

# Ridge Regression

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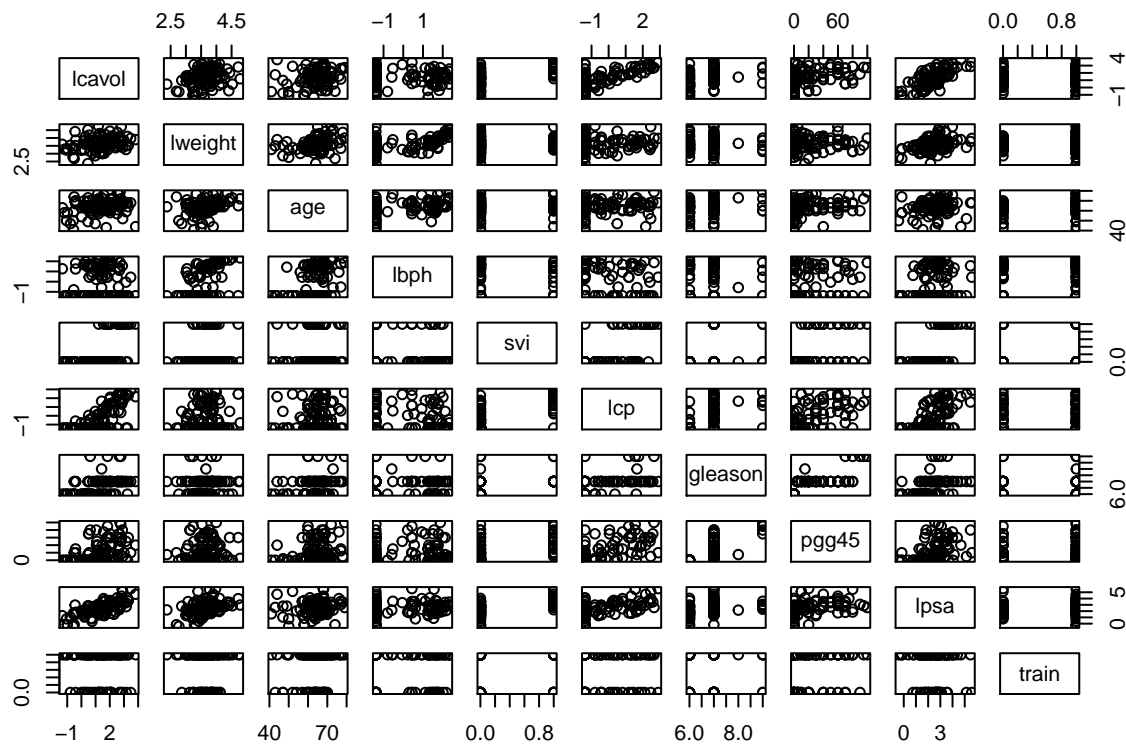
25/02/20

For the Assignment about Ridge Regression, we compute a function to choose a penalization parameter. The theory about Ridge Regression is used to write basic functions. In order to test these functions the Boston Housing data is used with it. Alternatively, we proposed to use a package that deals with Ridge Regression in the background.

## Choosing the penalization parameter

Testdate (to be removed later!)

```
prostate <- read.table("prostate_data.txt", header=TRUE, row.names = 1)
plot(prostate)
```



```
train.sample <- which(prostate$train==TRUE) ##separate trainingsdata from testdata
val.sample <- which(prostate$train==FALSE)
```

```
Y_t <- scale( prostate$lpsa[train.sample], center=TRUE, scale=FALSE) ## center but not scale for respon
X_t <- scale( as.matrix(prostate[train.sample,1:8]), center=TRUE, scale=TRUE) ##scale and center for
```

```

Y_val <- scale( prostate$lpsa[val.sample], center=TRUE, scale=FALSE) ## center but not scale for respon
X_val <- scale( as.matrix(prostate[val.sample,1:8]), center=TRUE, scale=TRUE)

#predictors
p <- dim(X_t)[2]

XtX <- t(X_t)%*%X_t
d2 <- eigen(XtX,symmetric = TRUE, only.values = TRUE)$values #eigenvalues of xtx

(cond.number <- sqrt(max(d2)/min(d2)))

## [1] 4.435608

lambda.max = 2e4
n_lambdas <- 25 ## look at 25 different values
lambda.v <- exp(seq(0,log(lambda.max+1),length=n_lambdas))-1 #lambda vector

n_val <- length(Y_val)

PMSE_vs <- function(X_t, Y_t, X_val, Y_val, lambda){
  p <- dim(X_t)[2]
  n_lambdas <- length(lambda)

  XtX <- t(X_t)%*%X_t

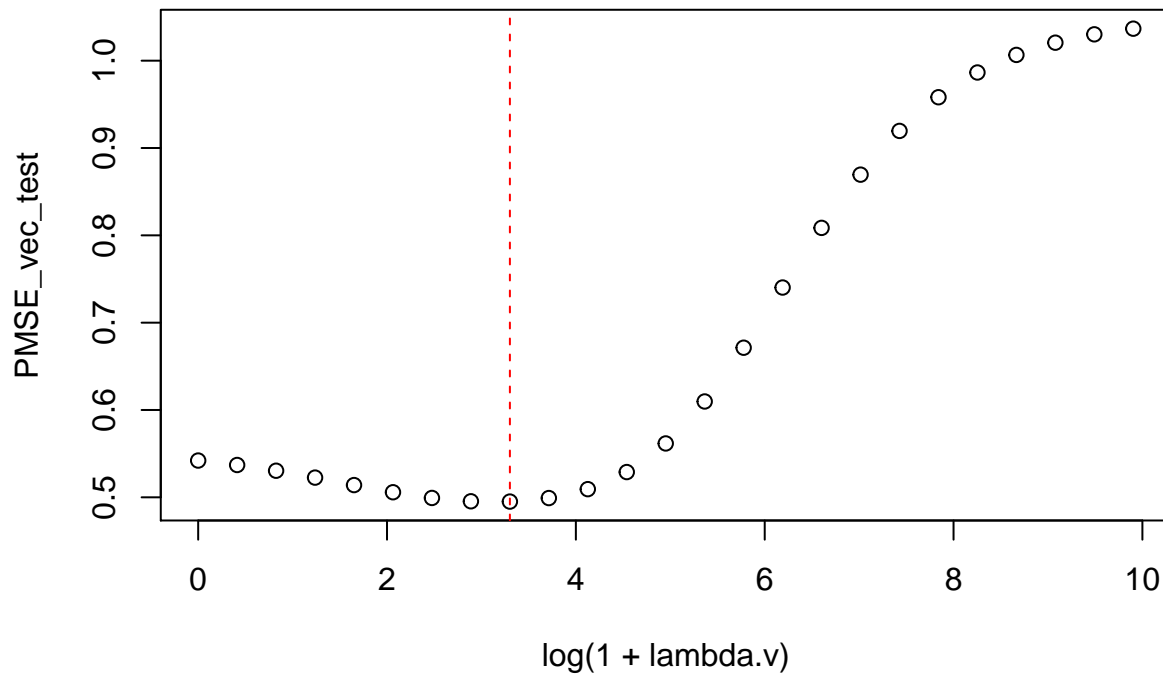
  PMSE_vec <- vector("numeric", length = n_lambdas)
  for(l in 1:n_lambdas){
    lambda <- lambda.v[l]
    beta_hat <- solve(XtX + lambda*diag(1,p)) %*% t(X_t) %*% Y_t
    #y_hat = X %*% beta_hat
    m_hat_vec <- vector("numeric", length = n_val)

    for (n in 1:n_val){
      m_hat_vec[n] <- (Y_val[n]-(X_val[n,]%*%beta_hat))^2
    }
    PMSE_vec[l]<- sum(m_hat_vec)/n_val
  }
  return (PMSE_vec)
}

PMSE_vec_test <- PMSE_vs(X_t, Y_t, X_val, Y_val, lambda.v)

lambda.CV <- lambda.v[which.min(PMSE_vec_test)]
plot(log(1+lambda.v), PMSE_vec_test)
abline(v=log(1+lambda.CV),col=2,lty=2)

```



```
##Task 2
```

```
X_t_shuffel <- X_t[sample(nrow(X_t)),]
```

```
k = 10
```

```
is.matrix(X_t_shuffel)
```

```
## [1] TRUE
```

```
#Assume we can delete the last ? values
```

```
length(X_t_shuffel)
```

```
## [1] 536
```

```
n_subset = as.integer(length(X_t_shuffel)/k)
```

```
n_subset
```

```
## [1] 53
```

```
k_subsets_matrix <- matrix(0, nrow=k, ncol = n_subset)
```

```
c = 1
```

```
for (i in 1:k){
```

```
  for (j in 1:n_subset){
```

```
    k_subsets_k <- X_t_shuffel[(n_subset*(i-1)+1):(n_subset*i)]
```

```
    c<- c + 1
```

```
  }
```

```
}
```

```
k_subsets_matrix
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13]
## [1,]    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```

## [2,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [3,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [4,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [5,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [6,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [7,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [8,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [9,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [10,] 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##      [,14] [,15] [,16] [,17] [,18] [,19] [,20] [,21] [,22] [,23] [,24] [,25]
## [1,] 0 0 0 0 0 0 0 0 0 0 0 0
## [2,] 0 0 0 0 0 0 0 0 0 0 0 0
## [3,] 0 0 0 0 0 0 0 0 0 0 0 0
## [4,] 0 0 0 0 0 0 0 0 0 0 0 0
## [5,] 0 0 0 0 0 0 0 0 0 0 0 0
## [6,] 0 0 0 0 0 0 0 0 0 0 0 0
## [7,] 0 0 0 0 0 0 0 0 0 0 0 0
## [8,] 0 0 0 0 0 0 0 0 0 0 0 0
## [9,] 0 0 0 0 0 0 0 0 0 0 0 0
## [10,] 0 0 0 0 0 0 0 0 0 0 0 0
##      [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34] [,35] [,36] [,37]
## [1,] 0 0 0 0 0 0 0 0 0 0 0 0
## [2,] 0 0 0 0 0 0 0 0 0 0 0 0
## [3,] 0 0 0 0 0 0 0 0 0 0 0 0
## [4,] 0 0 0 0 0 0 0 0 0 0 0 0
## [5,] 0 0 0 0 0 0 0 0 0 0 0 0
## [6,] 0 0 0 0 0 0 0 0 0 0 0 0
## [7,] 0 0 0 0 0 0 0 0 0 0 0 0
## [8,] 0 0 0 0 0 0 0 0 0 0 0 0
## [9,] 0 0 0 0 0 0 0 0 0 0 0 0
## [10,] 0 0 0 0 0 0 0 0 0 0 0 0
##      [,38] [,39] [,40] [,41] [,42] [,43] [,44] [,45] [,46] [,47] [,48] [,49]
## [1,] 0 0 0 0 0 0 0 0 0 0 0 0
## [2,] 0 0 0 0 0 0 0 0 0 0 0 0
## [3,] 0 0 0 0 0 0 0 0 0 0 0 0
## [4,] 0 0 0 0 0 0 0 0 0 0 0 0
## [5,] 0 0 0 0 0 0 0 0 0 0 0 0
## [6,] 0 0 0 0 0 0 0 0 0 0 0 0
## [7,] 0 0 0 0 0 0 0 0 0 0 0 0
## [8,] 0 0 0 0 0 0 0 0 0 0 0 0
## [9,] 0 0 0 0 0 0 0 0 0 0 0 0
## [10,] 0 0 0 0 0 0 0 0 0 0 0 0
##      [,50] [,51] [,52] [,53]
## [1,] 0 0 0 0
## [2,] 0 0 0 0
## [3,] 0 0 0 0
## [4,] 0 0 0 0
## [5,] 0 0 0 0
## [6,] 0 0 0 0
## [7,] 0 0 0 0
## [8,] 0 0 0 0
## [9,] 0 0 0 0
## [10,] 0 0 0 0

```

*#Different aproach*

k=10

n\_X\_t <- dim(X\_t)[1]

p\_X\_t <- dim(X\_t)[2] *#length of columns*

n\_subset <- as.integer((n\_X\_t)/k)+ 1

group <- rep(seq(1,k), times = n\_subset)

group <- group[1:n\_X\_t]

group\_random <- sample(group)

X\_t\_group <- cbind(X\_t, group\_random)

Y\_t\_group <- cbind(Y\_t, group\_random)

*#now we can start:*

PMSE <- list()

for (la in 1:n\_lambdas){

lambda <- lambda.v[la]

y\_hat <- list()

beta <- list()

h <- list()

y <- list()

for (l in 1:k){

new\_X\_t\_val <- subset(X\_t\_group, group\_random==1)[ ,1:p\_X\_t]

new\_X\_t\_test <- subset(X\_t\_group, group\_random!=1)[ ,1:p\_X\_t]

new\_Y\_t\_val <- subset.matrix(Y\_t\_group, group\_random==1)[,1]

new\_Y\_t\_test <- subset.matrix(Y\_t\_group, group\_random!=1)[,1]

p\_new <- dim(new\_X\_t\_test)[2]

p\_new\_v <- dim(new\_X\_t\_val)[2]

*#H.i <- new\_X\_t\_test%%solve(t(new\_X\_t\_test)%%new\_X\_t\_test + 1\*diag(1,p\_new))%% t(new\_X\_t\_test)*

beta[[l]] <- solve(t(new\_X\_t\_test)%%new\_X\_t\_test + lambda\*diag(1,p\_new))%% t(new\_X\_t\_test)%%(new\_Y\_t\_test)

*#y\_hat.i <- H.i %%(new\_Y\_t\_test)*

H\_val <- new\_X\_t\_val%%solve(t(new\_X\_t\_val)%%new\_X\_t\_val + (lambda+0.000000001)\*diag(1,p\_new\_v))%%(new\_Y\_t\_val)

*# singular matrix for lambda = 0 -> trick: add a very small number*

y\_hat[[l]] <- (new\_X\_t\_val)%%beta[[l]]

h[[l]] <- diag(H\_val)

y[[l]] <- new\_Y\_t\_val

}

y\_hat <- c(do.call(rbind, y\_hat))

beta <- c(do.call(cbind, beta))

h <- c(do.call(rbind, h))

y <- c(do.call(rbind, y))

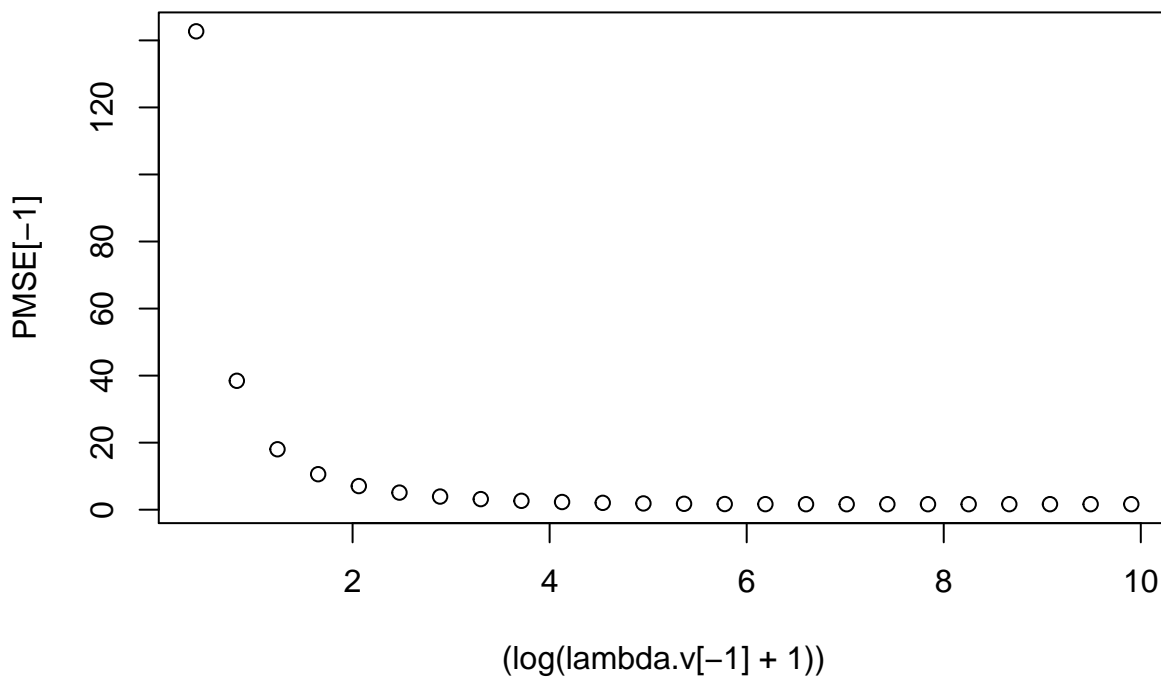
PMSE[[la]] <- 1/n\_X\_t \* sum(((y-y\_hat)/(1-h))^2)

```
#PMSE_vec[l]<- #sum(m_hat_vec)/n_val #not this but something
}  
PMSE
```

```
## [[1]]  
## [1] 8.557086e+18  
##  
## [[2]]  
## [1] 142.6991  
##  
## [[3]]  
## [1] 38.4593  
##  
## [[4]]  
## [1] 18.02619  
##  
## [[5]]  
## [1] 10.58874  
##  
## [[6]]  
## [1] 7.053541  
##  
## [[7]]  
## [1] 5.103468  
##  
## [[8]]  
## [1] 3.922699  
##  
## [[9]]  
## [1] 3.161826  
##  
## [[10]]  
## [1] 2.64993  
##  
## [[11]]  
## [1] 2.295553  
##  
## [[12]]  
## [1] 2.04723  
##  
## [[13]]  
## [1] 1.875265  
##  
## [[14]]  
## [1] 1.761405  
##  
## [[15]]  
## [1] 1.692151  
##  
## [[16]]  
## [1] 1.655292  
##  
## [[17]]  
## [1] 1.639532
```

```
##
## [[18]]
## [1] 1.635647
##
## [[19]]
## [1] 1.637288
##
## [[20]]
## [1] 1.640784
##
## [[21]]
## [1] 1.644366
##
## [[22]]
## [1] 1.647368
##
## [[23]]
## [1] 1.649654
##
## [[24]]
## [1] 1.651307
##
## [[25]]
## [1] 1.652464
```

```
plot((log(lambda.v[-1]+1)), PMSE[-1]) #First lambda is super high
```



### Task 3

```
#Different aproach
```

```

k=5
n_X_t <- dim(X_t)[1]
p_X_t <- dim(X_t)[2] #length of columns
n_subset <- as.integer((n_X_t)/k)+ 1
group <- rep(seq(1,k), times = n_subset)
group <- group[1:n_X_t]

group_random <- sample(group)

X_t_group <- cbind(X_t, group_random)
Y_t_group <- cbind(Y_t, group_random)

#now we can start:
PMSE <- list()

for (la in 1:n_lambdas){

  lambda <- lambda.v[la]

  y_hat <- list()
  beta <- list()
  h <- list()
  y <- list()

  for (l in 1:k){
    new_X_t_val <- subset(X_t_group, group_random==1)[ ,1:p_X_t]
    new_X_t_test <- subset(X_t_group, group_random!=1)[ ,1:p_X_t]

    new_Y_t_val <- subset.matrix(Y_t_group, group_random==1)[,1]
    new_Y_t_test <- subset.matrix(Y_t_group, group_random!=1)[,1]

    p_new <- dim(new_X_t_test)[2]
    p_new_v <- dim(new_X_t_val)[2]
    #H.i <- new_X_t_test%%solve(t(new_X_t_test)%%new_X_t_test + 1*diag(1,p_new))%% t(new_X_t_test)
    beta[[l]] <- solve(t(new_X_t_test)%%new_X_t_test + lambda*diag(1,p_new))%% t(new_X_t_test)%%(new
    #y_hat.i <- H.i %% (new_Y_t_test)
    H_val <- new_X_t_val%%solve(t(new_X_t_val)%%new_X_t_val + (lambda+0.000000001)*diag(1,p_new_v))%
    # singular matrix for lambda = 0 -> trick: add a very small number
    y_hat[[l]] <- (new_X_t_val)%%beta[[l]]
    h[[l]] <- diag(H_val)
    y[[l]] <- new_Y_t_val

  }
  y_hat <- c(do.call(rbind, y_hat))
  beta <- c(do.call(cbind, beta))
  h <- c(do.call(rbind, h))
  y <- c(do.call(rbind, y))

  PMSE[[la]] <- 1/n_X_t * sum(((y-y_hat)/(1-h))^2)
  #PMSE_vec[l]<- #sum(m_hat_vec)/n_val #not this but something
}

```



```

## Warning in (function (... , deparse.level = 1) : number of columns of result is
## not a multiple of vector length (arg 3)

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## Warning in y - y_hat: Länge des längeren Objektes
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```

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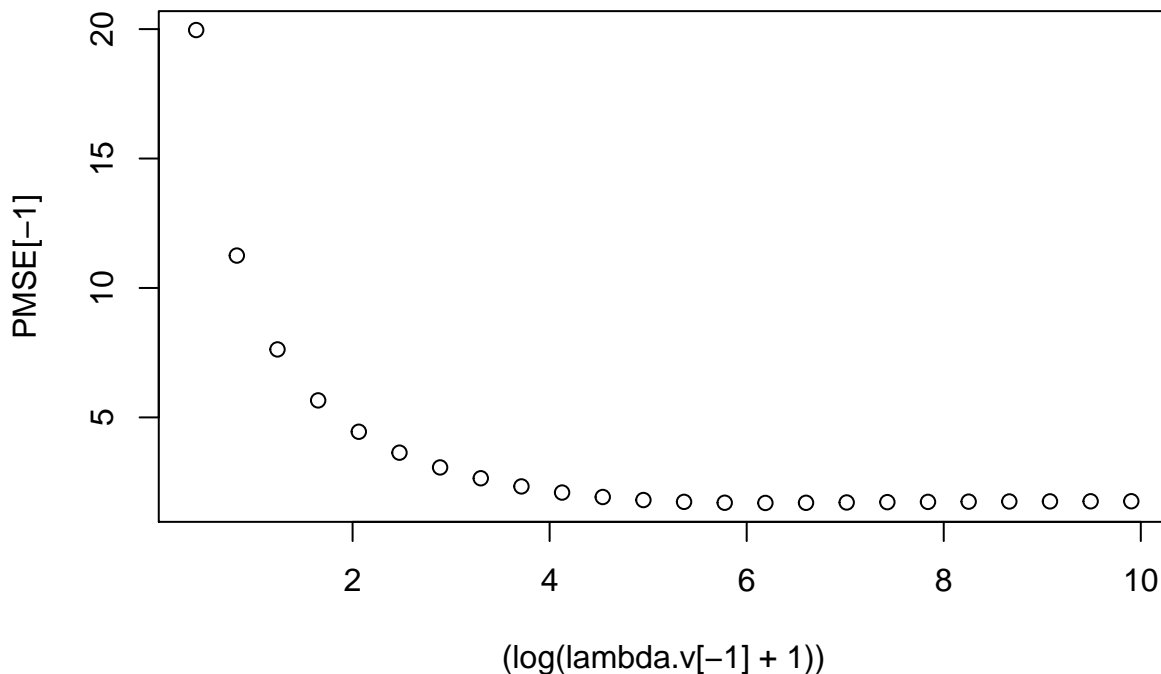
## Warning in y - y_hat: Länge des längeren Objektes
##      ist kein Vielfaches der Länge des kürzeren Objektes
```

```
PMSE
```

```
## [[1]]
## [1] 111.2021
##
## [[2]]
## [1] 19.9631
##
## [[3]]
## [1] 11.2515
##
## [[4]]
## [1] 7.625774
##
## [[5]]
## [1] 5.657326
##
## [[6]]
## [1] 4.445332
##
## [[7]]
## [1] 3.637422
##
## [[8]]
```

```
## [1] 3.067352
##
## [[9]]
## [1] 2.648486
##
## [[10]]
## [1] 2.333651
##
## [[11]]
## [1] 2.097093
##
## [[12]]
## [1] 1.924684
##
## [[13]]
## [1] 1.807473
##
## [[14]]
## [1] 1.737147
##
## [[15]]
## [1] 1.70363
##
## [[16]]
## [1] 1.69533
##
## [[17]]
## [1] 1.701251
##
## [[18]]
## [1] 1.71302
##
## [[19]]
## [1] 1.725545
##
## [[20]]
## [1] 1.736429
##
## [[21]]
## [1] 1.744959
##
## [[22]]
## [1] 1.751249
##
## [[23]]
## [1] 1.755716
##
## [[24]]
## [1] 1.758811
##
## [[25]]
## [1] 1.760923
```

```
plot((log(lambda.v[-1]+1)), PMSE[-1])
```



## Ridge Regression for the Boston Housing data

Loading the (corrected) Boston Housing data

```
library(MASS)
data(Boston)
help(Boston)
```

```
boston <- load("boston.Rdata")
```

## Alternative solution for Ridge Regression for the Boston Housing data

There exists a package called 'glmnet' that deals with elastic nets. Specifying  $\alpha = 0$  Ridge Regression is applied on the data.

```
#install.packages("glmnet")
library(glmnet)
```

```
## Loading required package: Matrix
```

```
## Loaded glmnet 3.0-2
```

```
response <- "MEDV"
```

```
explanatory <- c("CRIM", "ZN", "INDUS", "CHAS", "NOX", "RM", "AGE", "DIS", "RAD", "TAX", "PTRATIO", "B")
```

```
# cv.glmnet cannot handel factors -> "CHAS" is a factor
```

```
boston.c$CHAS <- as.numeric(boston.c$CHAS)
```

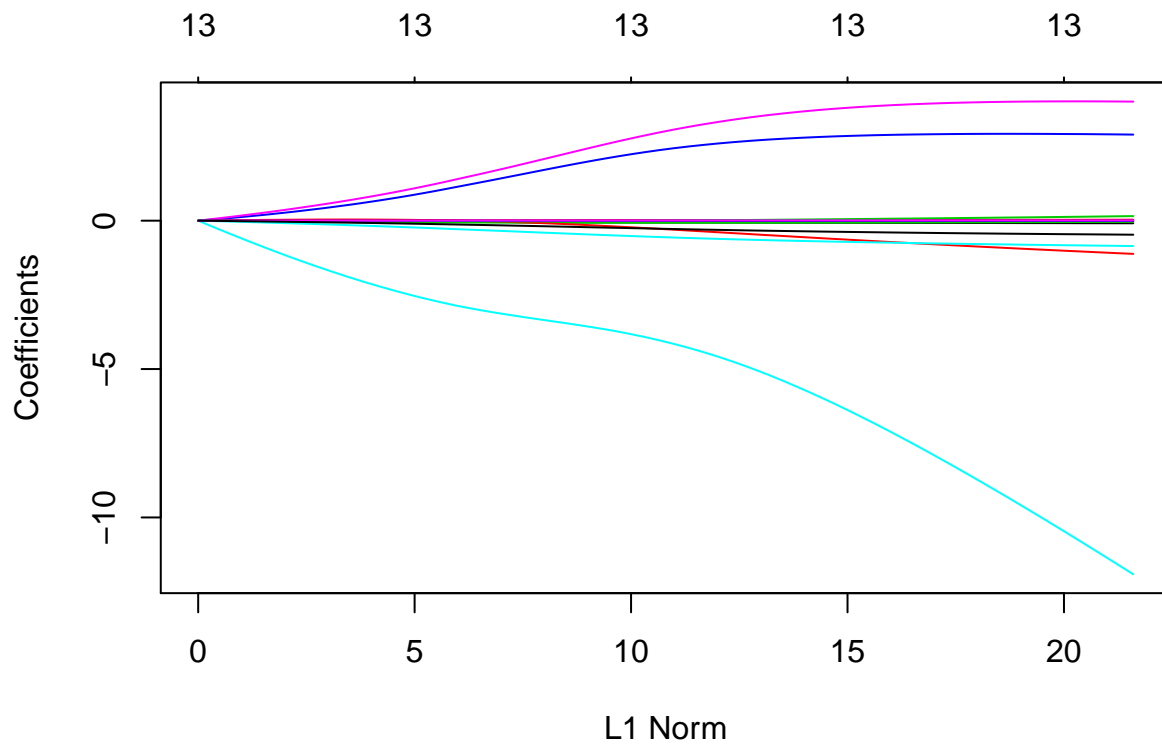
```
(ridge <- glmnet(y = boston.c$MEDV, x = as.matrix(boston.c[, explanatory]), alpha = 0))
```

```
##
## Call: glmnet(x = as.matrix(boston.c[, explanatory]), y = boston.c$MEDV,      alpha = 0)
##
##      Df      %Dev Lambda
## 1    13 0.00000 6778.0
## 2    13 0.00792 6176.0
## 3    13 0.00868 5627.0
## 4    13 0.00952 5127.0
## 5    13 0.01043 4672.0
## 6    13 0.01143 4257.0
## 7    13 0.01253 3878.0
## 8    13 0.01372 3534.0
## 9    13 0.01503 3220.0
## 10   13 0.01646 2934.0
## 11   13 0.01802 2673.0
## 12   13 0.01972 2436.0
## 13   13 0.02159 2219.0
## 14   13 0.02362 2022.0
## 15   13 0.02583 1843.0
## 16   13 0.02824 1679.0
## 17   13 0.03087 1530.0
## 18   13 0.03372 1394.0
## 19   13 0.03683 1270.0
## 20   13 0.04020 1157.0
## 21   13 0.04386 1054.0
## 22   13 0.04783  960.7
## 23   13 0.05213  875.4
## 24   13 0.05678  797.6
## 25   13 0.06180  726.7
## 26   13 0.06721  662.2
## 27   13 0.07304  603.4
## 28   13 0.07932  549.8
## 29   13 0.08605  500.9
## 30   13 0.09326  456.4
## 31   13 0.10100  415.9
## 32   13 0.10920  378.9
## 33   13 0.11790  345.3
## 34   13 0.12720  314.6
## 35   13 0.13710  286.6
## 36   13 0.14750  261.2
## 37   13 0.15840  238.0
## 38   13 0.16990  216.8
## 39   13 0.18200  197.6
## 40   13 0.19450  180.0
## 41   13 0.20760  164.0
## 42   13 0.22110  149.5
## 43   13 0.23510  136.2
## 44   13 0.24940  124.1
## 45   13 0.26420  113.1
## 46   13 0.27920  103.0
## 47   13 0.29450   93.9
## 48   13 0.31000   85.5
## 49   13 0.32570   77.9
## 50   13 0.34150   71.0
```

```
## 51 13 0.35730 64.7
## 52 13 0.37320 59.0
## 53 13 0.38900 53.7
## 54 13 0.40470 48.9
## 55 13 0.42030 44.6
## 56 13 0.43570 40.6
## 57 13 0.45090 37.0
## 58 13 0.46590 33.7
## 59 13 0.48060 30.7
## 60 13 0.49490 28.0
## 61 13 0.50900 25.5
## 62 13 0.52270 23.2
## 63 13 0.53600 21.2
## 64 13 0.54890 19.3
## 65 13 0.56140 17.6
## 66 13 0.57340 16.0
## 67 13 0.58500 14.6
## 68 13 0.59610 13.3
## 69 13 0.60660 12.1
## 70 13 0.61670 11.1
## 71 13 0.62620 10.1
## 72 13 0.63530 9.2
## 73 13 0.64380 8.4
## 74 13 0.65170 7.6
## 75 13 0.65920 6.9
## 76 13 0.66610 6.3
## 77 13 0.67260 5.8
## 78 13 0.67860 5.2
## 79 13 0.68410 4.8
## 80 13 0.68920 4.4
## 81 13 0.69390 4.0
## 82 13 0.69820 3.6
## 83 13 0.70210 3.3
## 84 13 0.70570 3.0
## 85 13 0.70900 2.7
## 86 13 0.71200 2.5
## 87 13 0.71480 2.3
## 88 13 0.71730 2.1
## 89 13 0.71960 1.9
## 90 13 0.72170 1.7
## 91 13 0.72360 1.6
## 92 13 0.72530 1.4
## 93 13 0.72690 1.3
## 94 13 0.72830 1.2
## 95 13 0.72960 1.1
## 96 13 0.73080 1.0
## 97 13 0.73190 0.9
## 98 13 0.73280 0.8
## 99 13 0.73370 0.7
## 100 13 0.73450 0.7
```

```
# alpha = 0: Ridge Regression
# alpha = 1: Lasso Regression
plot(ridge)
```





```
(cv.ridge <- cv.glmnet(y = boston.c$MEDV, x = as.matrix(boston.c[, explanatory]), alpha = 0))

##
## Call:  cv.glmnet(x = as.matrix(boston.c[, explanatory]), y = boston.c$MEDV,      alpha = 0)
##
## Measure: Mean-Squared Error
##
##      Lambda Measure      SE Nonzero
## min  0.678    24.38  4.253         13
## 1se  5.248    28.47  5.206         13

plot(cv.ridge)
```

