## K-FoldCV Test

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```
library(readr)
feature matrix <- read csv("feature matrix.csv")</pre>
## Parsed with column specification:
## cols(
##
     .default = col_double(),
     Primer_Name_L = col_character(),
##
##
     Seq_L = col_character(),
     exp = col_character(),
##
##
     flank_L = col_logical(),
     Primer_Name_R = col_character(),
##
     Seq_R = col_character(),
##
     flank_R = col_character(),
##
     sample_id = col_character(),
##
     sample_name = col_character(),
##
     species = col_character(),
##
     strain = col_logical()
## )
## See spec(...) for full column specifications.
View(feature_matrix)
data <- feature_matrix</pre>
data <- data %>% select(is.numeric)
## Warning: Predicate functions must be wrapped in 'where()'.
##
##
     data %>% select(is.numeric)
##
##
     # Good
##
     data %>% select(where(is.numeric))
##
## i Please update your code.
## This message is displayed once per session.
X <- select(data, -n_reads)</pre>
y <- data$n_reads
X <- as.matrix(X)</pre>
```

```
X.scaled <- scale(X)</pre>
# K-Fold CV stuff
n.folds <- 5
set.seed(1)
fold.vec <- rep(sample(1:n.folds), 1 = nrow(X.scaled))</pre>
table(fold.vec)
## fold.vec
## 1 2 3 4 5
## 40 39 39 39 39
for(test.fold in 1:n.folds){
  test.fold <- 1
  is.test <- fold.vec == test.fold</pre>
  is.train <- !is.test</pre>
  X.train = X.scaled[is.train, ]
  y.train = y[is.train]
  X.test <- X.scaled[is.test, ]</pre>
  y.test <- y[is.test]</pre>
  lambdas <-10^{seq}(2, -3, by = -.1)
  # Setting alpha = 1 implements lasso regression
  lasso_reg <- cv.glmnet(X.train, y.train, alpha = 1, lambda = lambdas, standardize = TRUE, nfolds = 5)
  plot(lasso_reg)
  # Best
  lambda_best <- lasso_reg$lambda.min</pre>
  lambda_best
  lasso_model <- glmnet(X.train, y.train, alpha = 1, lambda = lambda_best, standardize = TRUE)</pre>
}
```





