Model Selection - readmission_180d

Eduardo Yuki Yada

Global parameters

```
k <- params$k # Number of folds for cross validation
grid_size <- params$grid_size # Number of parameter combination to tune on each model
repeats <- params$repeats
RUN_ALL_MODELS <- params$RUN_ALL_MODELS
Hmisc::list.tree(params)
```

```
##  params = list 5 (968 bytes)
## .  outcome_column = character 1= readmission_180d
## .  k = double 1= 10
## .  grid_size = double 1= 20
## .  repeats = double 1= 2
## .  RUN_ALL_MODELS = logical 1= FALSE
```

Minutes to run: 0

Imports

```
library(tidyverse)
library(yaml)
library(tidymodels)
library(usemodels)
library(vip)
library(bonsai)
library(lightgbm)
library(caret)
library(pROC)

source("aux_functions.R")
```

Minutes to run: 0

Loading data

```
load('dataset/processed_data.RData')
load('dataset/processed_dictionary.RData')

columns_list <- yaml.load_file("./auxiliar/columns_list.yaml")

outcome_column <- params$outcome_column
features_list <- params$features_list

df <- mutate(df, across(where(is.character), as.factor))
```

Minutes to run: 0.005

```
dir.create(file.path("./auxiliar/model_selection/hyperparameters/"),
           showWarnings = FALSE,
           recursive = TRUE)
```

```
dir.create(file.path("./auxiliar/model_selection/performance/"),
           showWarnings = FALSE,
           recursive = TRUE)
```

Minutes to run: 0

Eligible features

```
cat_features_list = readRDS(sprintf(
  "./auxiliar/significant_columns/categorical_%s.rds",
  outcome_column
))

num_features_list = readRDS(sprintf(
  "./auxiliar/significant_columns/numerical_%s.rds",
  outcome_column
))

features_list = c(cat_features_list, num_features_list)
```

Minutes to run: 0

```
eligible_columns = df_names %>%
  filter(momento.aquisicao == 'Admissão t0') %>%
  .$variable.name

exception_columns = c('death_intraop', 'death_intraop_1', 'disch_outcomes_t0')

correlated_columns = c('year_procedure_1', # com year_adm_t0
                       'age_surgery_1', # com age
                       'admission_t0', # com admission_pre_t0_count
                       'atb', # com meds_antimicrobianos
                       'classe_meds_cardio_qtde', # com classe_meds_qtde
                       'suporte_hemod', # com proced_invasivos_qtde,
                       'radiografia', # com exames_imagem_qtde
                       'ecg' # com metodos_graficos_qtde
                       )

eligible_features = eligible_columns %>%
  base::intersect(c(columns_list$categorical_columns, columns_list$numerical_columns)) %>%
  setdiff(c(exception_columns, correlated_columns))

features = base::intersect(eligible_features, features_list)

gluedown::md_order(features, seq = TRUE, pad = TRUE)
```

```
## 01. sex
## 02. age
## 03. education_level
## 04. patient_state
## 05. underlying_heart_disease
## 06. heart_disease
## 07. nyha_basal
## 08. prior_mi
## 09. heart_failure
## 10. af
## 11. cardiac_arrest
## 12. transplant
## 13. valvopathy
## 14. endocardites
## 15. diabetes
```

```
## 16. renal_failure
## 17. hemodialysis
## 18. copd
## 19. comorbidities_count
## 20. procedure_type_1
## 21. reop_type_1
## 22. procedure_type_new
## 23. cied_final_1
## 24. cied_final_group_1
## 25. admission_pre_t0_count
## 26. admission_pre_t0_180d
## 27. icu_t0
## 28. dialysis_t0
## 29. n_procedure_t0
## 30. admission_t0_emergency
## 31. aco
## 32. antiarritmico
## 33. betabloqueador
## 34. ieca_bra
## 35. dva
## 36. digoxina
## 37. estatina
## 38. diuretico
## 39. vasodilatador
## 40. insuf_cardiaca
## 41. espironolactona
## 42. bloq_calcio
## 43. antiplaquetario_ev
## 44. insulina
## 45. anticonvulsivante
## 46. psicofarmacos
## 47. antifungico
## 48. antiviral
## 49. antiretroviral
## 50. classe_meds_qtde
## 51. meds_cardiovasc_qtde
## 52. meds_antimicrobianos
## 53. vni
## 54. ventilacao_mecanica
## 55. cec
## 56. transplante_cardiaco
## 57. cir_toracica
## 58. outros_proced_cirurgicos
## 59. icp
## 60. intervencao_cv
## 61. angioplastia
## 62. cateterismo
## 63. eletrofisiologia
## 64. cateter_venoso_central
## 65. proced_invasivos_qtde
## 66. cve_desf
## 67. transfusao
## 68. interconsulta
## 69. equipe_multiprof
## 70. holter
## 71. teste_esforco
## 72. espiro_ergoespiro
## 73. tilt_teste
## 74. metodos_graficos_qtde
## 75. laboratorio
## 76. cultura
```

```
## 77. analises_clinicas_qtde
## 78. citologia
## 79. biopsia
## 80. histopatologia_qtde
## 81. angio_rm
## 82. angio_tc
## 83. arteriografia
## 84. cintilografia
## 85. ecocardiograma
## 86. endoscopia
## 87. flebografia
## 88. pet_ct
## 89. ultrassom
## 90. tomografia
## 91. ressonancia
## 92. exames_imagem_qtde
## 93. bic
## 94. mpp
## 95. hospital_stay
```

Minutes to run: 0

Train test split (70%/30%)

```
set.seed(42)

if (outcome_column == 'readmission_30d') {
  df_split <- readRDS("./dataset/split_object.rds")
} else {
  df_split <- initial_split(df, prop = .7, strata = all_of(outcome_column))
}

df_train <- training(df_split) %>% dplyr::select(all_of(c(features, outcome_column)))
df_test <- testing(df_split) %>% dplyr::select(all_of(c(features, outcome_column)))

df_folds <- vfold_cv(df_train, v = k,
                     strata = all_of(outcome_column))
```

Minutes to run: 0.001

Boosted Tree (XGBoost)

```
xgboost_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula, data = df_train) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
  step_dummy(all_nominal_predictors())

xgboost_spec <- boost_tree(
  trees = tune(),
  min_n = tune(),
  tree_depth = tune(),
  learn_rate = tune(),
) %>%
  set_engine("xgboost",
             nthread = 8) %>%
  set_mode("classification")

xgboost_grid <- grid_latin_hypercube(
```

```
  trees(range = c(25L, 150L)),
  min_n(range = c(2L, 100L)),
  tree_depth(range = c(2L, 15L)),
  learn_rate(range = c(-3, -1), trans = log10_trans()),
  size = grid_size
)

xgboost_workflow <-
  workflow() %>%
  add_recipe(xgboost_recipe) %>%
  add_model(xgboost_spec)

xgboost_tune <-
  xgboost_workflow %>%
  tune_grid(resamples = df_folds,
            grid = xgboost_grid)

xgboost_tune %>%
  show_best("roc_auc")

best_xgboost <- xgboost_tune %>%
  select_best("roc_auc")

autoplot(xgboost_tune, metric = "roc_auc")

final_xgboost_workflow <-
  xgboost_workflow %>%
  finalize_workflow(best_xgboost)

last_xgboost_fit <-
  final_xgboost_workflow %>%
  last_fit(df_split)

final_xgboost_fit <- extract_workflow(last_xgboost_fit)

xgboost_auc <- validation(final_xgboost_fit, df_test)

extract_vip(final_xgboost_fit, pred_wrapper = predict,
            reference_class = "0")

xgboost_parameters <- xgboost_tune %>%
  show_best("roc_auc", n = 1) %>%
  select(trees, min_n, tree_depth, learn_rate, loss_reduction) %>%
  as.list

saveRDS(
  xgboost_parameters,
  file = sprintf(
    "./auxiliar/model_selection/hyperparameters/xgboost_%s.rds",
    outcome_column
  )
)

preds <- predict(final_xgboost_fit, new_data = df_train, type = "prob") %>%
  rename_at(vars(starts_with(".pred_")), ~ str_remove(., ".pred_")) %>%
  .$`1`

hist(preds)
```

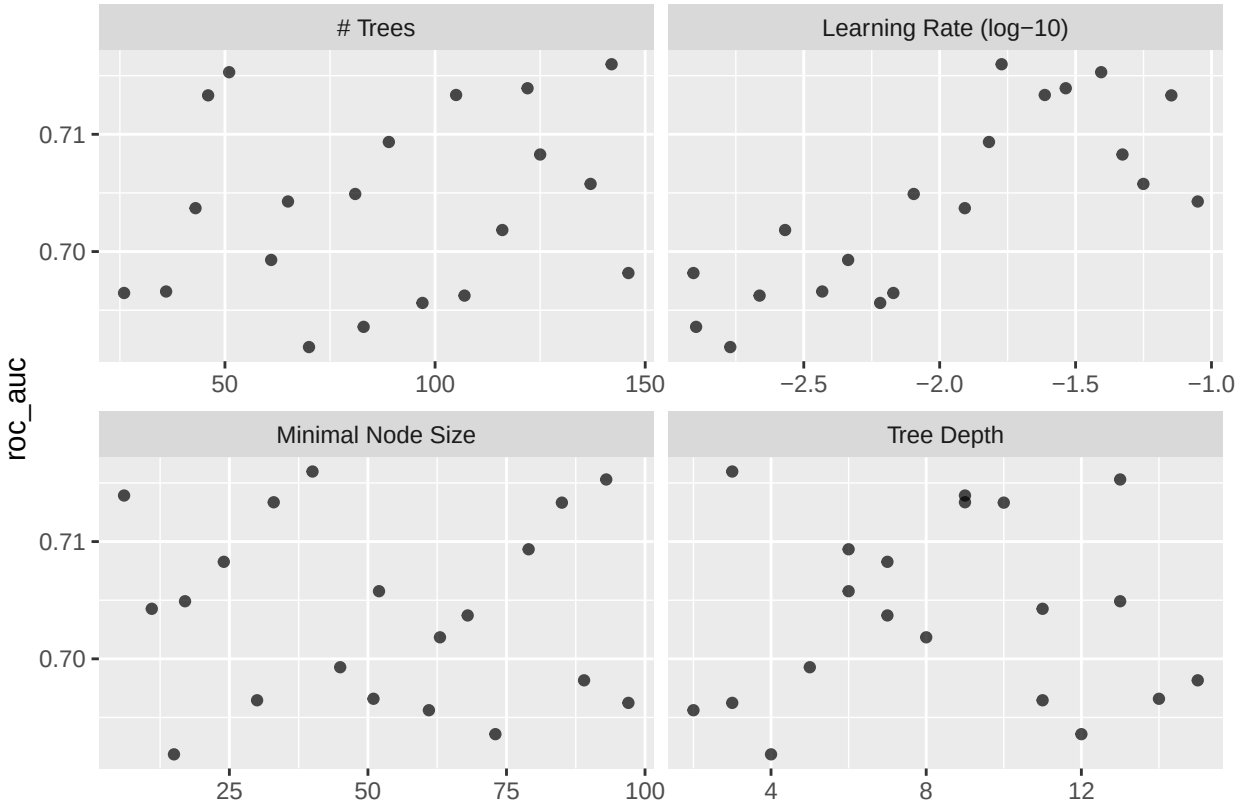
Minutes to run: 0

Boosted Tree (LightGBM)

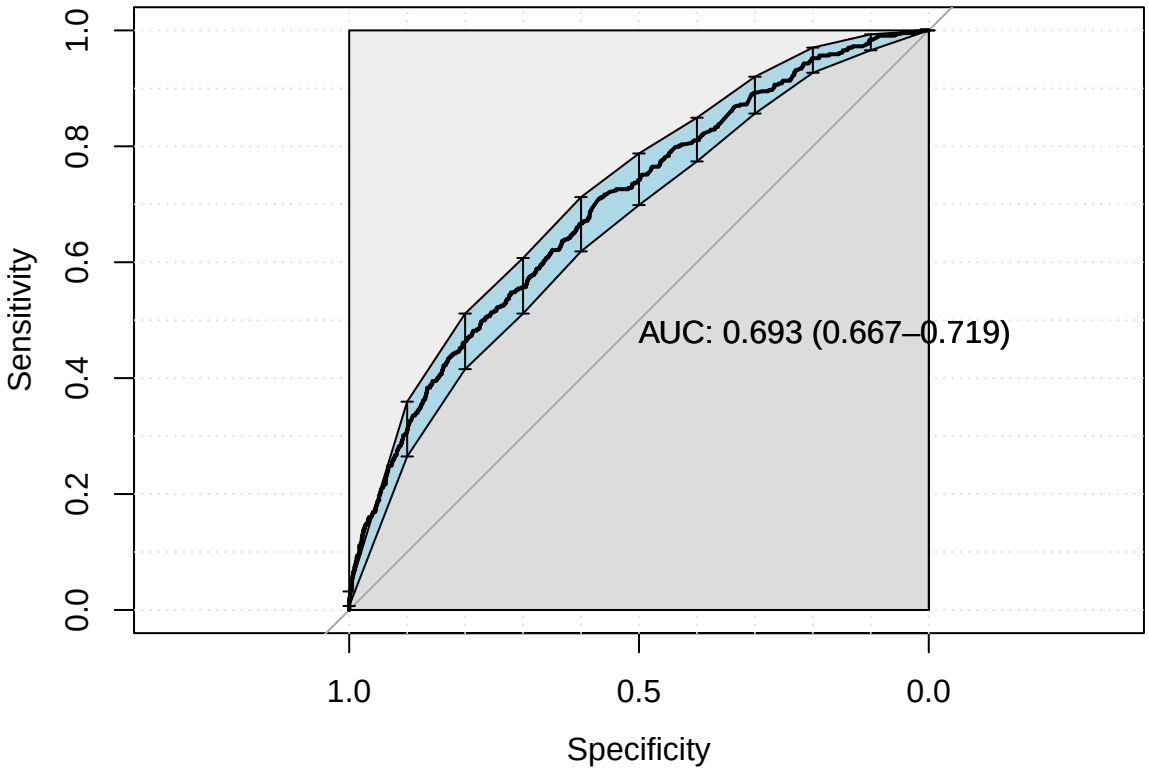
```
lightgbm_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula, data = df_train) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
  step_dummy(all_nominal_predictors())

lightgbm_spec <- boost_tree(
  trees = tune(),
  min_n = tune(),
  tree_depth = tune(),
  learn_rate = tune(),
  sample_size = 1
) %>%
  set_engine("lightgbm",
             nthread = 8) %>%
  set_mode("classification")

lightgbm_grid <- grid_latin_hypercube(
  trees(range = c(25L, 150L)),
  min_n(range = c(2L, 100L)),
  tree_depth(range = c(2L, 15L)),
  learn_rate(range = c(-3, -1), trans = log10_trans()),
  size = grid_size
)

lightgbm_workflow <-
  workflow() %>%
  add_recipe(lightgbm_recipe) %>%
  add_model(lightgbm_spec)

lightgbm_tune <-
  lightgbm_workflow %>%
  tune_grid(resamples = df_folds,
            grid = lightgbm_grid)

lightgbm_tune %>%
  show_best("roc_auc")
```

```
## # A tibble: 5 x 10
##   trees min_n tree_depth learn_rate .metric .estimator  mean     n std_err .config
##   <int> <int>      <int>      <dbl> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
## 1   142    40          3     0.0169 roc_auc binary     0.716    10  0.0100 Preprocessor1_Model08
## 2    51    93         13     0.0393 roc_auc binary     0.715    10  0.0120 Preprocessor1_Model19
## 3   122     6          9     0.0291 roc_auc binary     0.714    10  0.0122 Preprocessor1_Model01
## 4   105    33          9     0.0244 roc_auc binary     0.713    10  0.0119 Preprocessor1_Model07
## 5    46    85         10     0.0712 roc_auc binary     0.713    10  0.0130 Preprocessor1_Model17
```

```
best_lightgbm <- lightgbm_tune %>%
  select_best("roc_auc")

autoplot(lightgbm_tune, metric = "roc_auc")
```




```
final_lightgbm_workflow <-
  lightgbm_workflow %>%
  finalize_workflow(best_lightgbm)

last_lightgbm_fit <-
  final_lightgbm_workflow %>%
  last_fit(df_split)

final_lightgbm_fit <- extract_workflow(last_lightgbm_fit)

lightgbm_auc <- validation(final_lightgbm_fit, df_test)
```




```
## [1] "Optimal Threshold: 0.07"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 2442  127
##    1 1850  311
##
##                Accuracy : 0.582
##                  95% CI : (0.5678, 0.5961)
##     No Information Rate : 0.9074
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1009
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.5690
##             Specificity : 0.7100
##          Pos Pred Value : 0.9506
##          Neg Pred Value : 0.1439
##              Prevalence : 0.9074
##          Detection Rate : 0.5163
##    Detection Prevalence : 0.5431
##       Balanced Accuracy : 0.6395
##
##        'Positive' Class : 0
##
```

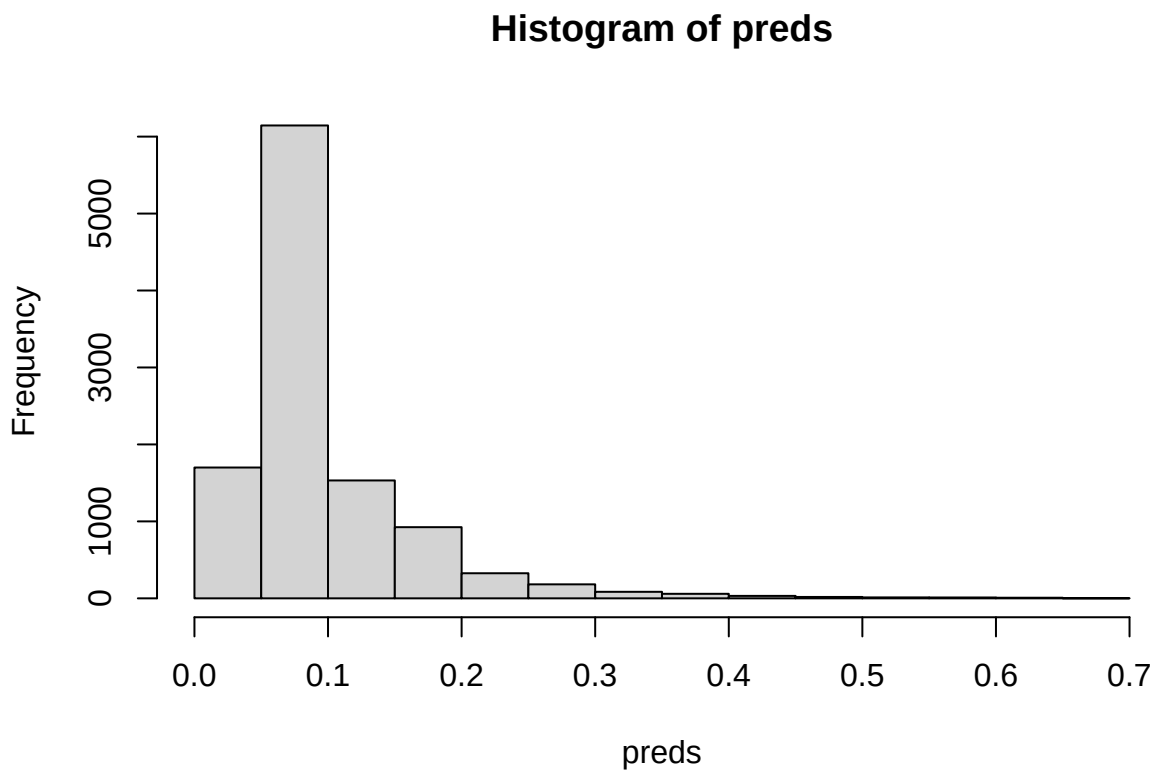
```
lightgbm_parameters <- lightgbm_tune %>%
  show_best("roc_auc", n = 1) %>%
  select(-.metric, -.estimator, -.config, -mean, -n, -std_err) %>%
  as.list
```

```
Hmisc::list.tree(lightgbm_parameters)
```

```
##  lightgbm_parameters = list 4 (736 bytes)
## .  trees = integer 1= 142
## .  min_n = integer 1= 40
## .  tree_depth = integer 1= 3
## .  learn_rate = double 1= 0.016901
```

```
saveRDS(
  lightgbm_parameters,
  file = sprintf(
    "./auxiliar/model_selection/hyperparameters/lightgbm_%s.rds",
    outcome_column
  )
)
```

Minutes to run: 3.781



Minutes to run: 0.006

GLM

```
glmnet_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula, data = df_train) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
  step_dummy(all_nominal_predictors()) %>%
  step_zv(all_predictors()) %>%
  step_normalize(all_numeric_predictors())

glmnet_spec <-
  logistic_reg(penalty = 0) %>%
  set_mode("classification") %>%
```

```
  set_engine("glmnet")

glmnet_workflow <-
  workflow() %>%
  add_recipe(glmnet_recipe) %>%
  add_model(glmnet_spec)

glm_fit <- glmnet_workflow %>%
  fit(df_train)

glmnet_auc <- validation(glm_fit, df_test)

pfun_glmnet <- function(object, newdata) predict(object, newx = newdata)

extract_vip(glm_fit, pred_wrapper = pfun_glmnet,
            reference_class = "1", method = 'model')

extract_vip(glm_fit, pred_wrapper = pfun_glmnet,
            reference_class = "1", method = 'permute')
```

Minutes to run: 0

Decision Tree

```
tree_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula, data = df_train) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
  step_dummy(all_nominal_predictors()) %>%
  step_zv(all_predictors())

tree_spec <-
  decision_tree(cost_complexity = tune(),
                tree_depth = tune(),
                min_n = tune()) %>%
  set_mode("classification") %>%
  set_engine("rpart")

tree_grid <- grid_latin_hypercube(cost_complexity(),
                                  tree_depth(),
                                  min_n(),
                                  size = grid_size)

tree_workflow <-
  workflow() %>%
  add_recipe(tree_recipe) %>%
  add_model(tree_spec)

tree_tune <-
  tree_workflow %>%
  tune_grid(resamples = df_folds,
            grid = tree_grid)

tree_tune %>%
  collect_metrics()

autoplot(tree_tune, metric = "roc_auc")

tree_tune %>%
```

```
  show_best("roc_auc")

best_tree <- tree_tune %>%
  select_best("roc_auc")

final_tree_workflow <-
  tree_workflow %>%
  finalize_workflow(best_tree)

last_tree_fit <-
  final_tree_workflow %>%
  last_fit(df_split)

final_tree_fit <- extract_workflow(last_tree_fit)

tree_auc <- validation(final_tree_fit, df_test)

extract_vip(final_tree_fit, pred_wrapper = predict,
            reference_class = "0", use_matrix = FALSE,
            method = 'model')

# extract_vip(final_tree_fit, pred_wrapper = predict,
#             reference_class = "1", use_matrix = FALSE,
#             method = 'permute')
```

Minutes to run: 0

Random Forest

```
rf_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula,
         data = df_train) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
  step_dummy(all_nominal_predictors()) %>%
  step_zv(all_predictors()) %>%
  step_impute_mean(all_numeric_predictors())

rf_spec <-
  rand_forest(mtry = tune(),
              trees = tune(),
              min_n = tune()) %>%
  set_mode("classification") %>%
  set_engine("randomForest",
             probability = TRUE,
             nthread = 8)

rf_grid <- grid_latin_hypercube(mtry(range = c(1L, 50L)),
                                trees(range = c(100L, 300L)),
                                min_n(),
                                size = grid_size)

rf_workflow <-
  workflow() %>%
  add_recipe(rf_recipe) %>%
  add_model(rf_spec)

rf_tune <-
  rf_workflow %>%
```

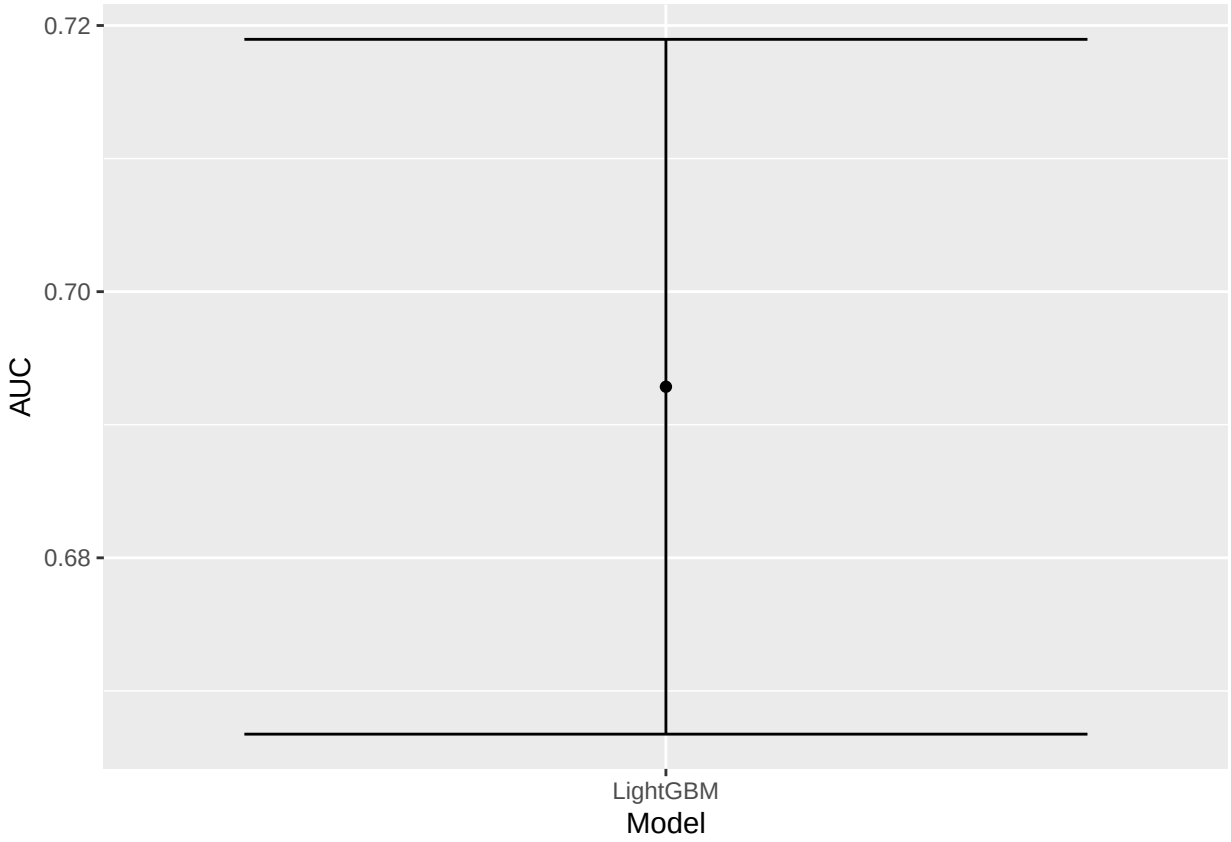
```
  tune_grid(resamples = df_folds,
            grid = rf_grid)

rf_tune %>%
  collect_metrics()

autoplot(rf_tune, metric = "roc_auc")

rf_tune %>%
  show_best("roc_auc")

best_rf <- rf_tune %>%
  select_best("roc_auc")

final_rf_workflow <-
  rf_workflow %>%
  finalize_workflow(best_rf)

last_rf_fit <-
  final_rf_workflow %>%
  last_fit(df_split)

final_rf_fit <- extract_workflow(last_rf_fit)

rf_auc <- validation(final_rf_fit, df_test)

pfun_rf <- function(object, newdata) predict(object, data = newdata)

extract_vip(final_rf_fit, pred_wrapper = predict,
            reference_class = "1", use_matrix = FALSE,
            method = 'model')

# extract_vip(final_rf_fit, pred_wrapper = predict,
#             reference_class = "1", use_matrix = FALSE,
#             method = 'permute')
```

Minutes to run: 0

Models Comparison

```
if (RUN_ALL_MODELS) {
  df_auc <- tibble::tribble(
    ~Model, ~`AUC`, ~`Lower Limit`, ~`Upper Limit`,
    'XGBoost', as.numeric(xgboost_auc$auc), xgboost_auc$ci[1], xgboost_auc$ci[3],
    'LightGBM', as.numeric(lightgbm_auc$auc), lightgbm_auc$ci[1], lightgbm_auc$ci[3],
    'GLM', as.numeric(glmnet_auc$auc), glmnet_auc$ci[1], glmnet_auc$ci[3],
    'Decision Tree', as.numeric(tree_auc$auc), tree_auc$ci[1], tree_auc$ci[3],
    'Random Forest', as.numeric(rf_auc$auc), rf_auc$ci[1], rf_auc$ci[3]
  ) %>%
    mutate(Target = outcome_column)
} else {
  df_auc <- tibble::tribble(
    ~Model, ~`AUC`, ~`Lower Limit`, ~`Upper Limit`,
    'LightGBM', as.numeric(lightgbm_auc$auc), lightgbm_auc$ci[1], lightgbm_auc$ci[3]
  ) %>%
    mutate(Target = outcome_column)
}

df_auc %>%
  ggplot(aes(x = Model, y = AUC, ymin = `Lower Limit`, ymax = `Upper Limit`)) +
```

```
    geom_point() +
    geom_errorbar()
```




```
saveRDS(df_auc, sprintf("./auxiliar/model_selection/performance/%s.RData", outcome_column))
```

Minutes to run: 0.002