Homework 1

Jingyi Zhang

2/6/21

Load dataset

```
sol_test <-
    read_csv("./data/solubility_test.csv") %>%
    janitor::clean_names()

sol_train <-
    read_csv("./data/solubility_train.csv") %>%
    janitor::clean_names()

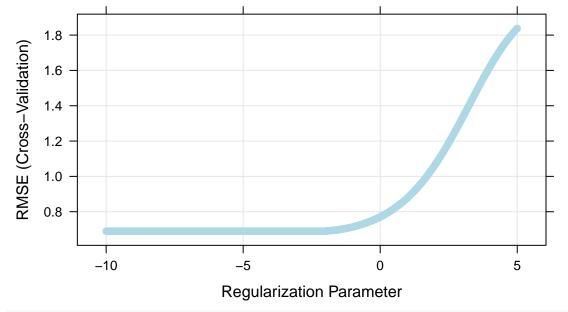
# training data
x_train <- model.matrix(solubility ~ ., sol_train)[ ,-1]
y_train <- sol_train$solubility

# test data
x_test <- model.matrix(solubility ~ ., sol_test)[ ,-1]
y_test <- sol_test$solubility</pre>
```

(a) Fit a linear model using least squares on the training data and calculate the mean squared error using the test data.

[1] 0.7455802

(b) Fit a ridge regression model on the training data, with lambda chosen by cross-validation. Report the test error.



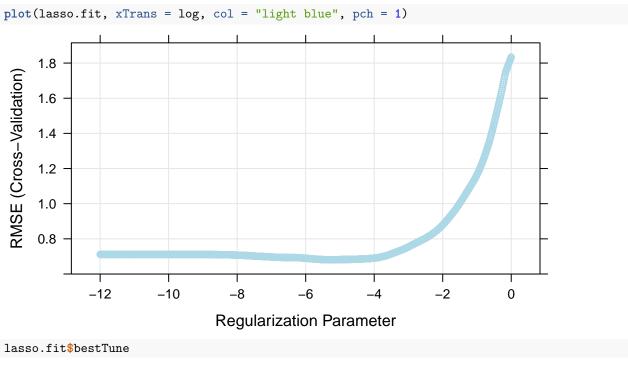
```
ridge.fit$bestTune

## alpha lambda
## 532     0 0.1317266

RMSE(predict(ridge.fit, s = "lambda.min", newx = sol_test), sol_test$solubility)

## [1] 2.929737
```

(c) Fit a lasso model on the training data, with lambda chosen by cross-validation. Report the test error and the number of non-zero coefficient estimates in your model.



```
## alpha lambda
## 565   1 0.005379148

RMSE(predict(lasso.fit, s = "lambda.min", newx = sol_test), sol_test$solubility)

## [1] 2.945769

sum(coef(lasso.fit$finalModel, lasso.fit$bestTune$lambda) != 0)

## [1] 144
```

(d) Fit a principle component regression model on the training data, with M chosen by cross-validation. Report the test error and the value of M selected by cross-validation.

```
ctrl2 <- trainControl(method = "cv", selectionFunction = "best")

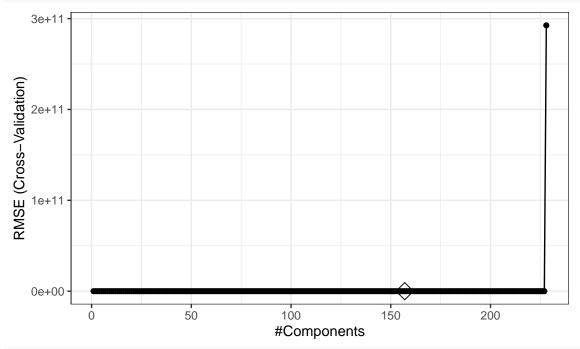
set.seed(7)
pcr.fit <-
    train(solubility~.,
        data = sol_train,
        method = "pcr",
        tuneGrid =
            data.frame(ncomp = seq(1, ncol(x_train))),
        trControl = ctrl2,
        preProcess = c("center", "scale"))</pre>
```

ncomp

```
## 157 157
```

[1] 0.549917

```
ggplot(pcr.fit, highlight = TRUE) + theme_bw()
```



```
RMSE(predict(pcr.fit, x_test), y_test)
```

```
## [1] 0.7415639
mean((predict(pcr.fit, x_test) - y_test)^2)
```

(e) Which model will you choose for predicting solubility?

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: linear, ridge, lasso, pcr
## Number of resamples: 10
##
## MAE
##
               Min.
                      1st Qu.
                                 Median
                                                     3rd Qu.
                                             Mean
## linear 0.4593506 0.5065095 0.5411760 0.5344250 0.5621513 0.5859706
## ridge 0.4668550 0.4842955 0.5407178 0.5266765 0.5569412 0.5790663
                                                                          0
## lasso 0.4525769 0.5013758 0.5336942 0.5218328 0.5459192 0.5795652
                                                                          0
## pcr
          0.4656072 0.5114016 0.5661166 0.5496161 0.5754840 0.6400421
                                                                          0
```

```
##
## RMSE
                                  Median
##
               Min.
                       1st Qu.
                                               Mean
                                                      3rd Qu.
## linear 0.5909568 0.6670690 0.7017143 0.7105437 0.7616208 0.8228557
                                                                            0
## ridge 0.5973602 0.6364183 0.7209517 0.6899735 0.7373330 0.7517499
                                                                            0
## lasso 0.5898579 0.6472640 0.6943397 0.6805959 0.7227745 0.7486055
                                                                            0
## pcr
          0.6027874 \ 0.6742055 \ 0.7316448 \ 0.7123739 \ 0.7559649 \ 0.7862302
                                                                            0
##
## Rsquared
##
               Min.
                       1st Qu.
                                  Median
                                                      3rd Qu.
                                                                    Max. NA's
                                               Mean
## linear 0.8217876 0.8718251 0.8843464 0.8798403 0.9035411 0.9143856
                                                                            0
## ridge 0.8469126 0.8680781 0.8851333 0.8862387 0.9084998 0.9200666
                                                                            0
## lasso 0.8505948 0.8737344 0.8867085 0.8893925 0.9120246 0.9230088
                                                                            0
          0.8412169 0.8662138 0.8763487 0.8790284 0.8972487 0.9220060
## pcr
                                                                            0
bwplot(resamp, metric = "RMSE")
  pcr
ridge
linear
lasso
           0.60
                                      0.70
                        0.65
                                                    0.75
                                                                 0.80
                                      RMSE
```

Based on the numeric and graph outputs, lasso model has the smallest mean RMSE among all four models. Lasso will be chosen for predicting solubility.