ML-HW3

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```
library('splines')        ## for 'bs'
library('dplyr')          ## for 'select', 'filter', and others
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library('magrittr')       ## for '%<>%' operator
#install.packages('glmnet')
library('glmnet')         ## for 'glmnet'
```

```
## Loading required package: Matrix

## Loaded glmnet 4.1-6
```

1. Use the prostate cancer data.

```
## load prostate data
prostate <-
  read.table(url(
    'https://web.stanford.edu/~hastie/ElemStatLearn/datasets/prostate.data'))
```

2. Use the cor function to reproduce the correlations listed in HTF Table 3.1, page 50.

```
cor(prostate)
```

```
##              lcavol      lweight       age         lbph         svi
## lcavol   1.00000000  0.280521380 0.2249999  0.027349703  0.53884500
## lweight  0.28052138  1.000000000 0.3479691  0.442264399  0.15538490
## age      0.22499988  0.347969112 1.0000000  0.350185896  0.11765804
## lbph     0.02734970  0.442264399 0.3501859  1.000000000 -0.08584324
## svi      0.53884500  0.155384903 0.1176580 -0.085843238  1.00000000
## lcp      0.67531048  0.164537142 0.1276678 -0.006999431  0.67311118
## gleason  0.43241706  0.056882093 0.2688916  0.077820447  0.32041222
## pgg45    0.43365225  0.107353785 0.2761124  0.078460018  0.45764762
## lpsa     0.73446033  0.433319382 0.1695928  0.179809404  0.56621822
## train   -0.04654347 -0.009940658 0.1776155 -0.029939957  0.02679950
##                 lcp      gleason      pgg45        lpsa        train
## lcavol   0.675310484  0.43241706 0.43365225  0.73446033 -0.046543468
## lweight  0.164537142  0.05688209 0.10735379  0.43331938 -0.009940658
## age      0.127667752  0.26889160 0.27611245  0.16959284  0.177615517
## lbph    -0.006999431  0.07782045 0.07846002  0.17980940 -0.029939957
## svi      0.673111185  0.32041222 0.45764762  0.56621822  0.026799505
## lcp      1.000000000  0.51483006 0.63152825  0.54881317 -0.037427296
## gleason  0.514830063  1.00000000 0.75190451  0.36898681 -0.044171456
## pgg45    0.631528246  0.75190451 1.00000000  0.42231586  0.100516371
## lpsa     0.548813175  0.36898681 0.42231586  1.00000000 -0.033889743
## train   -0.037427296 -0.04417146 0.10051637 -0.03388974  1.000000000
```

```
# heatmap(cor(prostate), Rowv=NA, Colv=NA, symm=T,
#          main='Correlation among inputs' )
```

3. Treat lcavol as the outcome, and use all other variables in the data set as predictors. & 4. With the training subset of the prostate data, train a least-squares regression model with all predictors using the lm function.

```
## split prostate into testing and training subsets
prostate_train <- prostate %>%
  filter(train == TRUE) %>%
  select(-train)

summary(prostate_train)
```

```
##      lcavol          lweight           age             lbph
##  Min.   :-1.3471   Min.   :2.375   Min.   :41.00   Min.   :-1.38629
##  1st Qu.: 0.4883   1st Qu.:3.330   1st Qu.:61.00   1st Qu.:-1.38629
##  Median : 1.4679   Median :3.599   Median :65.00   Median :-0.05129
##  Mean   : 1.3135   Mean   :3.626   Mean   :64.75   Mean   : 0.07144
##  3rd Qu.: 2.3491   3rd Qu.:3.884   3rd Qu.:69.00   3rd Qu.: 1.54751
##  Max.   : 3.8210   Max.   :4.780   Max.   :79.00   Max.   : 2.32630
##       svi              lcp             gleason          pgg45       
##  Min.   :0.0000   Min.   :-1.3863   Min.   :6.000   Min.   :  0.00  
##  1st Qu.:0.0000   1st Qu.:-1.3863   1st Qu.:6.000   1st Qu.:  0.00  
##  Median :0.0000   Median :-0.7985   Median :7.000   Median : 15.00  
##  Mean   :0.2239   Mean   :-0.2142   Mean   :6.731   Mean   : 26.27  
##  3rd Qu.:0.0000   3rd Qu.: 0.9948   3rd Qu.:7.000   3rd Qu.: 50.00  
##  Max.   :1.0000   Max.   : 2.6568   Max.   :9.000   Max.   :100.00  
##       lpsa        
##  Min.   :-0.4308  
##  1st Qu.: 1.6673  
##  Median : 2.5688  
##  Mean   : 2.4523  
##  3rd Qu.: 3.3652  
##  Max.   : 5.4775
```

```
prostate_test <- prostate %>%
  filter(train == FALSE) %>%
  select(-train)

## predict lcavol consider all other predictors
## lm fits using L2 loss
fit <- lm(lcavol ~ ., data=prostate_train)
summary(fit)
```

```
## 
## Call:
## lm(formula = lcavol ~ ., data = prostate_train)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.71027 -0.50138  0.03103  0.51352  1.35376 
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)    
## (Intercept) -2.173357   1.526699  -1.424    0.160    
## lweight     -0.113370   0.236639  -0.479    0.634    
## age          0.020102   0.013571   1.481    0.144    
## lbph        -0.056981   0.072525  -0.786    0.435    
## svi          0.035116   0.313526   0.112    0.911    
## lcp          0.418455   0.099521   4.205 9.16e-05 ***
## gleason      0.224387   0.198812   1.129    0.264    
## pgg45       -0.009113   0.005451  -1.672    0.100 .  
## lpsa         0.575455   0.107235   5.366 1.47e-06 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
## 
## Residual standard error: 0.7116 on 58 degrees of freedom
## Multiple R-squared:  0.7118, Adjusted R-squared:  0.672 
## F-statistic:  17.9 on 8 and 58 DF,  p-value: 3.999e-13
```

```
coef(fit)
```

```
## (Intercept)      lweight          age         lbph          svi          lcp
## -2.17335699 -0.11336968  0.02010188 -0.05698125  0.03511645  0.41845469
##     gleason       pgg45        lpsa
##  0.22438690 -0.00911273  0.57545508
```

```r
residuals(fit)
```

```
##           1           2           3           4           5           6
##  0.30510051 -0.36214995 -0.31372527 -0.57604668  1.00855250 -0.80121337
##           8          11          12          13          14          16
##  0.93154303 -0.04430734 -1.45525306  1.00784627  0.84369636  1.05697269
##          17          18          19          20          21          23
## -1.07296621  1.10894970 -0.58433985 -0.20987943  0.73401898 -0.96212934
##          24          27          29          30          31          33
##  0.60155186  0.08773062  0.30844179  0.46587959 -0.39203706  0.51616536
##          35          37          38          39          40          41
## -1.00794601 -1.08327905 -0.58060313  0.68114682 -0.52751225 -0.16747733
##          43          45          46          47          51          52
## -0.46010692  0.15965010  0.70751569  0.13993772  0.20829842  0.83814762
##          56          58          59          60          61          63
##  0.30174358 -0.21418255 -0.61609540  0.27427103 -0.59282089  0.37445320
##          67          68          69          70          71          72
##  0.20410928  0.51088167 -1.71027355 -0.30736902 -0.18635786 -0.24666610
##          75          76          77          78          79          81
##  0.03553988  0.23104706  0.17458591  0.89281112 -0.27734203 -0.62839982
##          82          83          85          86          87          88
## -0.06963027  0.03103464 -0.65441115  0.38724844  0.66414753 -0.63266711
##          89          90          91          92          93          94
## -0.25266290 -0.87963313  1.35375660  0.70838106 -0.13844098  0.62802337
##          96
## -0.47525498
```

5. Use the testing subset to compute the test error (average squared-error loss) using the fitted least-squares regression model.

```r
## functions to compute testing/training error w/lm
L2_loss <- function(y, yhat)
  (y-yhat)^2
error <- function(dat, fit, loss=L2_loss)
  mean(loss(dat$lcavol, predict(fit, newdata=dat)))

## testing error
error(prostate_test, fit)
```

```
## [1] 0.5084068
```

6. Train a ridge regression model using the glmnet function, and tune the value of lambda (i.e., use guess and check to find the value of lambda that approximately minimizes the test error).

```r
## use glmnet to fit lasso
## glmnet fits using penalized L2 loss
## first create an input matrix and output vector
form  <- lcavol ~  lweight + age + lbph + lcp + pgg45 + lpsa + svi + gleason
x_inp <- model.matrix(form, data=prostate_train)
y_out <- prostate_train$lcavol
fit <- glmnet(x=x_inp, y=y_out, lambda=seq(0.5, 0, -0.05))
print(fit$beta)
```

```
## 9 x 11 sparse Matrix of class "dgCMatrix"

##    [[ suppressing 11 column names 's0', 's1', 's2' ... ]]

##
## (Intercept) .         .         .         .         .         .
## lweight     .         .         .         .         .         .
## age         .         .         .         .         .         .
## lbph        .         .         .         .         .         .
## lcp         0.1473018 0.1714414 0.1955919 0.2197423 0.2438928 0.2680433
## pgg45       .         .         .         .         .         .
## lpsa        0.2535992 0.2816134 0.3096214 0.3376294 0.3656374 0.3936454
## svi         .         .         .         .         .         .
## gleason     .         .         .         .         .         .
##
## (Intercept) .         .            .            .            .
## lweight     .         .            .            .           -0.113959029
## age         .         0.0006179005 0.005823836  0.010987417  0.020114429
## lbph        .         .            .           -0.004060083 -0.056959719
## lcp         0.2921937 0.3160341041 0.337951116  0.352226351  0.418442122
## pgg45       .         .            .            .           -0.009110807
## lpsa        0.4216534 0.4489636282 0.470877681  0.491246304  0.575583816
## svi         .         .            .            0.026126960  0.035184640
## gleason     .         .            .            0.011159844  0.224210312
```

```r
## functions to compute testing/training error with glmnet
error <- function(dat, fit, lam, form, loss=L2_loss) {
  x_inp <- model.matrix(form, data=dat)
  y_out <- dat$lcavol
  y_hat <- predict(fit, newx=x_inp, s=lam)  ## see predict.elnet
  mean(loss(y_out, y_hat))
}

## train_error at lambda=0
error(prostate_train, fit, lam=0, form=form)
```

```
## [1] 0.4383709
## testing error at lambda=0
error(prostate_test, fit, lam=0, form=form)
```

```
## [1] 0.5084581
```

```
## train_error at lambda=0.03
error(prostate_train, fit, lam=0.05, form=form)
```

```
## [1] 0.4708637
```

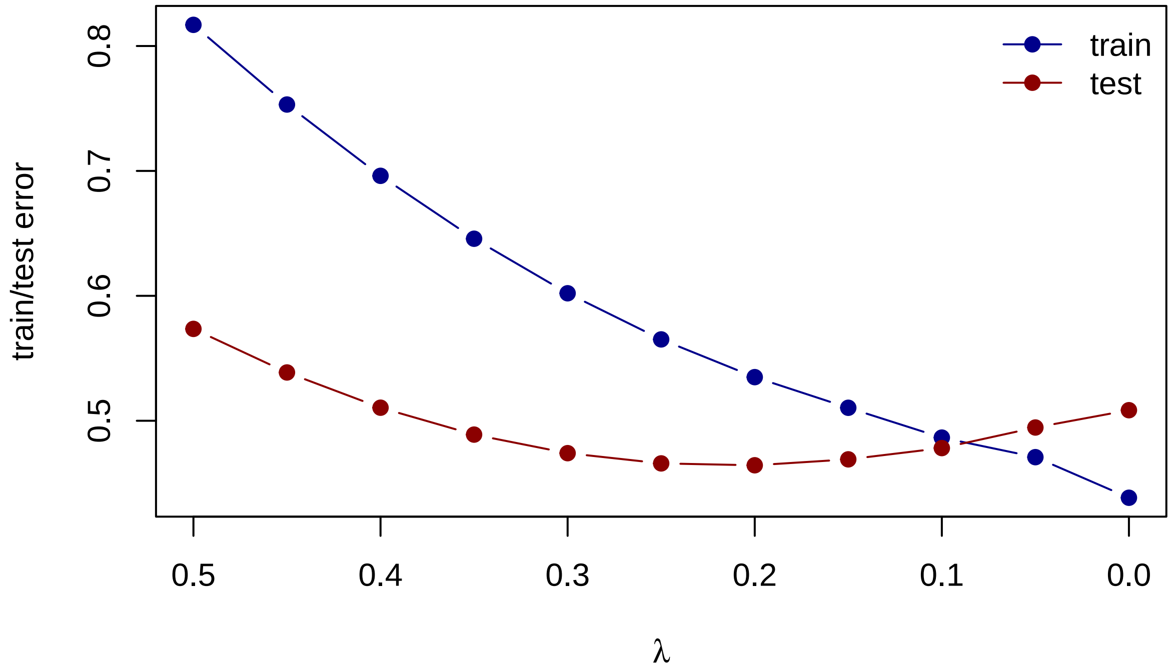
```
## testing error at lambda=0.03
error(prostate_test, fit, lam=0.05, form=form)
```

```
## [1] 0.4945864
```

7. Create a figure that shows the training and test error associated with ridge regression as a function of lambda

```
## compute training and testing errors as function of lambda
err_train_1 <- sapply(fit$lambda, function(lam)
  error(prostate_train, fit, lam, form))
err_test_1 <- sapply(fit$lambda, function(lam)
  error(prostate_test, fit, lam, form))

## plot test/train error
plot(x=range(fit$lambda),
     y=range(c(err_train_1, err_test_1)),
     xlim=rev(range(fit$lambda)),
     type='n',
     xlab=expression(lambda),
     ylab='train/test error')
points(fit$lambda, err_train_1, pch=19, type='b', col='darkblue')
points(fit$lambda, err_test_1, pch=19, type='b', col='darkred')
legend('topright', c('train','test'), lty=1, pch=19,
       col=c('darkblue','darkred'), bty='n')
```

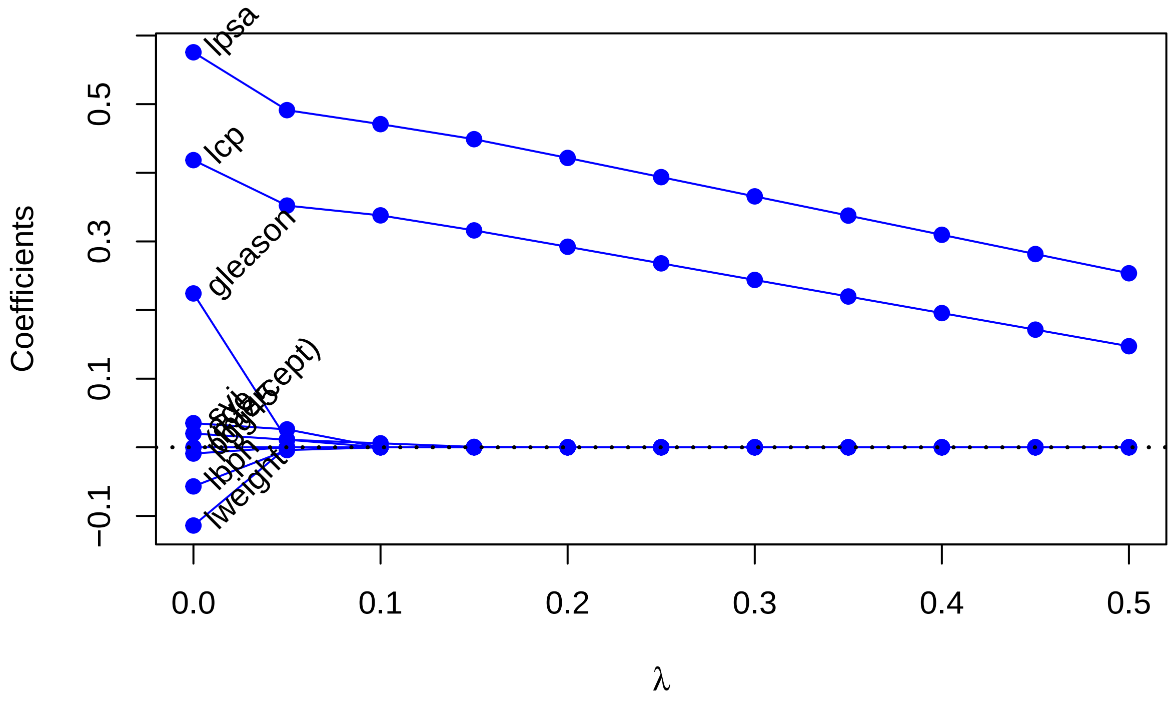


```r
colnames(fit$beta) <- paste('lam =', fit$lambda)
print(fit$beta %>% as.matrix)
```

```
##             lam = 0.5 lam = 0.45 lam = 0.4 lam = 0.35 lam = 0.3 lam = 0.25
## (Intercept) 0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
## lweight     0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
## age         0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
## lbph        0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
## lcp         0.1473018  0.1714414 0.1955919  0.2197423 0.2438928  0.2680433
## pgg45       0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
## lpsa        0.2535992  0.2816134 0.3096214  0.3376294 0.3656374  0.3936454
## svi         0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
## gleason     0.0000000  0.0000000 0.0000000  0.0000000 0.0000000  0.0000000
##             lam = 0.2   lam = 0.15   lam = 0.1   lam = 0.05      lam = 0
## (Intercept) 0.0000000 0.0000000000 0.000000000  0.000000000  0.000000000
## lweight     0.0000000 0.0000000000 0.000000000  0.000000000 -0.113959029
## age         0.0000000 0.0006179005 0.005823836  0.010987417  0.020114429
## lbph        0.0000000 0.0000000000 0.000000000 -0.004060083 -0.056959719
## lcp         0.2921937 0.3160341041 0.337951116  0.352226351  0.418442122
## pgg45       0.0000000 0.0000000000 0.000000000  0.000000000 -0.009110807
## lpsa        0.4216534 0.4489636282 0.470877681  0.491246304  0.575583816
## svi         0.0000000 0.0000000000 0.000000000  0.026126960  0.035184640
## gleason     0.0000000 0.0000000000 0.000000000  0.011159844  0.224210312
```

8. Create a path diagram of the ridge regression analysis, similar to HTF Figure 3.8

```
## plot path diagram
plot(x=range(fit$lambda),
     y=range(as.matrix(fit$beta)),
     type='n',
     xlab=expression(lambda),
     ylab='Coefficients')
for(i in 1:nrow(fit$beta)) {
  points(x=fit$lambda, y=fit$beta[i,], pch=19, col='blue')
  lines(x=fit$lambda, y=fit$beta[i,], col='blue')
}
text(x=0, y=fit$beta[,ncol(fit$beta)],
     labels=rownames(fit$beta),
     xpd=NA, pos=4, srt=45)
abline(h=0, lty=3, lwd=2)
```


lpsa
lcp
gleason
(Intercept)
svi
age
pgg45
lbph
lweight
Coefficients
λ