

1) Models used:

- Least squares: `fit.ls = lm(Y ~ ., data = data.train)`
- Stepwise
`fit.start = lm(Y ~ 1, data = data.train)`
`fit.end = lm(Y ~ .^2, data = data.train)`
`step.BIC = step(fit.start, list(upper = fit.end), k = log(n.train), trace = 0)`
- Ridge
`lambda.vals = seq(from = 0, to = 100, by = 0.05)`
`fit.ridge = lm.ridge(Y ~ ., lambda = lambda.vals, data = data.train)`
- LASSO: `all.LASSOs = cv.glmnet(x = matrix.train, y = Y.train)`
- GAM: `fit.gam = gam(data=data.train,`
`formula = Y ~ s(X1) + s(X2) + s(X3) + X4 + s(X5) + s(X6) +`
`s(X7) + s(X8) + s(X9) + X10 + s(X11) + X12 + s(X13) + s(X14) + s(X15),`
`family = gaussian(link=identity))`
- PPR: `fit.ppr.best = ppr(Y ~ ., data = data.train,`
`max.terms = 15, nterms = best.terms, sm.method = "gcv spline")`
- Regression trees:
 - `fit.tree = rpart(Y ~., data = data.train, cp = 0, method = "anova")`

2) I used a 10-fold Cross validation on the data. I first split the "Data2020.csv" into a training set and a validation set. For each process, I then calculated the MSPE for the 10 folds. I then chose the model with minimum MSPE and used that on the "Data2020testX.csv".

3) Tuning:

- Ridge&LASSO:
 - used lambda values: `lambda.vals = seq(from = 0, to = 100, by = 0.05)`
- PLS:
 - For optimal number of components:
`CV.pls = fit.pls$validation # Info from training data`
`PRESS.pls = CV.pls$PRESS # Sum of squared CV residuals`
`CV.MSPE.pls = PRESS.pls / nrow(data.train) # MSPE for internal CV`
`ind.best.pls = which.min(CV.MSPE.pls) # Optimal # of components`
- Regression trees:
 - For pruning min and se
`ind.min = which.min(info.tree[, "xerror"])`
`CP.min.raw = info.tree[ind.min, "CP"]`
`if(ind.min == 1){`
`### If minimum CP is in row 1, store this value`
`CP.min = CP.min.raw`
`} else{`
`CP.above = info.tree[ind.min-1, "CP"]`

`### (Geometric) average`
`CP.min = sqrt(CP.min.raw * CP.above)`
`}`

4)

```
library(pls)
library(mgcv)
library(rpart)
data_raw <- read.csv("Data2020.csv")
test_raw <- read.csv("Data2020testX.csv")
data <- na.omit(data_raw[, c(1:16)])
test <- na.omit(test_raw, c(1:15))

source("Helper Functions (1).R")
set.seed(2928893)

get.folds = function(n, K) {
  ### Get the appropriate number of fold labels
  n.fold = ceiling(n / K) # Number of observations per fold (rounded up)
  fold.ids.raw = rep(1:K, times = n.fold) # Generate extra labels
  fold.ids = fold.ids.raw[1:n] # Keep only the correct number of labels

  ### Shuffle the fold labels
  folds.rand = fold.ids[sample.int(n)]

  return(folds.rand)
}
### Number of folds
K = 10

### Construct folds
n = nrow(data) # Sample size
folds = get.folds(n, K)

all.models = c("GAM")
all.MSPEs = array(0, dim = c(K, length(all.models)))
colnames(all.MSPEs) = all.models

for(i in 1:K){
  data.train = data[folds != i,]
  data.valid = data[folds == i,]
  n.train = nrow(data.train)
  X.train = data.train[, -1]
  X.valid = data.valid[, -1]
  ### Get response vectors
  Y.train = data.train$Y
  Y.valid = data.valid$Y
  fit.gam = gam(data=data.train,
    formula = Y ~ s(X1) + s(X2) + s(X3) + X4 + s(X5) + s(X6) +
```

```

        s(X7) + s(X8) + s(X9) + X10 + s(X11) + X12 + s(X13) + s(X14) + s(X15),
        family = gaussian(link=identity))
summary(fit.gam)
pred.gam = predict(fit.gam, data.valid)
MSPE.gam = get.MSPE(Y.valid, pred.gam)
all.MSPEs[i, "GAM"] = MSPE.gam
}

fit.gam = gam(data=data,
              formula = Y ~ s(X1) + s(X2) + s(X3) + X4 + s(X5) + s(X6) +
                s(X7) + s(X8) + s(X9) + X10 + s(X11) + X12 + s(X13) + s(X14) + s(X15),
                family = gaussian(link=identity))
summary(fit.gam)
pred.gam = predict(fit.gam, test)
#write.table(pred.gam, "/Users/dollina/Desktop/Submit.csv", sep = ",", row.names =
FALSE, col.names=FALSE)

```

5) Variables that are important: evaluated this used LASSO and BIC and then tested on PCA.

- X2
- X4
- X10
- X12