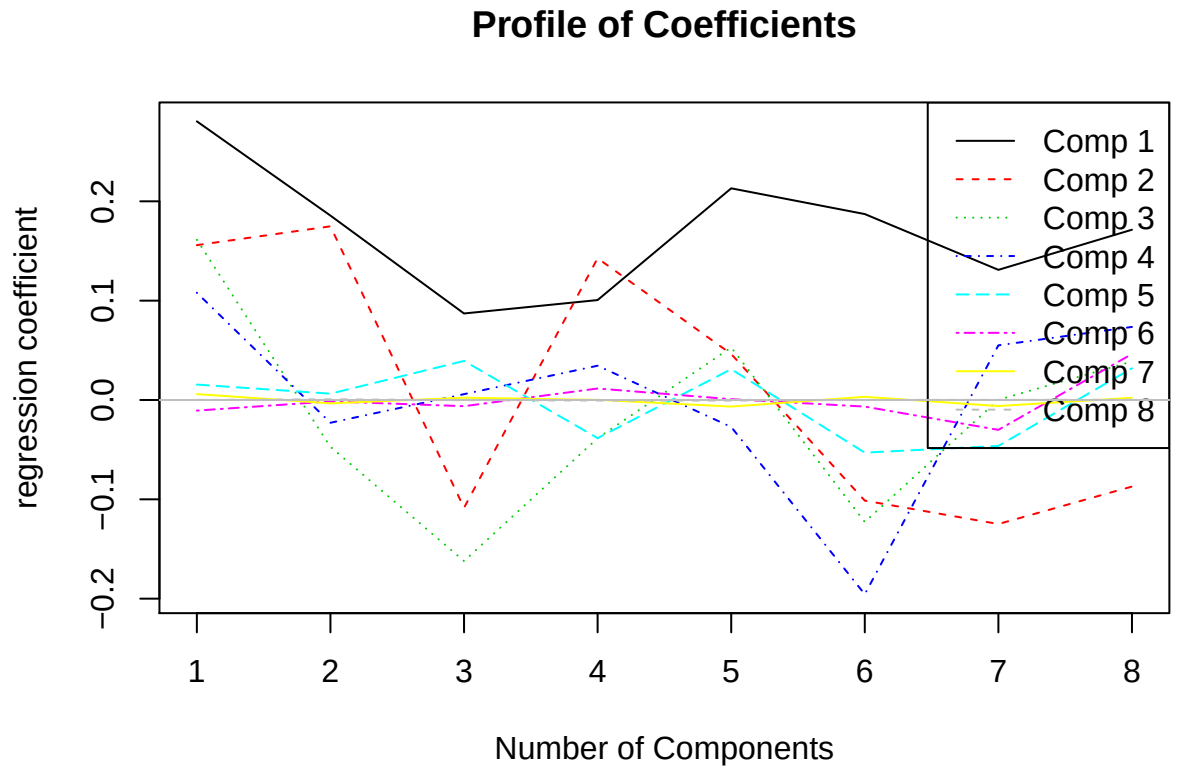
```
print("Associated coefficients of PLSR:")
```

```
## [1] "Associated coefficients of PLSR:"
```

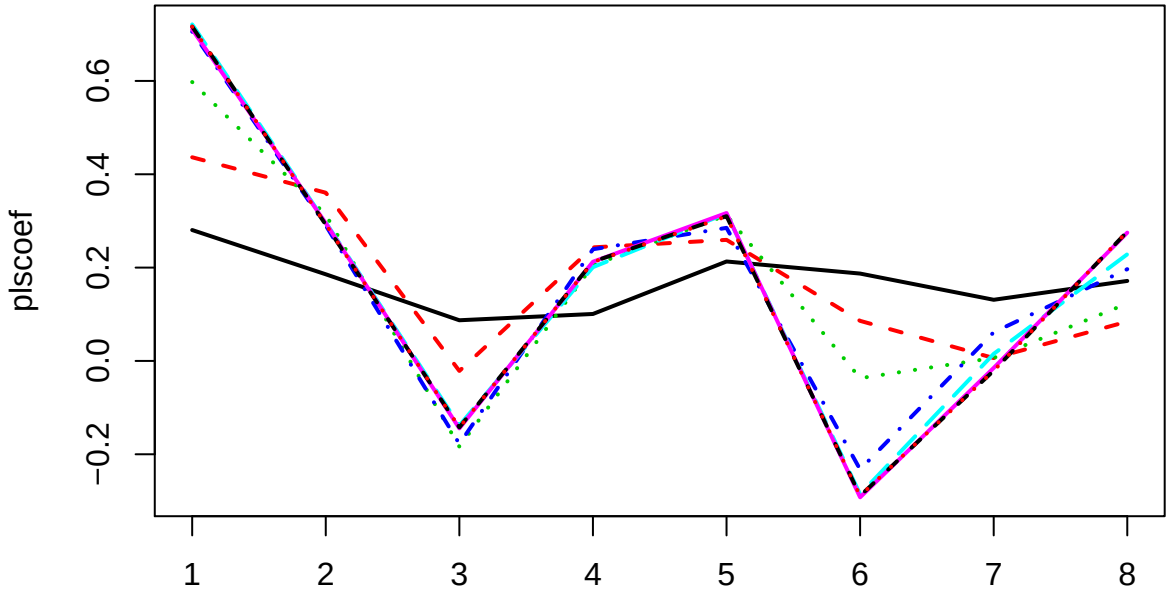
```
plsrfunc$coefficients[,,which.min(plsrfunc$validation$PRESS)]
```

```
##     lcavol    lweight        age       lbph        svi        lcp
##  0.7104094  0.2952801 -0.1446106  0.2124677  0.3169434 -0.2922292
##    gleason      pgg45
## -0.0149234  0.2748280
```

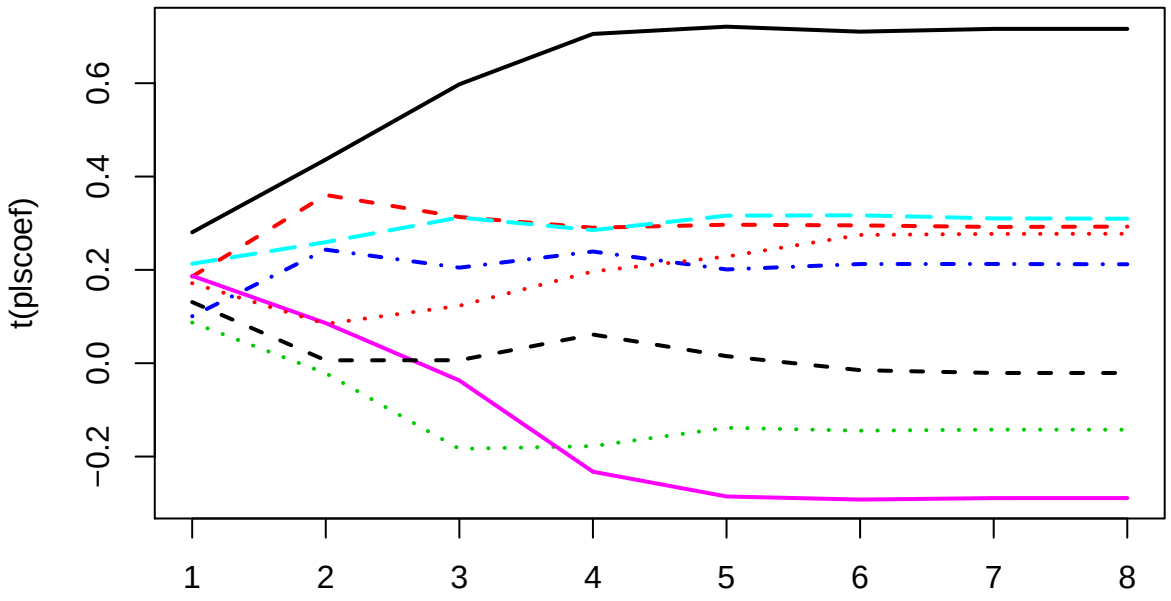
```
coefplot(plsrfunc, comps = 1:8, separate = F, intercept = T, xlab = "Number of Components",
         main = "Profile of Coefficients", legendpos = "topright")
```




```
plscoef <- apply(plsrfunc$coefficients, 3, function(x) x)
matplot(plscoef, type= 'l', lwd = 2)
```

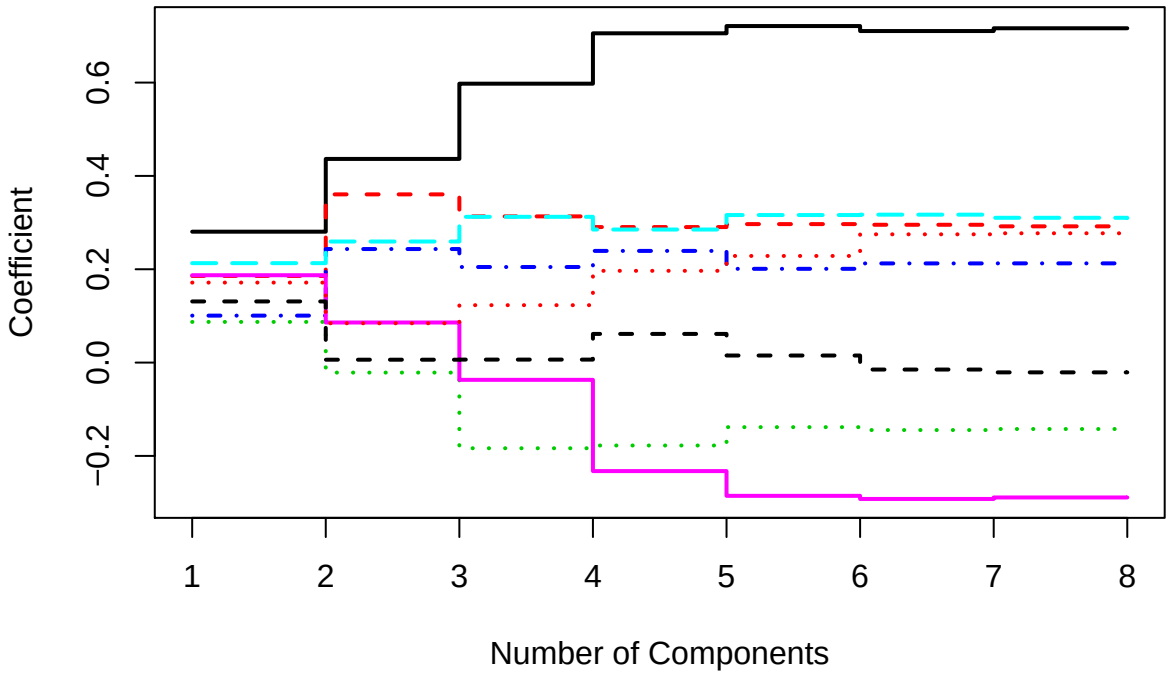



```
matplot(t(plscoef), type= 'l', lwd = 2)
```




```
matplot(t(plscoef), type= 's', lwd = 2, xlab = "Number of Components",
        main = "Profile of Coefficients", ylab = "Coefficient")
```

**Profile of Coefficients**



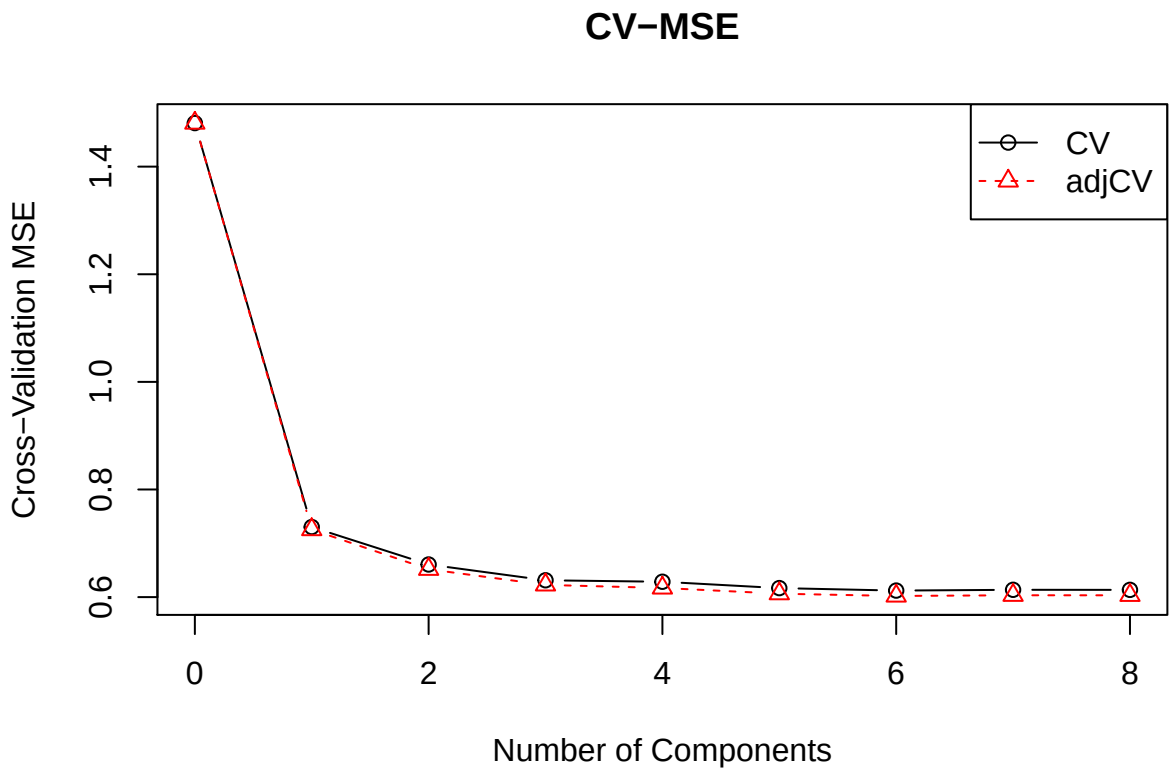

```
RMSEP(plsrfunc) #This is what we have from summary
```

```
##         (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV            1.217   0.8546   0.8128   0.7945   0.7928   0.7853   0.7824
## adjCV         1.217   0.8518   0.8073   0.7891   0.7855   0.7787   0.7760
##        7 comps  8 comps
## CV      0.7833   0.7833
## adjCV   0.7768   0.7767
```

```
MSEP(plsrfunc) #Output MSE
```

```
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           1.481   0.7303   0.6606   0.6313   0.6285   0.6168   0.6121
## adjCV        1.481   0.7255   0.6517   0.6227   0.6170   0.6064   0.6021
##        7 comps  8 comps
## CV      0.6136   0.6135
## adjCV   0.6034   0.6033
```

```
validationplot(plsrfunc, val.type = "MSEP", ncomp = 1:8, type = "b",
               legendpos = "topright", xlab = "Number of Components",
               ylab = "Cross-Validation MSE", main = "CV-MSE")
```




```
coef(plsrfunc, intercept = T)
```

```
## , , 8 comps
##
##                    lpsa
## (Intercept)  2.45234509
## lcavol       0.71640701
## lweight      0.29264240
## age         -0.14254963
## lbph         0.21200760
## svi          0.30961953
## lcp         -0.28900562
## gleason     -0.02091352
## pgg45        0.27734595
```

```
#PCR
pcrfunc <- pcr(formula = lpsa ~., data = as.data.frame(trainxscale_only), validation = "CV")
summary(pcrfunc)
```

```
## Data:    X dimension: 67 8
##  Y dimension: 67 1
## Fit method: svdpc
## Number of components considered: 8
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           1.217   0.9217   0.8875   0.8158   0.8109   0.8166   0.8362
## adjCV        1.217   0.9197   0.8863   0.8125   0.8074   0.8135   0.8324
##        7 comps  8 comps
## CV      0.7967   0.7521
## adjCV   0.7915   0.7474
##
## TRAINING: % variance explained
##       1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X       42.83    63.24    76.20    83.92    89.61    94.32    97.82
## lpsa    45.18    50.84    59.58    61.00    61.17    62.08    66.36
##       8 comps
## X      100.00
## lpsa    69.44
```

```
paste("Tuning parameter is", which.min(pcrfunc$validation$PRESS))
```

```
## [1] "Tuning parameter is 8"
```

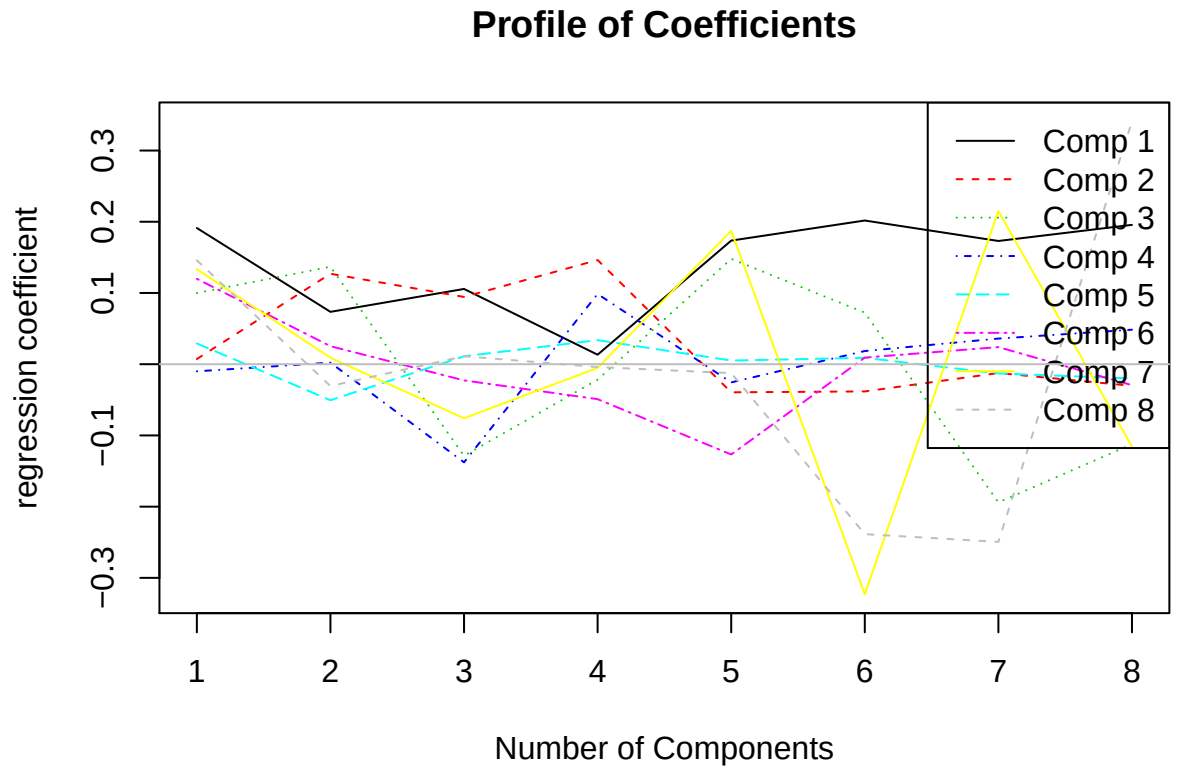
```
print("Associated coefficients of PCR:")
```

```
## [1] "Associated coefficients of PCR:"
```

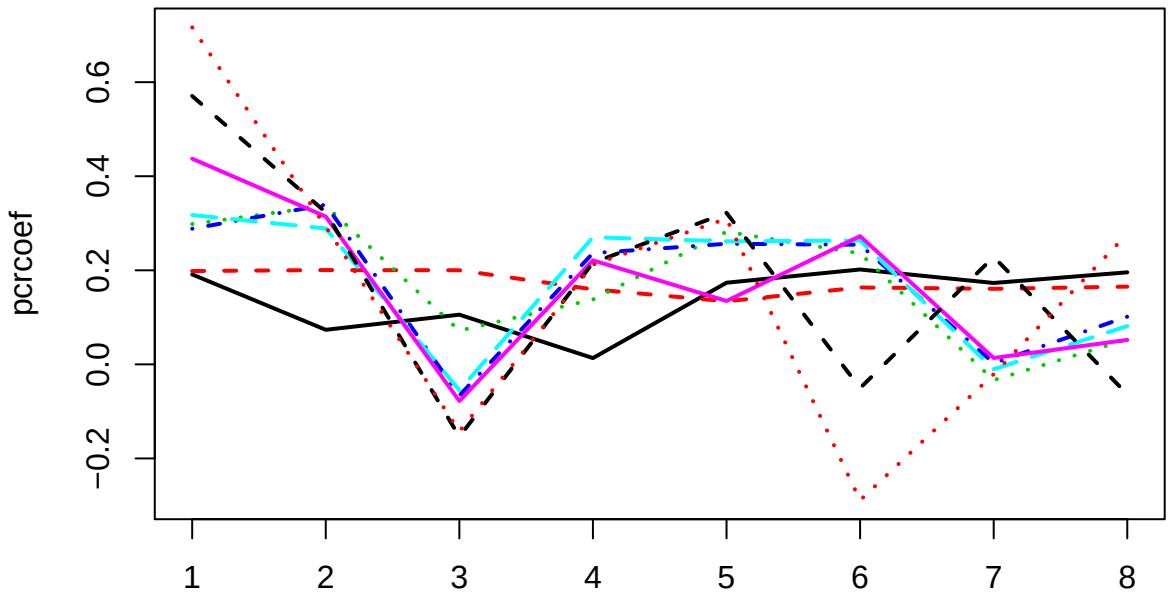
```
pcrfunc$coefficients[,,which.min(pcrfunc$validation$PRESS)]
```

```
##      lcavol     lweight         age        lbph         svi         lcp
##  0.71640701  0.29264240 -0.14254963  0.21200760  0.30961953 -0.28900562
##     gleason       pgg45
## -0.02091352  0.27734595
```

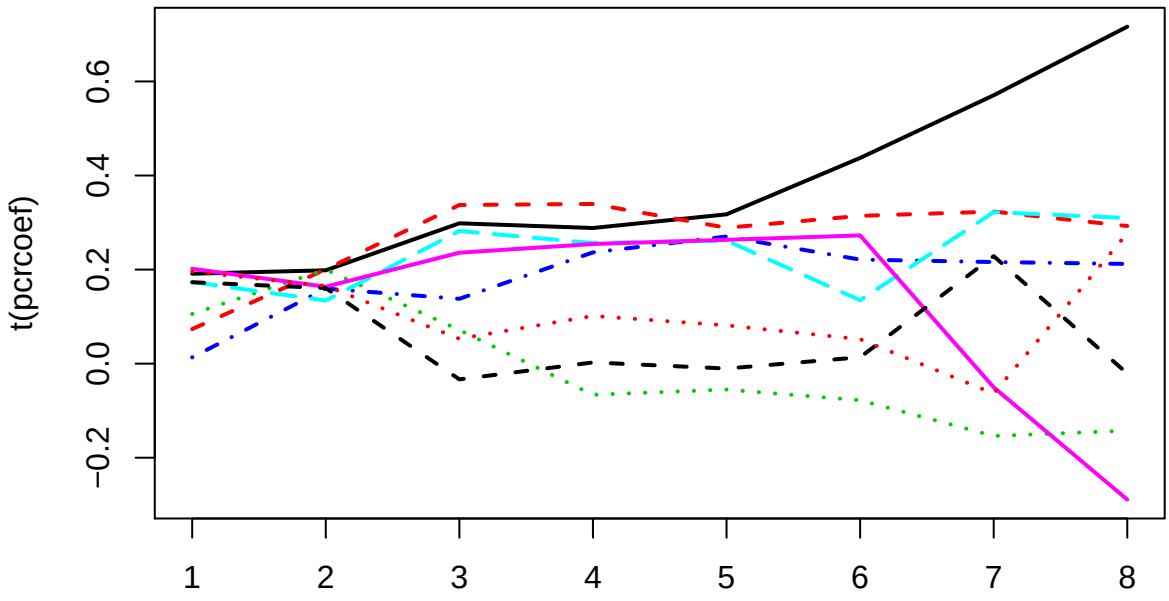
```
coefplot(pcrfunc, comps = 1:8, separate = F, xlab = "Number of Components",
         main = "Profile of Coefficients", legendpos = "topright")
```




```
pcrcoef <- apply(pcrfunc$coefficients, 3, function(x) x)
matplot(pcrcoef, type= 'l', lwd = 2)
```

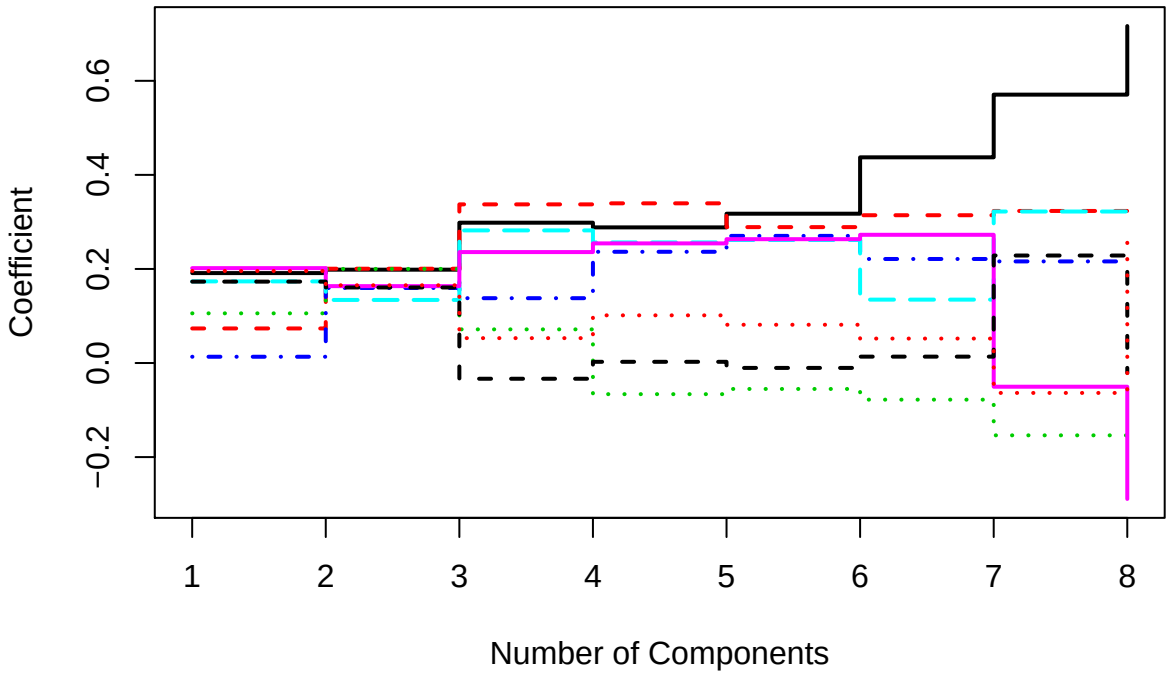



```
matplot(t(pcrcoef), type= 'l', lwd = 2)
```




```
matplot(t(pcrcoef), type= 's', lwd = 2, xlab = "Number of Components",
        main = "Profile of Coefficients", ylab = "Coefficient")
```

**Profile of Coefficients**



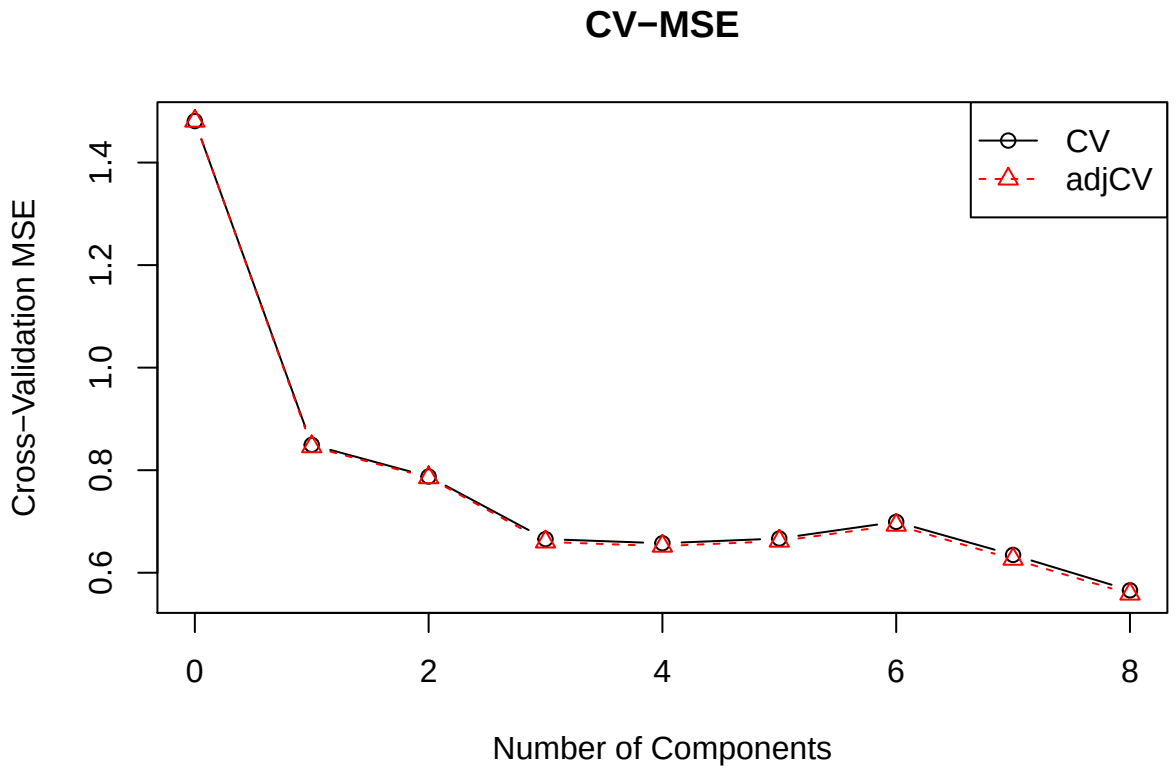

```
RMSEP(pcrfunc) #This is what we have from summary
```

```
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           1.217   0.9217   0.8875   0.8158   0.8109   0.8166   0.8362
## adjCV        1.217   0.9197   0.8863   0.8125   0.8074   0.8135   0.8324
##        7 comps  8 comps
## CV      0.7967   0.7521
## adjCV   0.7915   0.7474
```

```r
MSEP(pcrfunc) #Output MSE
```

```
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           1.481   0.8495   0.7876   0.6656   0.6575   0.6668   0.6992
## adjCV        1.481   0.8459   0.7855   0.6601   0.6520   0.6618   0.6928
##        7 comps  8 comps
## CV      0.6347   0.5657
## adjCV   0.6265   0.5586
```

```r
validationplot(pcrfunc, val.type = "MSEP", ncomp = 1:8, type = "b",
               legendpos = "topright", xlab = "Number of Components",
               ylab = "Cross-Validation MSE", main = "CV-MSE")
```




```r
coef(pcrfunc, intercept = T)
```

```
## , , 8 comps
##
##                    lpsa
## (Intercept)  2.45234509
## lcavol       0.71640701
## lweight      0.29264240
## age         -0.14254963
## lbph         0.21200760
## svi          0.30961953
## lcp         -0.28900562
## gleason     -0.02091352
## pgg45        0.27734595
```

*Comment:*

Tuning parameter/Number of components is *8 (using all variables)*, since this has the smallest CV-RMSE

(root square of MSE of prediction).

Just for knowledge, plsr and pcr will have the same coefficients if we are using full coefficients.

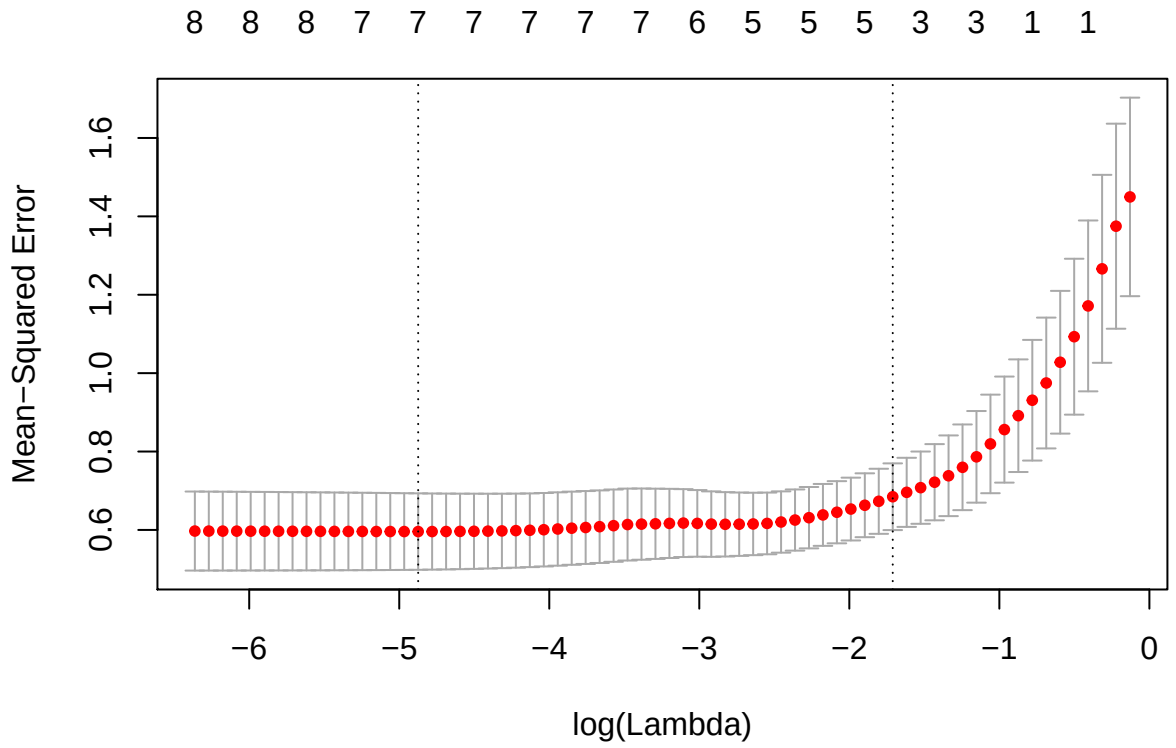
Q. How to "refit a model with chosen minimum lambda. This will allow you to recover the associated coefficients of the chosen model"? Q. What is tuning parameter here? What does it mean? Q. Why are the coefficients of Ridge and Lasso so different with the table's? Also, I have pgg45 coefficient for lasso while table on the instruction does not have it?

**RR and Lasso (40 pts)**

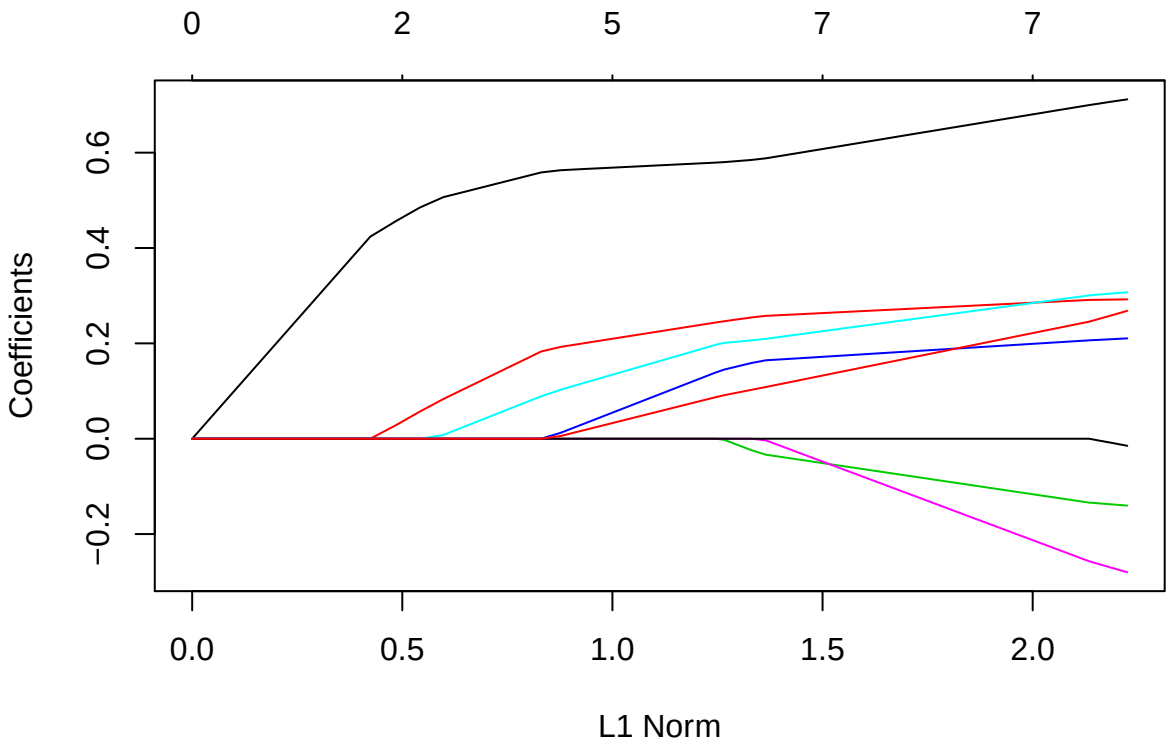
```
set.seed(10)
#Lasso
lasso <- cv.glmnet(trainxscale_only[,1:8], trainxscale_only[,9], nfolds = 10, alpha = 1)

paste("Tuning parameter is", round(lasso$lambda.min, 4))
```

```
## [1] "Tuning parameter is 0.0076"
```

```
plot.cv.glmnet(lasso)
```




```
lasso2 <- glmnet(trainxscale_only[,1:8], trainxscale_only[,9], alpha = 1)
plot.glmnet(lasso2)
```




```
coef(lasso) #include s (lambda) if wanted
```

```
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                       1
## (Intercept) 2.45234509
## lcavol      0.56536414
## lweight     0.19936439
## age         .
## lbph        0.02917609
## svi         0.11532140
## lcp         .
## gleason     .
## pgg45       0.01647872
```

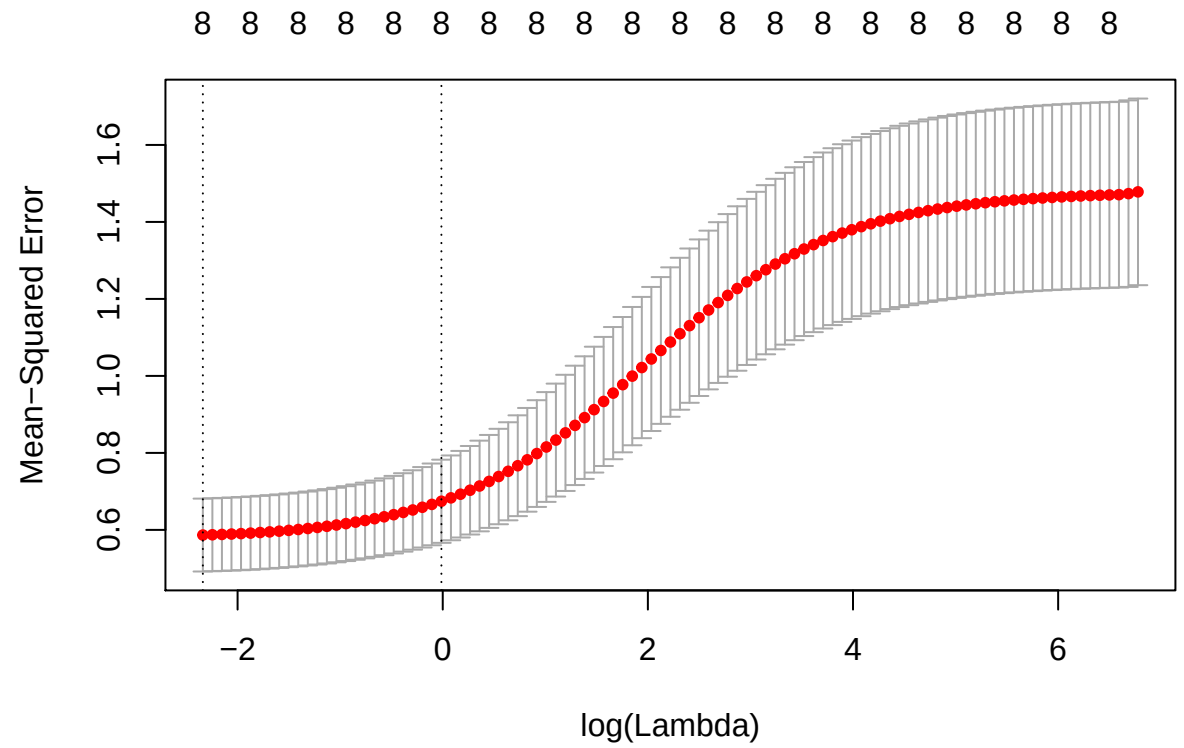
```
coef(lasso, s = "lambda.min")
```

```
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                       1
## (Intercept)  2.4523451
## lcavol       0.6918697
## lweight      0.2887031
## age         -0.1268621
## lbph         0.2033674
## svi          0.2940763
## lcp         -0.2389979
## gleason      .
## pgg45        0.2357199
```

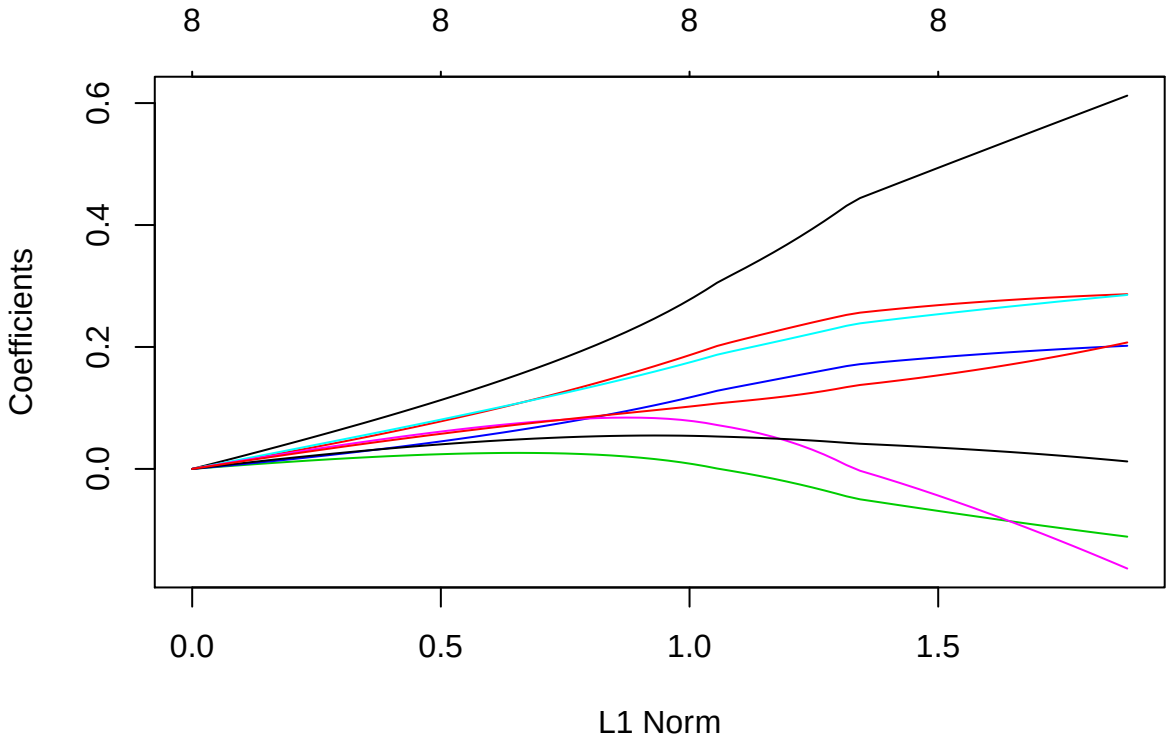
```
#Ridge
ridge <- cv.glmnet(trainxscale_only[,1:8], trainxscale_only[,9], nfolds = 10, alpha = 0)

paste("Tuning paremeter is", round(ridge$lambda.min, 4))
```

```
## [1] "Tuning paremeter is 0.0965"
```

```
plot.cv.glmnet(ridge)
```




```
ridge2 <- glmnet(trainxscale_only[,1:8], trainxscale_only[,9], alpha = 0)
plot.glmnet(ridge2)
```



```r
coef(ridge)
```

```
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                        1
## (Intercept)  2.452345085
## lcavol       0.317607465
## lweight      0.207749630
## age         -0.003245594
## lbph         0.132737031
## svi          0.192527220
## lcp          0.067982376
## gleason      0.052456497
## pgg45        0.109563765
```

Q. I have different MSE.... even with my friends who have the same set.seed number...

**Model Selection (20 pts)**

```r
subsetcoeffill <- matrix(0, 9, 1)
subsetcoeffill <- unname(rbind(as.matrix(subsetcoef), NA, NA, NA, NA, NA, NA)) #Fill NA for empty

Lasso <- coef(lasso)[,1]
Lasso[c(4, 7, 8)] <- NA
Lasso <- unname(Lasso)


models <- data.frame(
      LS = as.vector(table3.2[,1]), "Best Subset" = subsetcoeffill,
      Ridge = as.vector(coef(ridge)), Lasso = Lasso,
      PCR = unname(coef(pcrfunc, intercept = T)),
      PLS = unname(coef(plsrfunc, intercept = T))
      )


#I need to add intercept for PCR and PLSR, then add them into the models.
PCR = unname(pcrfunc$coefficients[,,8])
      PLS = as.vector(plsrfunc$coefficients[,,8])


mse <- c()
#add 6, 7 into the for loop after adding pcr and pls into models.
for (i in c(1, 3, 5, 6)){
  yhat <- as.matrix(cbind(1, testing[,-9])) %*% models[,i]
  mse[i] <- sum((testing[,9] - yhat)^2) / nrow(testing)
}
```

```r
subset_yhat <- as.matrix(cbind(1, testing[,1:2])) %*% models[,3][1:3] #Have NA so calculate separately.
mse[2] <- sum((testing[,9] - subset_yhat)^2) / nrow(testing)

lasso_yhat <- as.matrix(cbind(1, testing[,c(1, 2, 4, 5, 8)])) %*% na.omit(models[,4])
mse[4] <- sum((testing[,9] - lasso_yhat)^2) / nrow(testing)

print("Here is the mse for 6 models:")
```

```
## [1] "Here is the mse for 6 models:"
```

```r
mse
```

```
## [1] 45.245761  1.915015 20.252751  3.795633 45.245761 45.245761
```

```r
models <- rbind(models, mse)
rownames(models) <- c("Intercept", "lcavol", "lweight",
                      "age", "lbph", "svi", "lcp", "gleason",
                      "pgg45", "Test Error")
models
```

```
##                     LS Best.Subset        Ridge      Lasso          PCR
## Intercept   2.45234509   2.4523451  2.452345085 2.45234509  2.45234509
## lcavol      0.71640701   0.7798589  0.317607465 0.56536414  0.71640701
## lweight     0.29264240   0.3519101  0.207749630 0.19936439  0.29264240
## age        -0.14254963          NA -0.003245594         NA -0.14254963
## lbph        0.21200760          NA  0.132737031 0.02917609  0.21200760
## svi         0.30961953          NA  0.192527220 0.11532140  0.30961953
## lcp        -0.28900562          NA  0.067982376         NA -0.28900562
## gleason    -0.02091352          NA  0.052456497         NA -0.02091352
## pgg45       0.27734595          NA  0.109563765 0.01647872  0.27734595
## Test Error 45.24576149   1.9150154 20.252750581 3.79563253 45.24576149
##                    PLS
## Intercept   2.45234509
## lcavol      0.71640701
## lweight     0.29264240
## age        -0.14254963
## lbph        0.21200760
## svi         0.30961953
## lcp        -0.28900562
## gleason    -0.02091352
## pgg45       0.27734595
## Test Error 45.24576149
```

*Comment:*

From the table I got,