Lab 5: Regularization and Dimension Reduction

We will use the Hitters data set in the ISLR package to predict Salary for baseball players.

```
library(ISLR)
library(tidyverse)
library(knitr)
str(Hitters)
## 'data.frame':
                    322 obs. of 20 variables:
   $ AtBat : int 293 315 479 496 321 594 185 298 323 401 ...
## $ Hits
               : int 66 81 130 141 87 169 37 73 81 92 ...
## $ HmRun : int 1 7 18 20 10 4 1 0 6 17 ...
## $ Runs : int 30 24 66 65 39 74 23 24 26 49 ...
## $ RBI : int 29 38 72 78 42 51 8 24 32 66 ...
## $ Walks : int 14 39 76 37 30 35 21 7 8 65 ...
   $ Years : int 1 14 3 11 2 11 2 3 2 13 ...
##
## $ CAtBat : int 293 3449 1624 5628 396 4408 214 509 341 5206 ...
## $ CHits : int 66 835 457 1575 101 1133 42 108 86 1332 ... ## $ CHmRun : int 1 69 63 225 12 19 1 0 6 253 ...
## $ CRuns : int 30 321 224 828 48 501 30 41 32 784 ...
##
   $ CRBI : int 29 414 266 838 46 336 9 37 34 890 ...
## $ CWalks : int 14 375 263 354 33 194 24 12 8 866 ...
## $ League : Factor w/ 2 levels "A", "N": 1 2 1 2 2 1 2 1 2 1 ...
   $ Division : Factor w/ 2 levels "E","W": 1 2 2 1 1 2 1 2 2 1 ...
## $ PutOuts : int 446 632 880 200 805 282 76 121 143 0
   $ Assists : int 33 43 82 11 40 421 127 283 290 0 ...
## $ Errors : int 20 10 14 3 4 25 7 9 19 0 ...
## $ Salary : num NA 475 480 500 91.5 750 70 100 75 1100 ...
   $ NewLeague: Factor w/ 2 levels "A","N": 1 2 1 2 2 1 1 1 2 1 ...
```

0.1 Data Processing

- 1. Remove records with missing data. Create a new (complete) version of your data set. (Hint: drop_na in tidyr could be helpful.)
- 2. You may need to create dummy variables for categorical variables in your recipes.

```
step dummy(all nominal predictors()) is a good way to do this.
```

3. You may need to standardize all variables in your recipes. step_normalize(all_predictors()) is a good way to do this.

0.2 Ridge Regression

The linear_reg() specification can perform both ridge regression and the lasso. This is done with the specification of a parameter mixture. If mixture = 0 then a ridge regression model is fit and if mixture = 1 then the lasso is fit. Here is an example for ridge regression with penalty = λ :

```
ridge_spec <- linear_reg(mixture = 0, penalty = lambda) |>
  set_mode("regression") |>
  set_engine("glmnet")
```

- 1. Create a vector of λ values from $\lambda = .01$ to $\lambda = 10^10$ of length 100.
- 2. Fit a ridge regression model for each λ in your grid. Be sure to normalize your predictors.
- 3. Make a line plot of coefficient corresponding to each λ . You should have an individual line for each variable with coefficient value on the y-axis and λ on the x axis. What happens to your coefficients as λ increases?
- 4. Perform 10-fold cross validation and get an estimate of the test MSE for each λ in your grid. Which λ would you choose and why? (Hint: look at the tune package for a fast way to do this.)

0.3 Lasso

- 1. Fit the lasso model for each λ in your grid.
- 2. Make a line plot of coefficient corresponding to each λ . You should have an individual line for each variable with coefficient value on the y-axis and λ on the x axis. (Hint: coef may be a useful function). What happens to your coefficients as λ increases?
- 3. Perform 10-fold cross validation and get an estimate of the test MSE for each λ in your grid. Which λ would you choose and why?

0.4 Principal Components Regression

The function call $step_pca(all_predictors(), num_comp = d)$ will compute d principal components of predictors in a data frame as a component in a recipe.

1. Fit the PCR model using 10-fold cross validation for values of M. Be sure to normalize your predictors.

- 2. Create a plot of the CV MSE vs. *M*.
- 3. When does the smallest cross-validation error occur? Which M would you choose for your final model?
- 4. How much variability in *Y* is explained for your chosen value of *M*?

0.5 Partial Least Squares

The function call $step_pls(all_predictors(), num_comp = d)$ will compute d partial least squares components of predictors in a data frame as a component in a recipe.

- 1. Fit the PLS model using 10-fold cross validation for values of M. Be sure to normalize your predictors.
- 2. Create a plot of the CV MSE vs. M.
- 3. When does the smallest cross-validation error occur? Which M would you choose for your final model?
- 4. How much variability in *Y* is explained for your chosen value of *M*?
- 5. Discuss the difference between PCR and PLS results. Which would you prefer?