# $Homework\_1$

### Jeffrey LIANG

2/4/2021

```
set.seed(123123)
sl_tr =
    read_csv(here::here("solubility_train.csv")) %>%
    janitor::clean_names()

sl_ts =
    read_csv(here::here("solubility_test.csv")) %>%
    janitor::clean_names()

x_ts = model.matrix(solubility ~ ., sl_ts)[, -1]

y_ts = sl_ts$solubility
```

## $\mathbf{Q}\mathbf{1}$

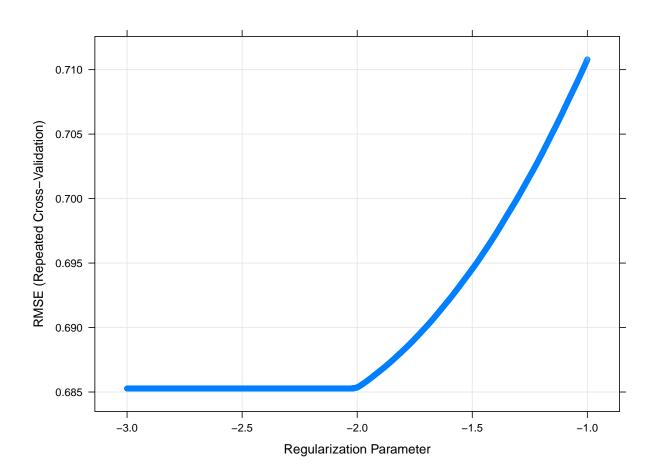
```
sl_lm =
  train(solubility~.,
    data = sl_tr,
    method = "lm",
    trControl =
       trainControl(
       method = "repeatedcv",
       number = 10,
       repeats = 5
    ))

RMSE(predict(sl_lm,newdata = sl_ts),sl_ts$solubility)
```

## [1] 0.746

### $\mathbf{Q2}$

```
sl_ridge =
  train(
    solubility ~ .,
```

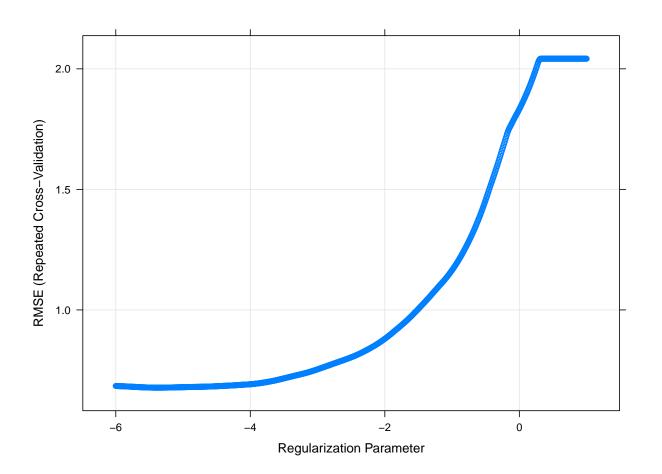


```
sl_ridge$bestTune
```

```
## alpha lambda
## 485     0     0.131

RMSE(predict(sl_ridge,s="lambda.min",newx = sl_ts),sl_ts$solubility)
```

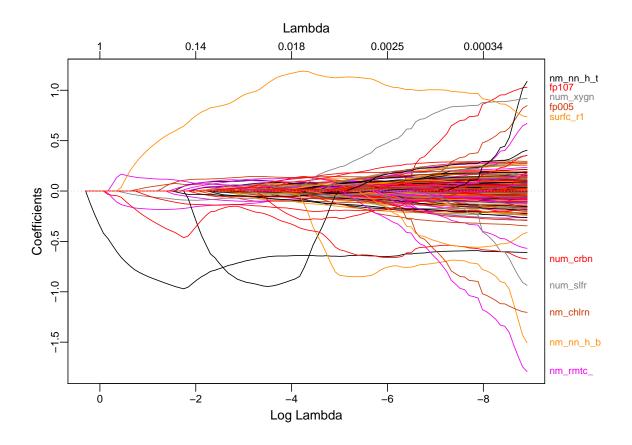
```
sl_lasso =
  train(
    solubility~.,
    data = sl_tr,
   method = "glmnet",
    tuneGrid =
      expand.grid(alpha = 1,
             lambda = exp(seq(-6, to=1, length = 1000))),
    trControl =
      trainControl(
        method = "repeatedcv",
        number = 10,
        repeats = 5
      ),
   preProcess =
      c("center","scale")
plot(sl_lasso,xTrans = log)
```



#### sl\_lasso\$bestTune

```
## alpha lambda
## 89   1 0.00459

plotmo::plot_glmnet(
   sl_lasso$finalModel
)
```



```
sum(coef(sl_lasso$finalModel, s = sl_lasso$bestTune$lambda)!=0)
```

```
## [1] 148
```

```
RMSE(predict(sl_lasso,s="lambda.min",newx = sl_ts),sl_ts$solubility)
```

## [1] 2.95

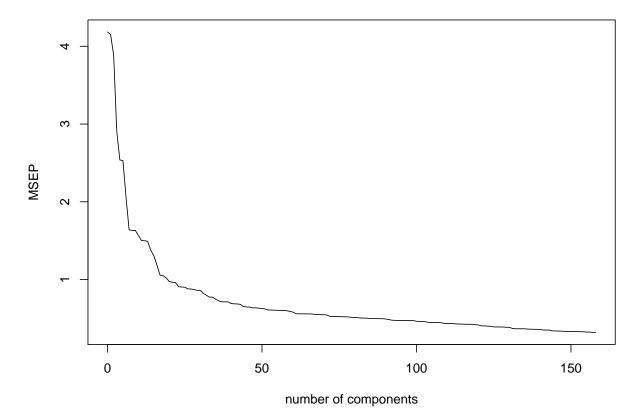
 $\mathbf{Q4}$ 

```
sl_pcr =
    train(
    solubility~.,
    data = sl_tr,
    method = "pcr",
    tuneGrid =
        expand.grid(ncomp = seq(1,ncol(sl_tr))),
    preProcess = c("center", "scale"),
    trControl =
        trainControl(
        method = "repeatedcv",
        number = 10,
        repeats = 5
    )
)
sl_pcr$bestTune
```

## ncomp ## 158 158

validationplot(sl\_pcr\$finalModel,val.type = "MSEP")

#### .outcome



```
RMSE(predict(sl_pcr,x_ts),y_ts)
## [1] 0.741
mean((predict(sl_pcr,x_ts)-y_ts)^2)
## [1] 0.549
resam =
 resamples(list(
  lm = sl_lm,
  ridge = sl_ridge,
  lasso = sl_lasso,
   pcr = sl_pcr
 ))
summary(resam)
##
## Call:
## summary.resamples(object = resam)
## Models: lm, ridge, lasso, pcr
## Number of resamples: 50
##
## MAE
##
        Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
        ## lm
## ridge 0.426 0.491 0.522 0.522 0.557 0.640
## lasso 0.444 0.498 0.512 0.519 0.543 0.606
                                               0
## pcr 0.445 0.514 0.541 0.544 0.574 0.643
##
## RMSE
        Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
##
        0.604   0.678   0.718   0.716   0.750   0.853
## lm
## ridge 0.547
               0.641 0.690 0.685
                                0.721 0.837
## lasso 0.558
               0.647 0.673 0.678
                                0.706 0.776
                                               0
## pcr
      0.609
               0.663 0.703 0.707
                                  0.748 0.808
##
## Rsquared
        Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
##
## lm
        ## ridge 0.822
             0.869 0.886 0.887
                                  0.912 0.932
                                               0
## lasso 0.850
             0.876 0.893 0.891
                                  0.903 0.929
## pcr 0.816 0.863 0.886 0.881
                                0.900 0.921
```