homework1

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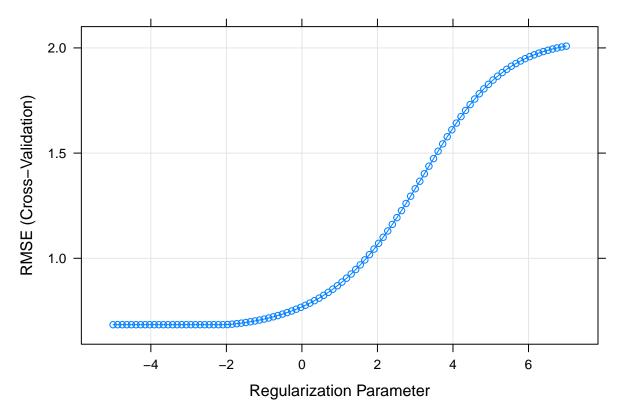
```
library(glmnet)
library(caret)
library(corrplot)
library(plotmo)
library(tidyverse)
library(pls)
train_data = read.csv("./data/solubility_train.csv")
train_data <- na.omit(train_data)</pre>
test_data = read.csv("./data/solubility_test.csv")
test_data <- na.omit(test_data)</pre>
train2 <- model.matrix(Solubility ~ .,train_data)[ ,-1]</pre>
test2 <- model.matrix(Solubility ~ ., test_data)[ ,-1]</pre>
#matrix of predictors
x <- train2
y1 <- test2
#vector of response
y <- train_data$Solubility
y2 <- test_data$Solubility
```

Part(a)

```
## [1] 0.5558898
```

The mean squared error using the test data is 0.5558898

Part(b)



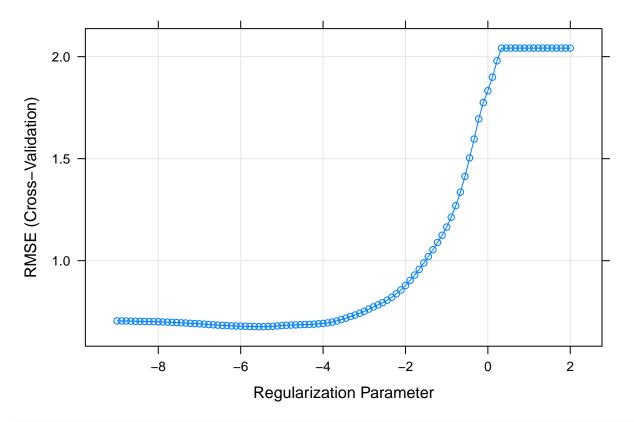
```
best_ridge = ridge.fit$bestTune

#calculate test error
ridge.pred <- predict(ridge.fit, newdata = test2)
mean((ridge.pred - test_data$Solubility)^2)</pre>
```

[1] 0.5134603

The chosen lambda is 0.1235747 and the test error is $0.5134603\,$

Part(c)



```
best_lasso = lasso.fit$bestTune

#calculate test error
lasso.pred <- predict(lasso.fit, newdata = test2)
mean((lasso.pred - test_data$Solubility)^2)

#find number of coefficient estimates
coef(lasso.fit$finalModel, lasso.fit$bestTune$lambda)</pre>
```

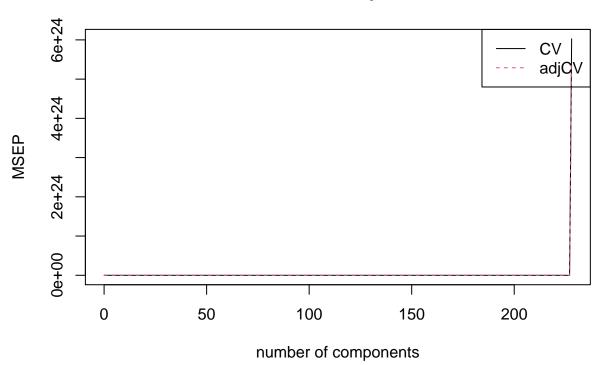
The chosen lambda is 0.00386592, the test error is 0.50333, and there are 149 non-zero coefficient estimates in the model.

Part(d)

```
#fit model using function pcr()
set.seed(1)
pcr.mod <- pcr(Solubility ~ .,
data = train_data,
scale = TRUE,
validation= "CV")
summary(pcr.mod)

validationplot(pcr.mod, val.type="MSEP", legendpos = "topright")</pre>
```

Solubility



```
trControl = ctrl1,
preProcess = c("center", "scale"))
```

The chosen M is 152 and the test error is 0.5477905