PSTAT131HW06

Yifei Zhang

2022-05-24

```
library(ggplot2)
library(tidyverse)
library(tidymodels)
library(corrplot)
library(klaR)
library(glmnet)
tidymodels_prefer()
Pokemon <- read_csv("Pokemon.csv")
library(janitor)
library(randomForest)
library(xgboost)
library(rpart.plot)
library(ranger)
library(vip)
```

Exercise 1

Read in the data and set things up as in Homework 5:

- Use `clean_names()`
- Filter out the rarer Pokémon types
- Convert `type_1` and `legendary` to factors

```
cleaned <- clean_names(Pokemon)
cleaned
```

```
## # A tibble: 800 x 13
##    number name      type_1 type_2 total    hp attack defense sp_atk sp_def speed
##     <dbl> <chr>     <chr>  <chr>  <dbl> <dbl>  <dbl>   <dbl>  <dbl>  <dbl> <dbl>
##  1      1 Bulbasaur Grass  Poison   318    45     49      49     65     65    45
##  2      2 Ivysaur   Grass  Poison   405    60     62      63     80     80    60
##  3      3 Venusaur  Grass  Poison   525    80     82      83    100    100    80
##  4      3 Venusaur~ Grass  Poison   625    80    100     123    122    120    80
##  5      4 Charmand~ Fire   <NA>     309    39     52      43     60     50    65
##  6      5 Charmele~ Fire   <NA>     405    58     64      58     80     65    80
##  7      6 Charizard Fire   Flying   534    78     84      78    109     85   100
##  8      6 Charizar~ Fire   Dragon   634    78    130     111    130     85   100
##  9      6 Charizar~ Fire   Flying   634    78    104      78    159    115   100
## 10      7 Squirtle  Water  <NA>     314    44     48      65     50     64    43
## # ... with 790 more rows, and 2 more variables: generation <dbl>,
## #   legendary <lgl>
```

```r
filtered <- cleaned %>% filter(
  type_1 == "Bug" | type_1 == "Fire" | type_1 == "Grass"
  | type_1 == "Normal" | type_1 == "Water" | type_1 == "Psychic"
  )
filtered
```

```
## # A tibble: 458 x 13
##    number name      type_1 type_2 total    hp attack defense sp_atk sp_def speed
##     <dbl> <chr>     <chr>  <chr>  <dbl> <dbl>  <dbl>   <dbl>  <dbl>  <dbl> <dbl>
##  1      1 Bulbasaur Grass  Poison   318    45     49      49     65     65    45
##  2      2 Ivysaur   Grass  Poison   405    60     62      63     80     80    60
##  3      3 Venusaur  Grass  Poison   525    80     82      83    100    100    80
##  4      3 Venusaur~ Grass  Poison   625    80    100     123    122    120    80
##  5      4 Charmand~ Fire   <NA>     309    39     52      43     60     50    65
##  6      5 Charmele~ Fire   <NA>     405    58     64      58     80     65    80
##  7      6 Charizard Fire   Flying   534    78     84      78    109     85   100
##  8      6 Charizar~ Fire   Dragon   634    78    130     111    130     85   100
##  9      6 Charizar~ Fire   Flying   634    78    104      78    159    115   100
## 10      7 Squirtle  Water  <NA>     314    44     48      65     50     64    43
## # ... with 448 more rows, and 2 more variables: generation <dbl>,
## #   legendary <lgl>
```

```r
data <- filtered %>%
  mutate(type_1 = factor(type_1),
         legendary = factor(legendary),
         generation = factor(generation)
         )
data
```

```
## # A tibble: 458 x 13
##    number name      type_1 type_2 total    hp attack defense sp_atk sp_def speed
##     <dbl> <chr>     <fct>  <chr>  <dbl> <dbl>  <dbl>   <dbl>  <dbl>  <dbl> <dbl>
##  1      1 Bulbasaur Grass  Poison   318    45     49      49     65     65    45
##  2      2 Ivysaur   Grass  Poison   405    60     62      63     80     80    60
##  3      3 Venusaur  Grass  Poison   525    80     82      83    100    100    80
##  4      3 Venusaur~ Grass  Poison   625    80    100     123    122    120    80
##  5      4 Charmand~ Fire   <NA>     309    39     52      43     60     50    65
##  6      5 Charmele~ Fire   <NA>     405    58     64      58     80     65    80
##  7      6 Charizard Fire   Flying   534    78     84      78    109     85   100
##  8      6 Charizar~ Fire   Dragon   634    78    130     111    130     85   100
##  9      6 Charizar~ Fire   Flying   634    78    104      78    159    115   100
## 10      7 Squirtle  Water  <NA>     314    44     48      65     50     64    43
## # ... with 448 more rows, and 2 more variables: generation <fct>,
## #   legendary <fct>
```

Do an initial split of the data; you can choose the percentage for splitting. Stratify on the outcome variable.

```r
set.seed(2022)
pokemon_split <- data %>%
  initial_split(strata = type_1, prop = 0.75)
pokemon_train <- training(pokemon_split)
pokemon_test <- testing(pokemon_split)
dim(pokemon_train)
```

```
## [1] 341  13
```

Fold the training set using *v*-fold cross-validation, with `v = 5`. Stratify on the outcome variable.

```
pokemon_folds <- vfold_cv(pokemon_train, v = 5, strata = 'type_1')
pokemon_folds
```

```
## #  5-fold cross-validation using stratification
## # A tibble: 5 x 2
##   splits           id
##   <list>           <chr>
## 1 <split [270/71]> Fold1
## 2 <split [271/70]> Fold2
## 3 <split [273/68]> Fold3
## 4 <split [274/67]> Fold4
## 5 <split [276/65]> Fold5
```

Set up a recipe to predict `type_1` with `legendary`, `generation`, `sp_atk`, `attack`, `speed`, `defense`, `hp`, and `sp_def`:

- Dummy-code `legendary` and `generation`;
- Center and scale all predictors.

```
pokemon_recipe <- recipe(type_1 ~ legendary + generation + sp_atk +
                           attack + speed + defense + hp + sp_def,
                         data = pokemon_train) %>%
  step_dummy(all_nominal_predictors()) %>%
  step_normalize(all_predictors())
```

Exercise 2

Create a correlation matrix of the training set, using the `corrplot` package. *Note: You can choose how to handle the continuous variables for this plot; justify your decision(s).*

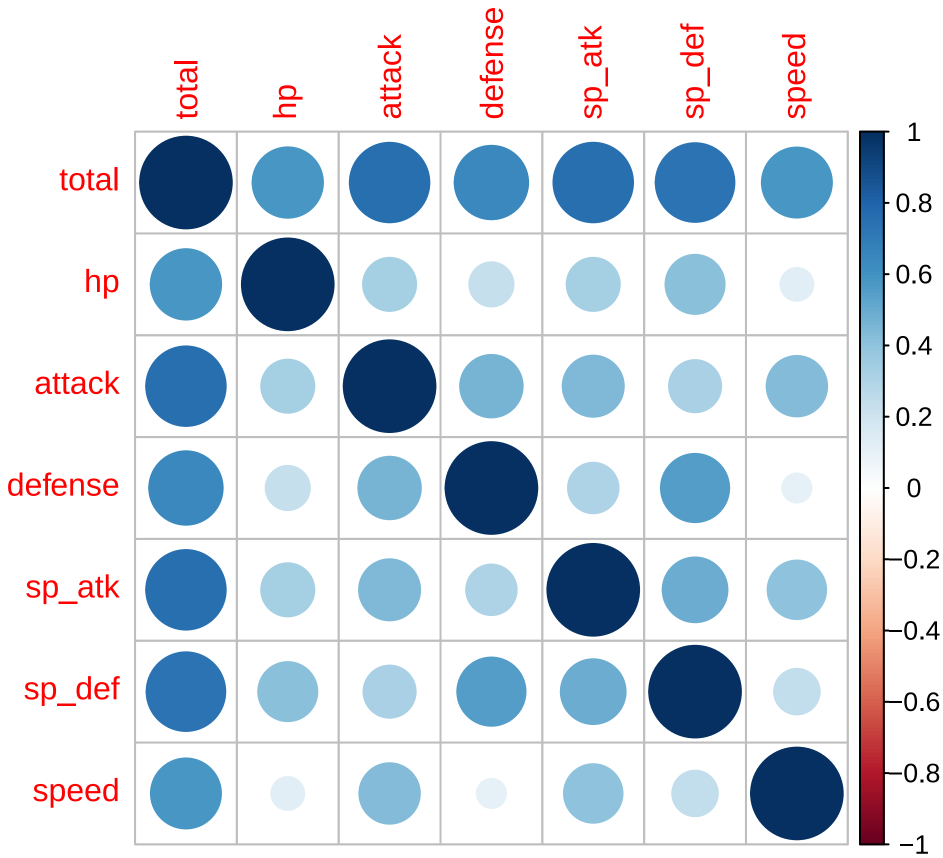
I droped all non numeric variables, becuase they can not fit into the correlation function. I think the hw question is phrased wrong. We are eliminating the non continous variables.

```
cordata <- subset (data, select = c( "total", "hp", "attack",
                                     "defense", "sp_atk", "sp_def",
                                     "speed"))
```

```
res <- cor(cordata)
res
```

```
##             total        hp   attack   defense    sp_atk    sp_def     speed
## total   1.0000000 0.5891580 0.7517256 0.6413857 0.7521862 0.7361142 0.5831479
## hp      0.5891580 1.0000000 0.3352739 0.2321308 0.3353892 0.4154919 0.1294510
## attack  0.7517256 0.3352739 1.0000000 0.4645177 0.4437926 0.3232667 0.4347855
## defense 0.6413857 0.2321308 0.4645177 1.0000000 0.3038973 0.5534584 0.1015110
## sp_atk  0.7521862 0.3353892 0.4437926 0.3038973 1.0000000 0.4992364 0.4077537
## sp_def  0.7361142 0.4154919 0.3232667 0.5534584 0.4992364 1.0000000 0.2471261
## speed   0.5831479 0.1294510 0.4347855 0.1015110 0.4077537 0.2471261 1.0000000
```

```r
corrplot(res, method = "circle")
```



What relationships, if any, do you notice? Do these relationships make sense to you?

All the variables have positive correlation with each other to some degree. All the variables have a positive correlation with total which makes sense. Other than that, speed is pretty positively correlated with attack and defense which also makes sense. Attack is positively correlated with sp attack and defense.Defense is also positively correlated with sp defense. They all make sense.

Exercise 3

First, set up a decision tree model and workflow. Tune the `cost_complexity` hyperparameter. Use the same levels we used in Lab 7 – that is, `range = c(-3, -1)`. Specify that the metric we want to optimize is `roc_auc`.

Print an `autoplot()` of the results. What do you observe? Does a single decision tree perform better with a smaller or larger complexity penalty?

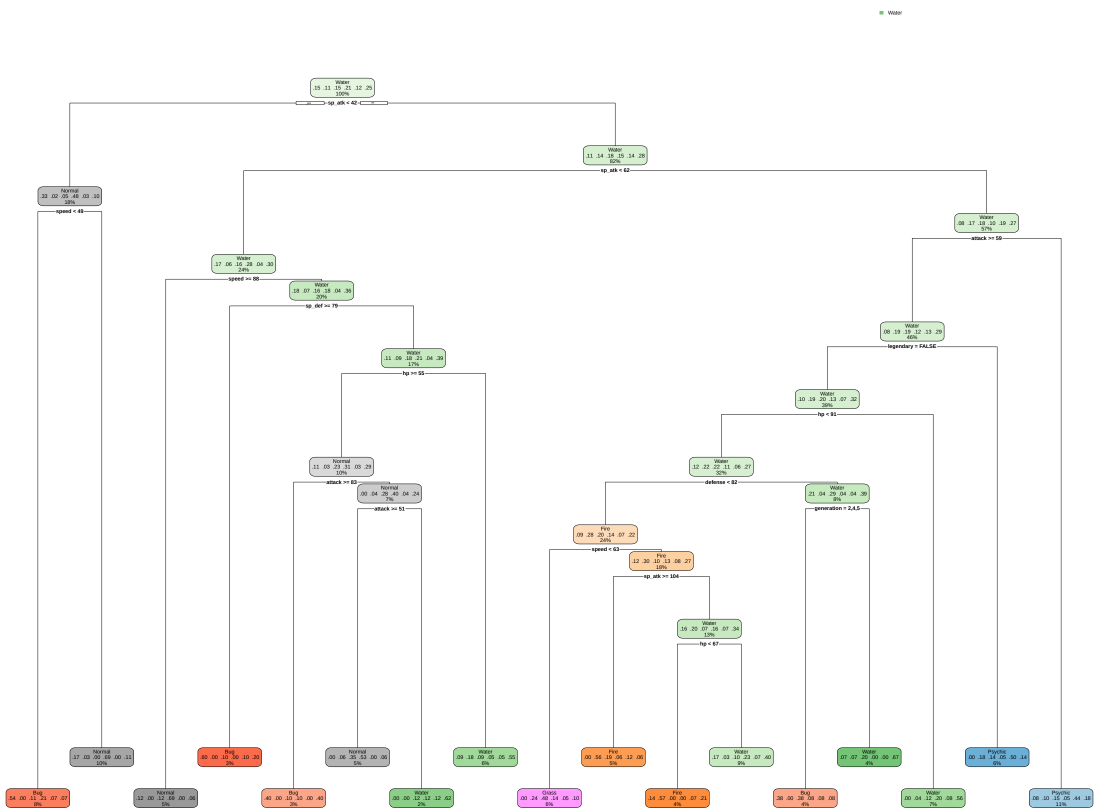
```r
tree_spec <- decision_tree() %>%
  set_engine("rpart")

class_tree_spec <- tree_spec %>%
  set_mode("classification")

class_tree_fit <- class_tree_spec %>%
  fit(type_1 ~ legendary + generation + sp_atk +
```

```
                           attack + speed + defense + hp + sp_def,
      data = pokemon_train)

class_tree_fit %>%
  extract_fit_engine() %>%
  rpart.plot() # this graph is for fun
```

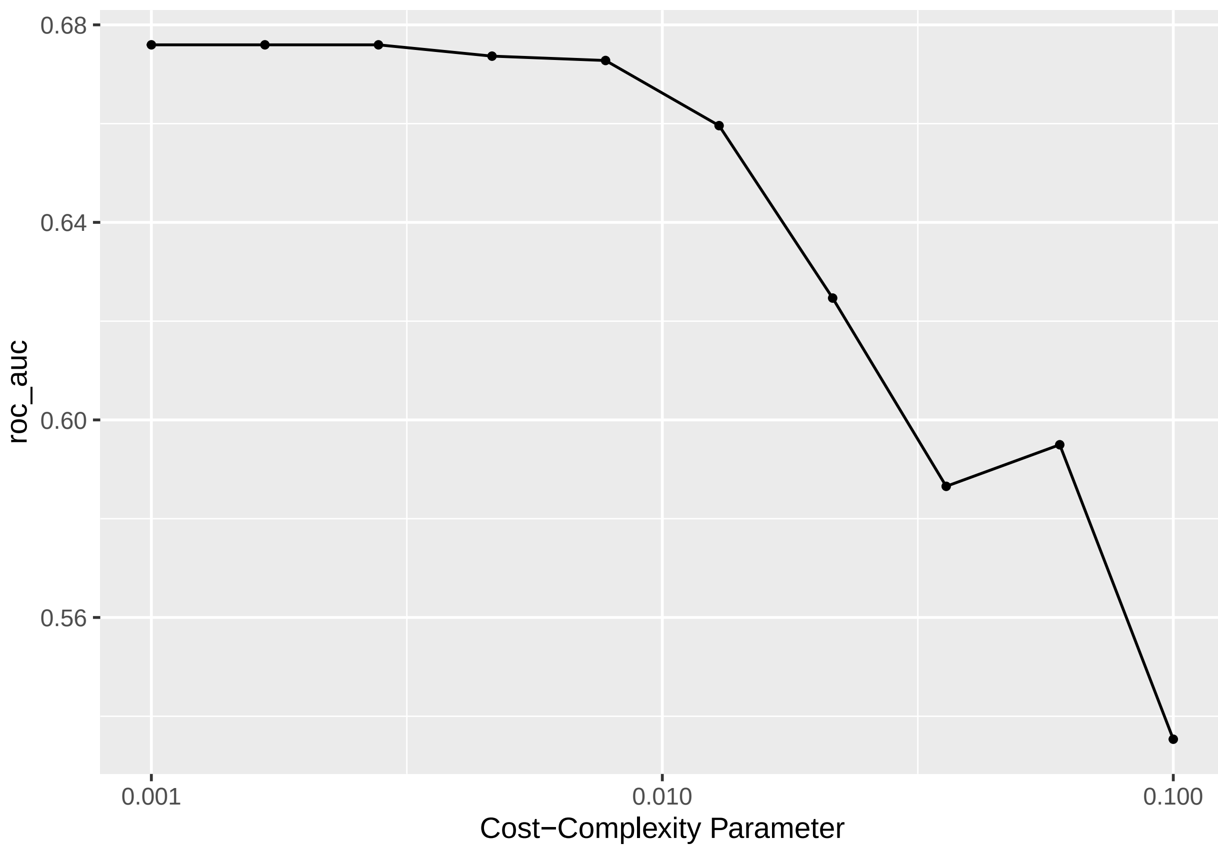


```
class_tree_wf <- workflow() %>%
  add_model(class_tree_spec %>% set_args(cost_complexity = tune())) %>%
  add_recipe(pokemon_recipe)
```

```
param_grid <- grid_regular(cost_complexity(range = c(-3, -1)), levels = 10)

tune_res <- tune_grid(
  class_tree_wf,
  resamples = pokemon_folds,
  grid = param_grid,
  metrics = metric_set(roc_auc)
)
```

```
autoplot(tune_res)
```



It is pretty steady at the beginning, and then it drastically dropped. It performs better with a lower complexity penalty, it will plumb if it is too large.

Exercise 4

What is the `roc_auc` of your best-performing pruned decision tree on the folds? *Hint: Use `collect_metrics()` and `arrange()`.*

The `roc_auc` of your best-performing pruned decision tree on the folds is 0.6759523

```
collect_metrics(tune_res) %>% arrange()
```

```
## # A tibble: 10 x 7
##    cost_complexity .metric .estimator  mean     n std_err .config
##              <dbl> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
##  1         0.001   roc_auc hand_till  0.676     5 0.0188  Preprocessor1_Model01
##  2         0.00167 roc_auc hand_till  0.676     5 0.0188  Preprocessor1_Model02
##  3         0.00278 roc_auc hand_till  0.676     5 0.0188  Preprocessor1_Model03
##  4         0.00464 roc_auc hand_till  0.674     5 0.0168  Preprocessor1_Model04
##  5         0.00774 roc_auc hand_till  0.673     5 0.0189  Preprocessor1_Model05
##  6         0.0129  roc_auc hand_till  0.660     5 0.0204  Preprocessor1_Model06
##  7         0.0215  roc_auc hand_till  0.625     5 0.0122  Preprocessor1_Model07
##  8         0.0359  roc_auc hand_till  0.587     5 0.00577 Preprocessor1_Model08
##  9         0.0599  roc_auc hand_till  0.595     5 0.0140  Preprocessor1_Model09
## 10         0.1     roc_auc hand_till  0.535     5 0.0218  Preprocessor1_Model10
```

```r
best_pruned <- select_best(tune_res, metric = "roc_auc")
best_pruned
```

```
## # A tibble: 1 x 2
##   cost_complexity .config
##             <dbl> <chr>
## 1           0.001 Preprocessor1_Model01
```

Exercise 5

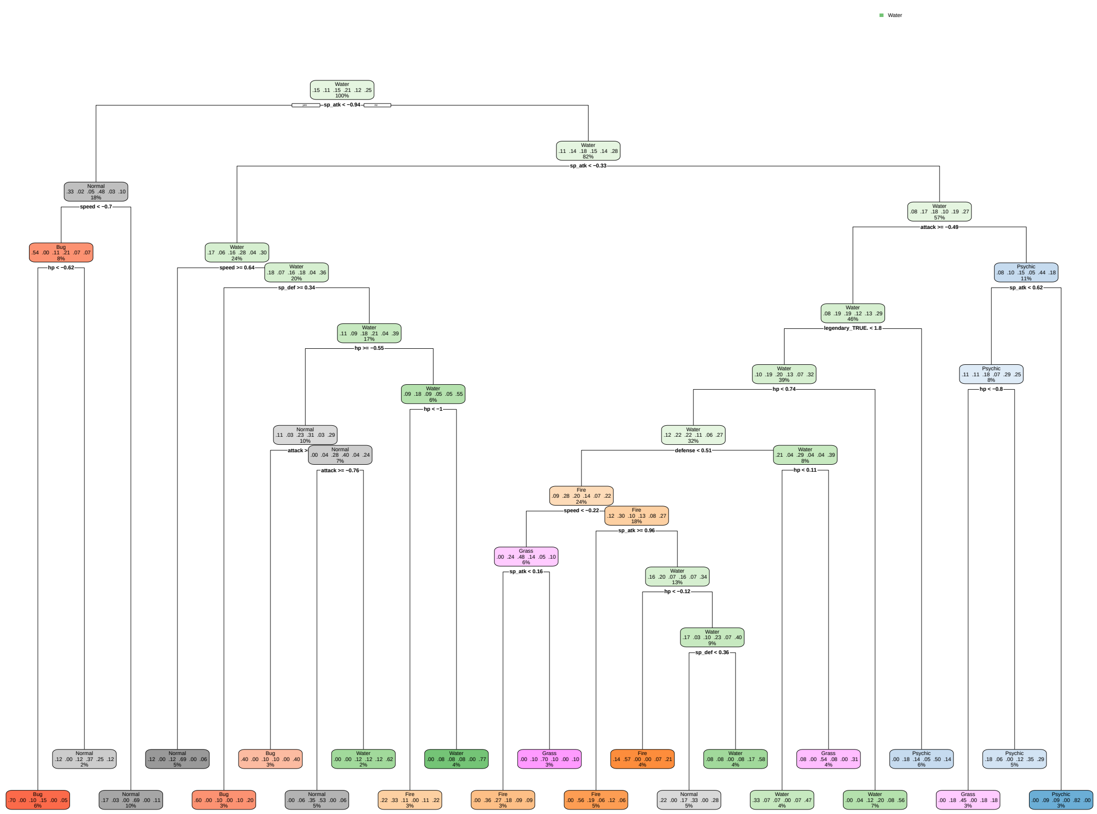
Using `rpart.plot`, fit and visualize your best-performing pruned decision tree with the *training* set.

```r
best_complexity <- select_best(tune_res)

class_tree_final <- finalize_workflow(class_tree_wf, best_complexity)

class_tree_final_fit <- fit(class_tree_final, data = pokemon_train)
```

```r
class_tree_final_fit %>%
  extract_fit_engine() %>%
  rpart.plot()
```



Exercise 5

Now set up a random forest model and workflow. Use the `ranger` engine and set `importance = "impurity"`. Tune `mtry`, `trees`, and `min_n`. Using the documentation for `rand_forest()`, explain in your own words what each of these hyperparameters represent.

mode is how we want our outcome to be reached. engine is the computation engine. mtry is the number of predictors we will resample each split. trees is the number of trees. min_n is the minimum number of data in a node

Create a regular grid with 8 levels each. You can choose plausible ranges for each hyperparameter. Note that `mtry` should not be smaller than 1 or larger than 8. **Explain why not. What type of model would `mtry = 8` represent?**

mtry represents the integer for the number of predictors that will be randomly sampled at each split when creating the tree models.We can not have less than 1 because then we are not sampling any predictors, more than 8 would be too many. So mtry = 8 means we are randomly sampling 8 predictors in each split when creating the tree models.

```
forest_spec <- rand_forest(
  mode = "classification",
  mtry = tune(),
  trees = tune(),
  min_n = tune()
)%>%
  set_engine("ranger", importance = "impurity")

forest_wf <- workflow() %>%
  add_model(forest_spec %>%
              set_args(mtry = tune(), trees = tune(),
                       min_n = tune()
                       )
            ) %>%
  add_recipe(pokemon_recipe)
```

```
forest_grid <- grid_regular(mtry(range = c(1, 8)),
                            trees(range = c(1, 100)),
                            min_n(range = c(1, 5)),
                            levels = 8)
forest_grid
```

```
## # A tibble: 320 x 3
##     mtry trees min_n
##    <int> <int> <int>
##  1     1     1     1
##  2     2     1     1
##  3     3     1     1
##  4     4     1     1
##  5     5     1     1
##  6     6     1     1
##  7     7     1     1
##  8     8     1     1
##  9     1    15     1
## 10     2    15     1
## # ... with 310 more rows
```

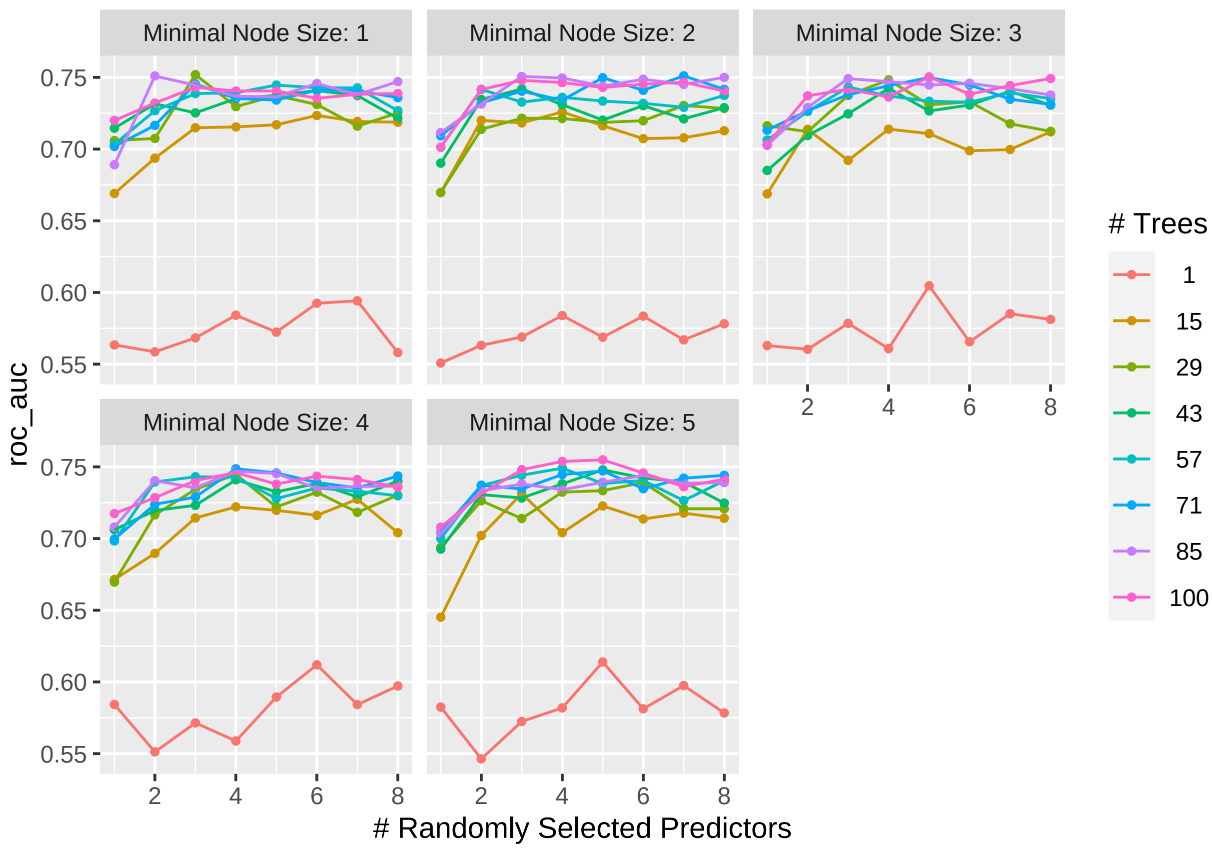
Exercise 6

Specify `roc_auc` as a metric. Tune the model and print an `autoplot()` of the results. What do you observe? What values of the hyperparameters seem to yield the best performance?

The general trend is that as the number of randomly selected predictors goes up, roc_auc goes up, the minimal node size does not matter much, and when tree is one, it performs the worst. When the hyperparameters has a high minimal node number, high tree number, and high randomly selected predictor, the model seems to yield the best performance.

```
forest_tune_res <- tune_grid(
  forest_wf,
  resamples = pokemon_folds,
  grid = forest_grid,
  metrics = metric_set(roc_auc)
)
```

```
autoplot(forest_tune_res)
```



Exercise 7

What is the `roc_auc` of your best-performing random forest model on the folds? *Hint: Use `collect_metrics()` and `arrange()`.*

The `roc_auc` of my best-performing random forest model on the folds is 0.7548953

```r
collect_metrics(forest_tune_res) %>% arrange()
```

```
## # A tibble: 320 x 9
##     mtry trees min_n .metric .estimator  mean     n std_err .config
##    <int> <int> <int> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
##  1     1     1     1 roc_auc hand_till  0.563     5 0.0188  Preprocessor1_Model~
##  2     2     1     1 roc_auc hand_till  0.559     5 0.0143  Preprocessor1_Model~
##  3     3     1     1 roc_auc hand_till  0.568     5 0.0127  Preprocessor1_Model~
##  4     4     1     1 roc_auc hand_till  0.584     5 0.0167  Preprocessor1_Model~
##  5     5     1     1 roc_auc hand_till  0.572     5 0.0176  Preprocessor1_Model~
##  6     6     1     1 roc_auc hand_till  0.592     5 0.0136  Preprocessor1_Model~
##  7     7     1     1 roc_auc hand_till  0.594     5 0.00865 Preprocessor1_Model~
##  8     8     1     1 roc_auc hand_till  0.558     5 0.0134  Preprocessor1_Model~
##  9     1    15     1 roc_auc hand_till  0.669     5 0.00878 Preprocessor1_Model~
## 10     2    15     1 roc_auc hand_till  0.694     5 0.0176  Preprocessor1_Model~
## # ... with 310 more rows
```

```r
best_forest <- select_best(forest_tune_res, metric = "roc_auc")
best_forest
```

```
## # A tibble: 1 x 4
##    mtry trees min_n .config
##   <int> <int> <int> <chr>
## 1     5   100     5 Preprocessor1_Model317
```

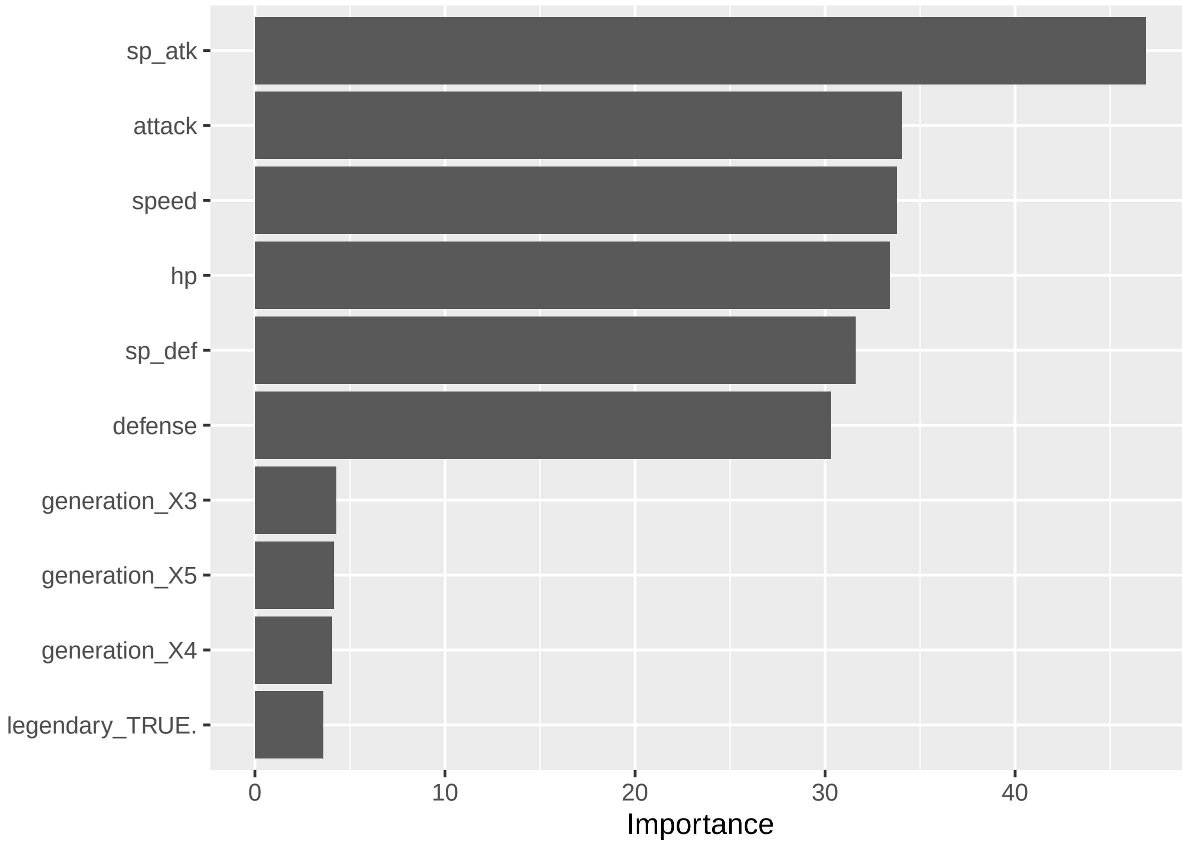
Exercise 8

Create a variable importance plot, using `vip()`, with your best-performing random forest model fit on the *training* set.

Which variables were most useful? Which were least useful? Are these results what you expected, or not?

The most useful variables are sp_attack, attack, speed, hp, sp_defense, and defense. Legendary or not is the least useful. They are about the same as I expected, since we have checked the correlations before.

```r
rf_final <- finalize_workflow(forest_wf, best_forest)
rf_fit_final <- fit(rf_final, data = pokemon_train)
rf_fit_final %>%
  pull_workflow_fit()%>%
  vip()
```



Exercise 9

Finally, set up a boosted tree model and workflow. Use the `xgboost` engine. Tune `trees`. Create a regular grid with 10 levels; let `trees` range from 10 to 2000. Specify `roc_auc` and again print an `autoplot()` of the results.

What do you observe?

What is the `roc_auc` of your best-performing boosted tree model on the folds? *Hint: Use `collect_metrics()` and `arrange()`.*

boost_spec <- boost_tree(trees = 5000, tree_depth = 4) %>% set_engine("xgboost") %>% set_mode("regression")

Exercise 10

Display a table of the three ROC AUC values for your best-performing pruned tree, random forest, and boosted tree models. Which performed best on the folds? Select the best of the three and use `select_best()`, `finalize_workflow()`, and `fit()` to fit it to the *testing* set.

Print the AUC value of your best-performing model on the testing set. Print the ROC curves. Finally, create and visualize a confusion matrix heat map.

Which classes was your model most accurate at predicting? Which was it worst at?