ST558_HW5

Keshav Ramesh

Task 1 Conceptual questions

1. What is the purpose of using cross-validation when fitting a random forest model?

   - cross validation is to check the performance and generalization of the random forest model. Although they already reduce over fitting, cross validation make a more accurate guess of how the model will perform on unseen data

2. Describe the bagged tree algorithm.

   - Bagging is an ensemble technique that builds decision tress on different bootstrapped samples of an original dataset. each tree is created independently and the results are averages creating a more stable and accurate prediction.

3. What is meant by a general linear model?

   - A general linear model is a statistical model where the outcome is a linear combination of predictors. This includes, simple linear regression, multiple linear regression. Y = X_B + e

4. When fitting a multiple linear regression model, what does adding an interaction term do? That is, what does it allow the model to do differently as compared to when it is not included in the model?

   - The interaction term allow for the model to check situation where one predictor depends on the value of another., It enables the model to check for more complex relationships between variables.

5. Why do we split our data into a training and test set?

   - Data is split into training and test sets to evaluate the model's ability to generalize. The model is trained on a portion of a set then used to see if that training holds up on unseen data. This prevents over fitting, and increases accuracy.

Task 2: Data Prep

Packages and Data

```
library(tidyverse)
```

```
Warning: package 'tidyverse' was built under R version 4.4.3
```

```
library(tidymodels)
library(caret)
```

```
Warning: package 'caret' was built under R version 4.4.3
```

```
library(yardstick)
library(glmnet)
```

```
Warning: package 'glmnet' was built under R version 4.4.3
```

```
heart = as_tibble(read_csv("heart.csv"))
```

Question 1

```
summary(heart)
```

```
      Age            Sex            ChestPainType        RestingBP     
 Min.   :28.00   Length:918         Length:918         Min.   :  0.0  
 1st Qu.:47.00   Class :character   Class :character   1st Qu.:120.0  
 Median :54.00   Mode  :character   Mode  :character   Median :130.0  
 Mean   :53.51                                         Mean   :132.4  
 3rd Qu.:60.00                                         3rd Qu.:140.0  
 Max.   :77.00                                         Max.   :200.0  
  Cholesterol      FastingBS       RestingECG            MaxHR      
 Min.   :  0.0   Min.   :0.0000   Length:918         Min.   : 60.0  
 1st Qu.:173.2   1st Qu.:0.0000   Class :character   1st Qu.:120.0  
 Median :223.0   Median :0.0000   Mode  :character   Median :138.0  
 Mean   :198.8   Mean   :0.2331                      Mean   :136.8  
```

```
 3rd Qu.:267.0   3rd Qu.:0.0000                      3rd Qu.:156.0
 Max.   :603.0   Max.   :1.0000                      Max.   :202.0
 ExerciseAngina        Oldpeak          ST_Slope          HeartDisease
 Length:918         Min.   :-2.6000   Length:918         Min.   :0.0000
 Class :character   1st Qu.: 0.0000   Class :character   1st Qu.:0.0000
 Mode  :character   Median : 0.6000   Mode  :character   Median :1.0000
                    Mean   : 0.8874                      Mean   :0.5534
                    3rd Qu.: 1.5000                      3rd Qu.:1.0000
                    Max.   : 6.2000                      Max.   :1.0000
```

a. heart disease is being treated as a quantitative variable, it is a storing values as either 1 or 0.
b. This does not make sense as we should eb treating the variables as categorical, as a yes or no response. While this does work in theory as a binary 1/0 response, it would be better to treat this as a facotrs with levels of yes or no, or T and F.

Question 2

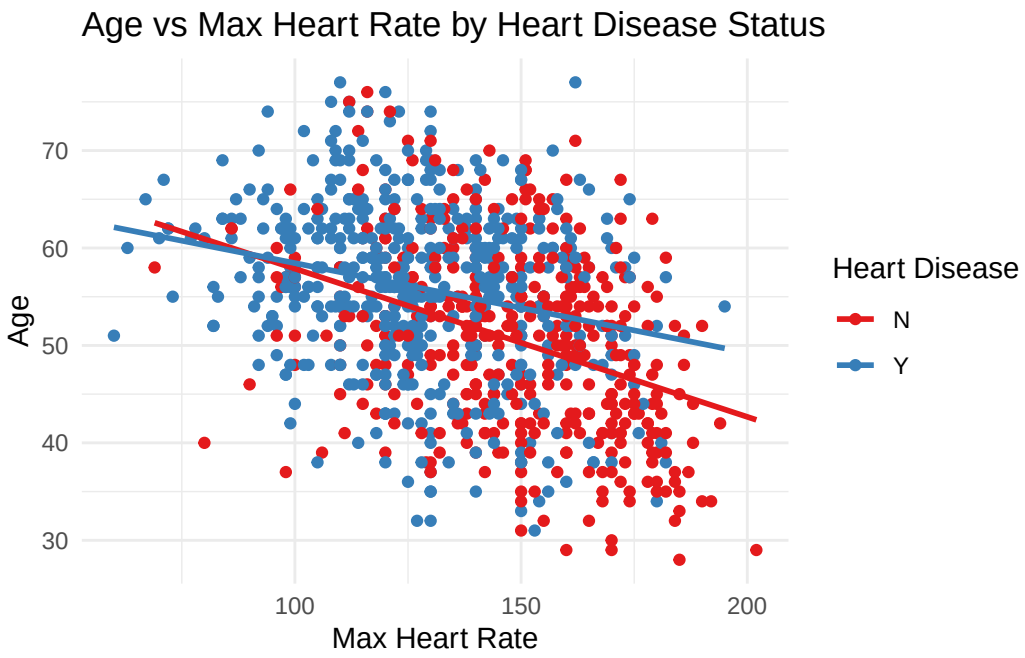
```
new_heart = heart %>%
  mutate(HeartDisease_FACTORED = factor(HeartDisease, levels = c(0,1), labels = c("N", "Y")))
  select(-ST_Slope, -HeartDisease)

head(new_heart)
```

```
# A tibble: 6 x 11
    Age Sex   ChestPainType RestingBP Cholesterol FastingBS RestingECG MaxHR
  <dbl> <chr> <chr>              <dbl>       <dbl>     <dbl> <chr>      <dbl>
1    40 M     ATA                  140         289         0 Normal       172
2    49 F     NAP                  160         180         0 Normal       156
3    37 M     ATA                  130         283         0 ST            98
4    48 F     ASY                  138         214         0 Normal       108
5    54 M     NAP                  150         195         0 Normal       122
6    39 M     NAP                  120         339         0 Normal       170
# i 3 more variables: ExerciseAngina <chr>, Oldpeak <dbl>,
#   HeartDisease_FACTORED <fct>
```

Task 3: EDA

```
new_heart %>%
  ggplot(
    aes(
      x = MaxHR,
      y = Age,
      colour = HeartDisease_FACTORED
    )
  ) +
  geom_point() +
  geom_smooth(method = "lm", se = F) +
  scale_color_brewer(palette = "Set1") +
  labs(
    title = "Age vs Max Heart Rate by Heart Disease Status",
    x = "Max Heart Rate",
    y = "Age",
    color = "Heart Disease"
  ) +
  theme_minimal()
```

```
`geom_smooth()` using formula = 'y ~ x'
```



Question 2

An interaction model would be more accurate. The relationship between max heart rate and age differed depending on whether or not the person has heart disease. The have different slops indicating that max hr depends on heart disease status. This is algined with an interactive model not an additive model.

Task 4: Testing and Training

```
set.seed(101)

heart_split = initial_split(new_heart, prop = 0.8)

train = training(heart_split)
test = testing(heart_split)
```

Task 5: OLS and LASSO

Question 1

```
ols_mlr = lm(Age ~ MaxHR + HeartDisease_FACTORED + MaxHR*HeartDisease_FACTORED, data = train)

summary(ols_mlr)
```

```
Call:
lm(formula = Age ~ MaxHR + HeartDisease_FACTORED + MaxHR * HeartDisease_FACTORED,
    data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-22.7703  -5.7966   0.4516   5.7772  20.6378

Coefficients:
                             Estimate Std. Error t value Pr(>|t|)
(Intercept)                  75.58896    3.07510  24.581  < 2e-16 ***
MaxHR                        -0.16992    0.02064  -8.233 8.43e-16 ***
HeartDisease_FACTOREDY       -8.58502    3.83433  -2.239  0.02546 *
MaxHR:HeartDisease_FACTOREDY  0.08343    0.02716   3.072  0.00221 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.478 on 730 degrees of freedom
Multiple R-squared:  0.1839,    Adjusted R-squared:  0.1806
F-statistic: 54.84 on 3 and 730 DF,  p-value: < 2.2e-16
```

Question 2

```
yardstick::rmse_vec(test$Age, predict(ols_mlr, test))
```

```
[1] 9.100206
```

Question 3

```
LASSO_recipe = recipe(Age ~ MaxHR + HeartDisease_FACTORED, data = train) %>%
  step_dummy(all_nominal_predictors()) %>%
  step_normalize(all_predictors()) %>%
  step_interact(~ MaxHR:starts_with("HeartDisease_FACTORED"))

LASSO_recipe
```

```
-- Recipe ----------------------------------------------------------------------



-- Inputs

Number of variables by role

outcome:   1
predictor: 2



-- Operations

* Dummy variables from: all_nominal_predictors()

* Centering and scaling for: all_predictors()

* Interactions with: MaxHR:starts_with("HeartDisease_FACTORED")
```

Question 4

```
set.seed(101)
cv_folds = vfold_cv(train, v = 10)

lasso_model = linear_reg(penalty = tune(), mixture = 1) %>%
  set_engine("glmnet")

lasso_workflow = workflow() %>%
  add_model(lasso_model) %>%
  add_recipe(LASSO_recipe)
lasso_workflow
```

```
== Workflow ====================================================================
Preprocessor: Recipe
Model: linear_reg()

-- Preprocessor ----------------------------------------------------------------
3 Recipe Steps

* step_dummy()
* step_normalize()
* step_interact()

-- Model -----------------------------------------------------------------------
Linear Regression Model Specification (regression)

Main Arguments:
  penalty = tune()
  mixture = 1

Computational engine: glmnet
```

```
LASSO_grid = lasso_workflow %>%
  tune_grid(resamples = cv_folds, grid = grid_regular(penalty(), levels = 200))

LASSO_grid
```

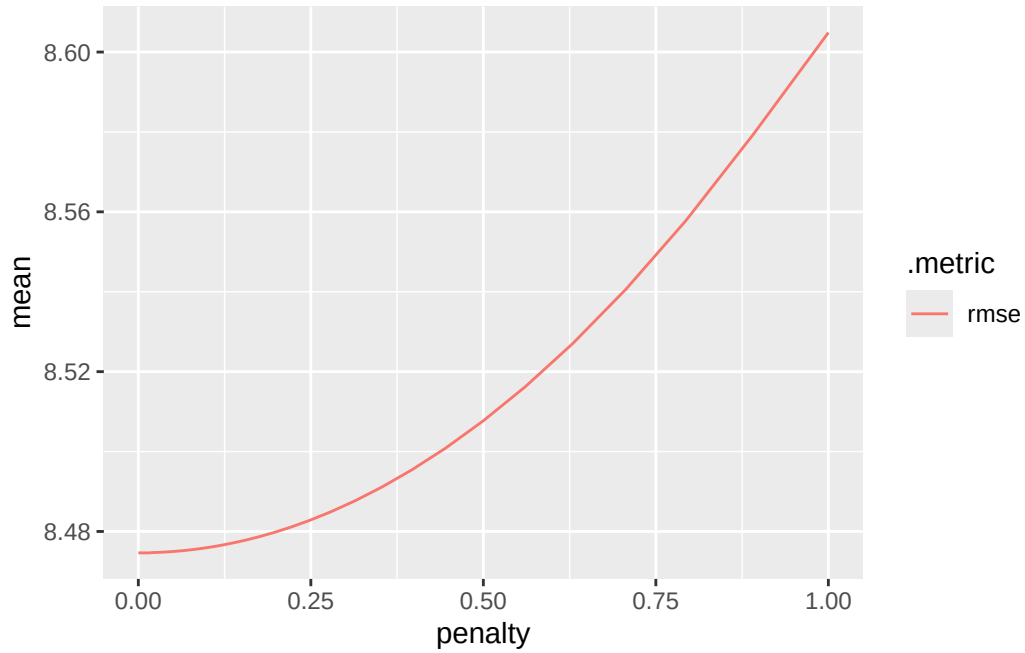
```
# Tuning results
# 10-fold cross-validation
```

```
# A tibble: 10 x 4
   splits           id     .metrics           .notes
   <list>           <chr>  <list>             <list>
 1 <split [660/74]> Fold01 <tibble [400 x 5]> <tibble [0 x 3]>
 2 <split [660/74]> Fold02 <tibble [400 x 5]> <tibble [0 x 3]>
 3 <split [660/74]> Fold03 <tibble [400 x 5]> <tibble [0 x 3]>
 4 <split [660/74]> Fold04 <tibble [400 x 5]> <tibble [0 x 3]>
 5 <split [661/73]> Fold05 <tibble [400 x 5]> <tibble [0 x 3]>
 6 <split [661/73]> Fold06 <tibble [400 x 5]> <tibble [0 x 3]>
 7 <split [661/73]> Fold07 <tibble [400 x 5]> <tibble [0 x 3]>
 8 <split [661/73]> Fold08 <tibble [400 x 5]> <tibble [0 x 3]>
 9 <split [661/73]> Fold09 <tibble [400 x 5]> <tibble [0 x 3]>
10 <split [661/73]> Fold10 <tibble [400 x 5]> <tibble [0 x 3]>
```

```
LASSO_grid %>%
  collect_metrics() %>%
  filter(.metric == "rmse")
```

```
# A tibble: 200 x 7
    penalty .metric .estimator  mean     n std_err .config
      <dbl> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
 1 1   e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model001
 2 1.12e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model002
 3 1.26e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model003
 4 1.41e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model004
 5 1.59e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model005
 6 1.78e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model006
 7 2.00e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model007
 8 2.25e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model008
 9 2.52e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model009
10 2.83e-10 rmse    standard    8.47    10   0.124 Preprocessor1_Model010
# i 190 more rows
```

```
LASSO_grid %>%
  collect_metrics() %>%
  filter(.metric == "rmse") %>%
  ggplot(aes(penalty, mean, color = .metric)) +
  geom_line()
```




```
lowest_rmse <- LASSO_grid %>%
  select_best(metric = "rmse")
lowest_rmse
```

```
# A tibble: 1 x 2
       penalty .config
         <dbl> <chr>
1 0.0000000001 Preprocessor1_Model001
```

```
lasso_workflow %>%
  finalize_workflow(lowest_rmse)
```

```
== Workflow ====================================================================
Preprocessor: Recipe
Model: linear_reg()

-- Preprocessor ----------------------------------------------------------------
3 Recipe Steps

* step_dummy()
* step_normalize()
```

```
* step_interact()

-- Model ---------------------------------------------------------------------
Linear Regression Model Specification (regression)

Main Arguments:
  penalty = 1e-10
  mixture = 1

Computational engine: glmnet
```

```
#fit it to the entire training set to see the model fit
LASSO_final <- lasso_workflow %>%
  finalize_workflow(lowest_rmse) %>%
  fit(train)


tidy(LASSO_final)
```

```
# A tibble: 4 x 3
  term                           estimate      penalty
  <chr>                             <dbl>        <dbl>
1 (Intercept)                       54.0  0.0000000001
2 MaxHR                             -3.08 0.0000000001
3 HeartDisease_FACTORED_Y            1.36 0.0000000001
4 MaxHR_x_HeartDisease_FACTORED_Y    1.03 0.0000000001
```

Question 5

I would expect the outputs to be generally the same between the OLS and LASSO models.

based on the tidy output of LASSO_final we can see that the LASSO model has the same predictors that the OLS model has. This would indiacte that RMSE would also be very similar.

Question 6

```
ols_mlr %>%
  predict(test) %>%
  rmse_vec(truth = test$Age)
```

```
[1] 9.100206
```

```
LASSO_final %>%
  predict(test) %>%
  pull() %>%
  rmse_vec(truth = test$Age)
```

```
[1] 9.095981
```

Question 7

They are both using the same predictors, and their interactions are also the same and simple.

Task 6: Logistic regression

Question 1

```
logrec1 <- recipe(HeartDisease_FACTORED ~ MaxHR, data = train) %>%
  step_normalize(MaxHR)

logrec2 <- recipe(HeartDisease_FACTORED ~ Age + Sex + ChestPainType + RestingBP, data = trai
  step_normalize(all_numeric(), -HeartDisease_FACTORED) %>%
  step_dummy(all_nominal_predictors())
```

```
set.seed(101)
cv_repeats <- vfold_cv(train, 10, 5)
```

```
log_spec <- logistic_reg() %>%
  set_engine("glm")
```

```
LR1_wkf <- workflow() |>
add_recipe(logrec1) |>
add_model(log_spec)


LR2_wkf <- workflow() |>
add_recipe(logrec2) |>
add_model(log_spec)
```

```
LR1_fit <- LR1_wkf |>
fit_resamples(cv_repeats, metrics = metric_set(accuracy, mn_log_loss))


LR2_fit <- LR2_wkf |>
fit_resamples(cv_repeats, metrics = metric_set(accuracy, mn_log_loss))
```

```
rbind(LR1_fit |> collect_metrics(),
LR2_fit |> collect_metrics())|>
mutate(Model = c("Model1", "Model1", "Model2", "Model2")) |>
select(Model, everything())
```

```
# A tibble: 4 x 7
  Model  .metric     .estimator  mean     n std_err .config
  <chr>  <chr>       <chr>      <dbl> <int>   <dbl> <chr>
1 Model1 accuracy    binary     0.677    50 0.00670 Preprocessor1_Model1
2 Model1 mn_log_loss binary     0.607    50 0.00550 Preprocessor1_Model1
3 Model2 accuracy    binary     0.776    50 0.00676 Preprocessor1_Model1
4 Model2 mn_log_loss binary     0.490    50 0.00913 Preprocessor1_Model1
```

```
mean(train$HeartDisease_FACTORED == "Y")
```

```
[1] 0.5694823
```

Model 2 was the better performing model it had the highest accuracy and the lowest loss.

Question 2

```
final_model <- LR2_wkf %>%
  fit(data = train)

predictions <- predict(final_model, test, type = "class") %>%
  bind_cols(test)

confusionMatrix(
  data = predictions$.pred_class,
  reference = predictions$HeartDisease_FACTORED
)
```

```
Confusion Matrix and Statistics

          Reference
Prediction  N  Y
         N 71 17
         Y 23 73

               Accuracy : 0.7826
                 95% CI : (0.716, 0.8399)
    No Information Rate : 0.5109
    P-Value [Acc > NIR] : 2.577e-14

                  Kappa : 0.5656

 Mcnemar's Test P-Value : 0.4292

            Sensitivity : 0.7553
            Specificity : 0.8111
         Pos Pred Value : 0.8068
         Neg Pred Value : 0.7604
             Prevalence : 0.5109
         Detection Rate : 0.3859
   Detection Prevalence : 0.4783
      Balanced Accuracy : 0.7832

       'Positive' Class : N
```

Question 3

The model's sensitivity was 0.7553: The model will miss about 24.5% of healthy patients. It will false flag almost 1/4 healthy people as diseased.

The model's specificity was 0.8111: The model correctly identified 81% of actual heart disease cases but will miss 19% of diseased patients.

The model is better at confirming positive cases than it is with ruling out disease.