Decision Trees and Random Forest

Stat 220

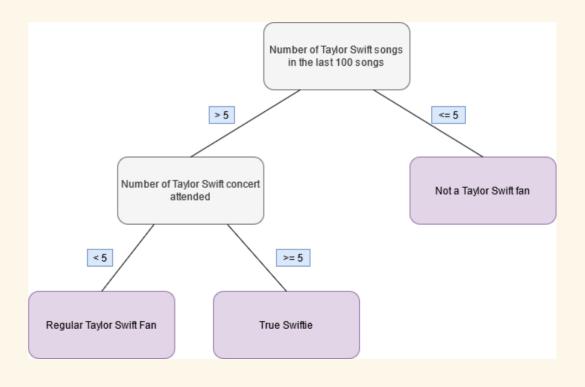
Bastola

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Decision Tree

 learns how to best split the dataset into smaller and smaller subsets to predict the target value

- Data is continuously split according to a certain parameter
- Two main entities:
 - o nodes: where the data is split
 - leaves: decisions or final outcomes



Decision Tree

Use features to make subsets of cases that are as similar ("pure") as possible with respect to the outcome

- Start with all observations in one group
- Find the variable/feature/split that best separates the outcome
- Divide the data into two groups (leaves) on the split (node)
- Within each split, find the best variable/split that separates the outcomes
- Continue until the groups are too small or sufficiently "pure"

Dataset

```
data(PimaIndiansDiabetes2)
db <- PimaIndiansDiabetes2 %>% drop_na() %>%
  mutate(diabetes = fct_relevel(diabetes, ref = "neg"))
```

```
glimpse(db)
Rows: 392
Columns: 9
$ pregnant <dbl> 1, 0, 3, 2, 1, 5, 0, 1, 1, 3, 11, 10, 1, 13, 3, 3, 4, 4, 3, 9...
$ glucose <dbl> 89, 137, 78, 197, 189, 166, 118, 103, 115, 126, 143, 125, 97,...
$ pressure <dbl> 66, 40, 50, 70, 60, 72, 84, 30, 70, 88, 94, 70, 66, 82, 76, 5...
$ triceps <dbl> 23, 35, 32, 45, 23, 19, 47, 38, 30, 41, 33, 26, 15, 19, 36, 1...
$ insulin <dbl> 94, 168, 88, 543, 846, 175, 230, 83, 96, 235, 146, 115, 140, ...
$ mass <dbl> 28.1, 43.1, 31.0, 30.5, 30.1, 25.8, 45.8, 43.3, 34.6, 39.3, 3...
$ pedigree <dbl> 0.167, 2.288, 0.248, 0.158, 0.398, 0.587, 0.551, 0.183, 0.529...
$ age <dbl> 21, 33, 26, 53, 59, 51, 31, 33, 32, 27, 51, 41, 22, 57, 28, 2...
$ diabetes <fct> neg, pos, pos, pos, pos, pos, neg, pos, neg, pos, pos, neg.
```

Data preparation and pre-processing

```
set.seed(314)
db_split <- initial_split(db, prop = 0.75)
db_train <- db_split %>% training()
db_test <- db_split %>% testing()
```

```
# scaling not needed
db_recipe <- recipe(diabetes ~ ., data = db_train) %>%
  step_dummy(all_nominal(), -all_outcomes()) %>%
  prep()
```

Model Specification

- cost_complexity: The cost complexity parameter, the minimum improvement in the model needed at each node
- tree_depth: The maximum depth of a tree
- min_n: The minimum number of data points in a node that are required for the node to be split further.

Workflow

Hyperparameter tuning

```
# Create folds for cross validation on the training data set
db_folds <- vfold_cv(db_train, v = 5, strata = diabetes)</pre>
```

View grid

```
tree_grid
# A tibble: 10 \times 3
  cost_complexity tree_depth min_n
            <dbl> <int> <int>
         5.28e-10
                                40
         2.99e- 6
         1.30e- 8
                                17
         1.94e- 2
                          13
                                19
         1.74e- 7
                          11
                                22
                               3
         8.11e- 7
                                10
         2.41e- 6
         1.01e- 5
                          14
                                40
         2.38e- 2
                                18
10
         2.68e- 6
                                39
                          15
```

Tuning Hyperparameters with tune_grid()

Best model

```
# Select best model based on accuracy
best_tree <- tree_tuning %>%
    select_best(metric = 'accuracy')
```

Finalize workflow

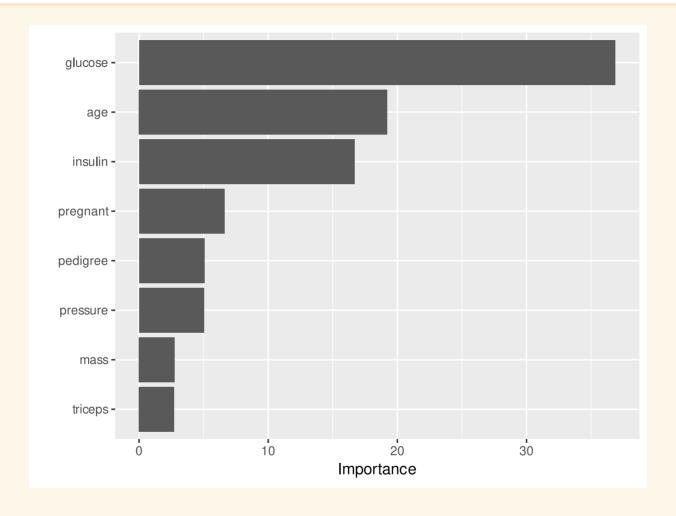
```
final_tree_workflow <- tree_workflow %>%
finalize_workflow(best_tree)
```

Fit the model

```
tree_wf_fit <- final_tree_workflow %>%
    fit(data = db_train)
```

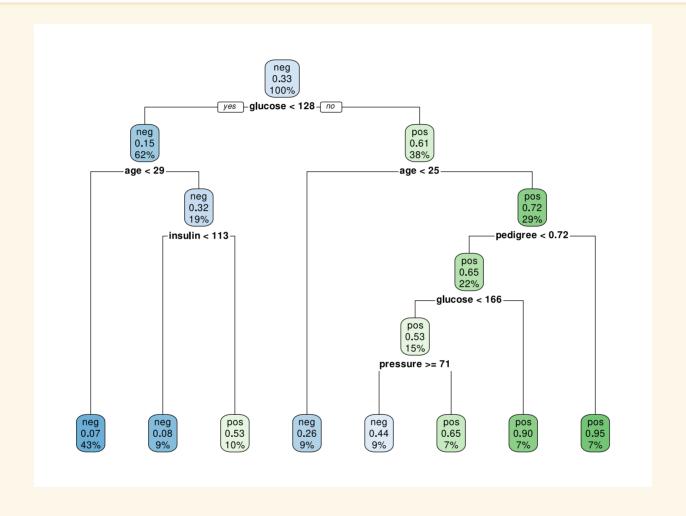
Extract fit

```
tree_fit <- tree_wf_fit %>%
extract_fit_parsnip()
```



Variable Importance

rpart.plot(tree_fit\$fit, roundint = FALSE)

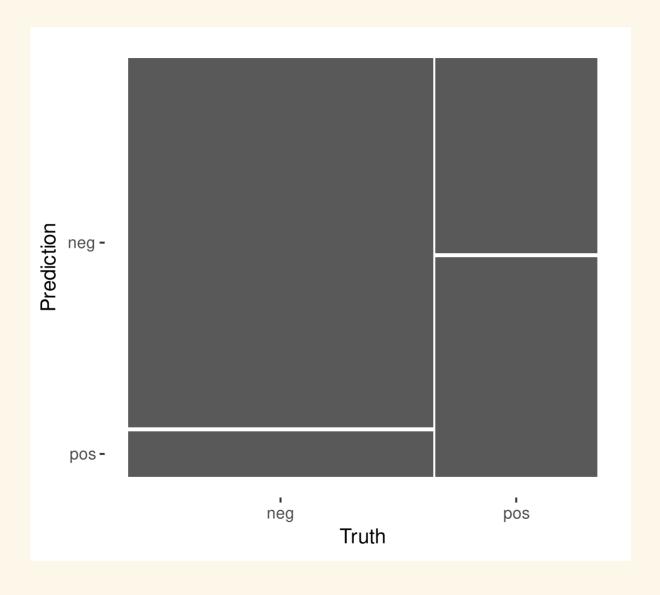


Decision Tree

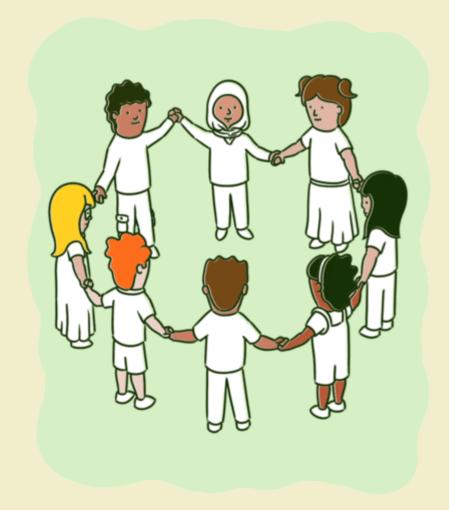
Train and Evaluate With last_fit()

```
tree_last_fit <- final_tree_workflow %>%
last_fit(db_split)
```

Confusion matrix



Group Activity 1



- Get the class activity 26.Rmd file from moodle
- Let's work on group activity 1 together

Now, let's talk about random forest

Random Forest

Random forests take decision trees and construct more powerful models in terms of prediction accuracy.

- Repeated sampling (with replacement) of the training data to produce a sequence of decision tree models.
- These models are then averaged to obtain a single prediction for a given value in the predictor space.
- The random forest model selects a random subset of predictor variables for splitting the predictor space in the tree building process.

Model Specification

- mtry: The number of predictors that will be randomly sampled at each split when creating the tree models
- trees: The number of decision trees to fit and ultimately average
- min_n: The minimum number of data points in a node that are required for the node to be split further

Model Specification

Workflow

```
rf_workflow <- workflow() %>%
    add_model(rf_model) %>%
    add_recipe(db_recipe)
```

Hyperparameter Tuning

View Grid

```
rf_grid
# A tibble: 15 × 3
   mtry trees min_n
   <int> <int> <int>
           609
                  32
 2
                   6
       5 1235
          1822
                  29
                  16
           678
           138
                  14
 6
                  19
          1218
                  14
           228
8
           873
                  4
 9
          1387
                  10
                   5
10
          1717
                   4
11
           436
12
          1175
                  16
13
         1909
                  33
14
                  4
         118
15
          1003
                  24
```

Tuning Hyperparameters with tune_grid()

Select best

```
## Select best model based on roc_auc
best_rf <- rf_tuning %>%
    select_best(metric = 'accuracy')
```

Finalize workflow

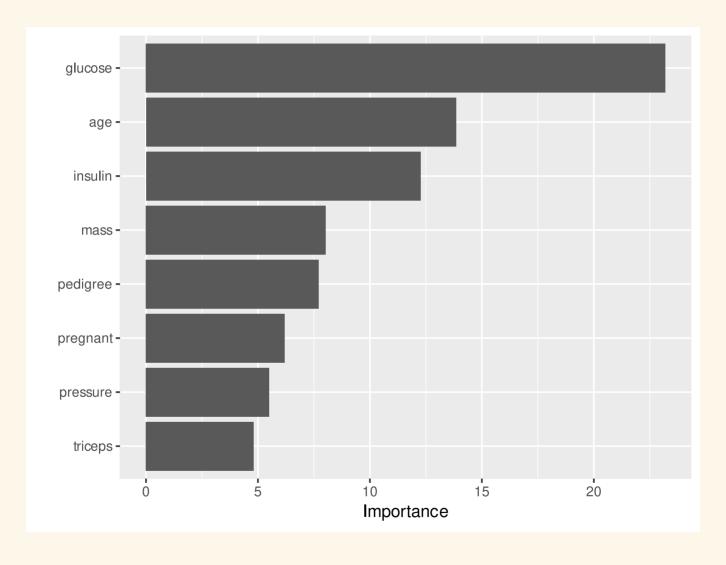
```
final_rf_workflow <- rf_workflow %>%
finalize_workflow(best_rf)
```

Variable Importance

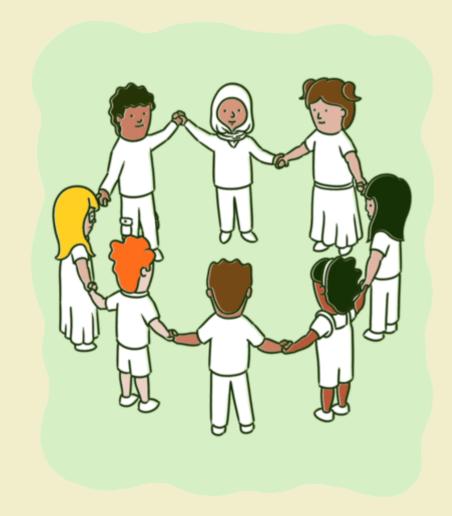
```
rf_wf_fit <- final_rf_workflow %>%
        fit(data = db_train)

rf_fit <- rf_wf_fit %>%
        extract_fit_parsnip()
```

Variable Importance



Group Activity 2



Please continue working on group activity 2