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= TRUE
```

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")
predict <- stats::predict
```

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: 0.007

```
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 = read_yaml(sprintf(
  "./auxiliar/significant_columns/categorical_%s.yaml",
  outcome_column
))

num_features_list = read_yaml(sprintf(
  "./auxiliar/significant_columns/numerical_%s.yaml",
  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

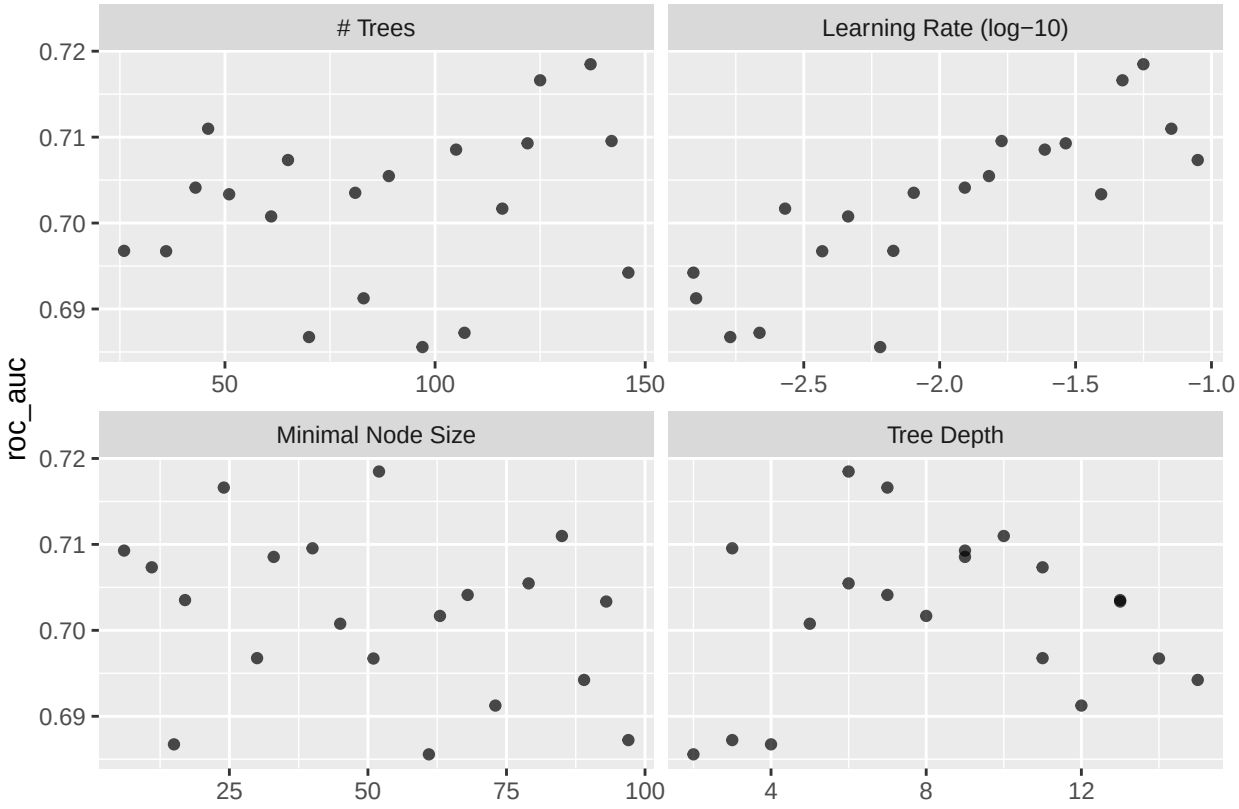
Boosted Tree (XGBoost)

```
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")
```

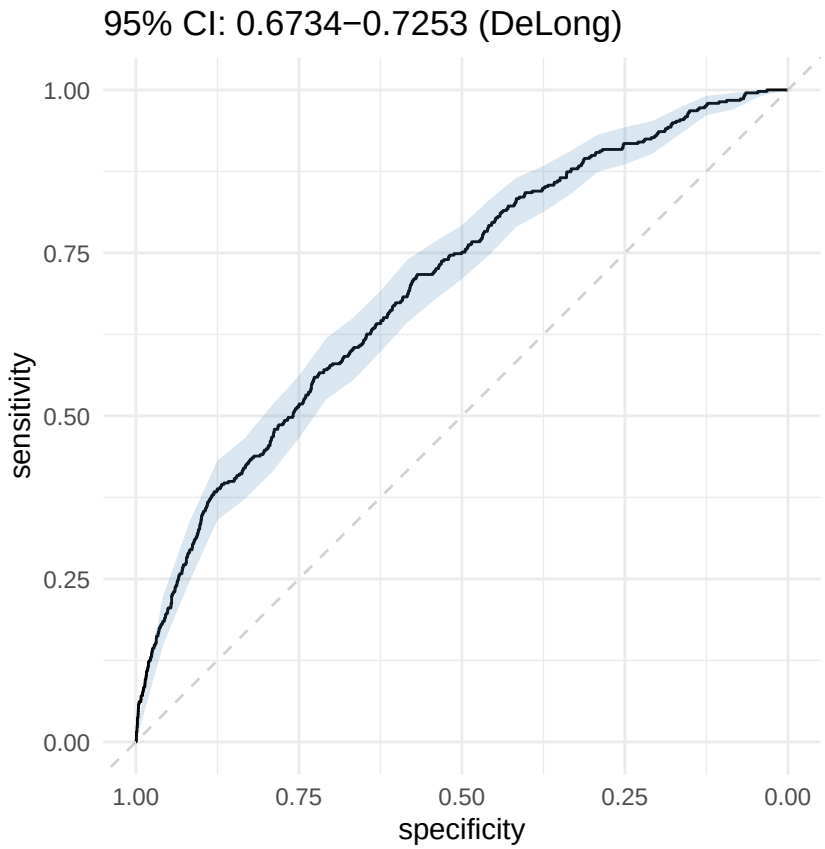
```
xgboost_grid <- grid_latin_hypercube(
  trees(range = c(25L, 150L)),
  min_n(range = c(2L, 100L)),
  tree_depth(range = c(2L, 15L)),
  learn_rate(range = c(-3, -1), trans = log10_trans()),
  size = grid_size
)

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")
```

```
## # 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   137    52          6     0.0562 roc_auc binary     0.718    10  0.0120 Prepro~
## 2   125    24          7     0.0471 roc_auc binary     0.717    10  0.0114 Prepro~
## 3    46    85         10     0.0712 roc_auc binary     0.711    10  0.0101 Prepro~
## 4   142    40          3     0.0169 roc_auc binary     0.710    10  0.0105 Prepro~
## 5   122     6          9     0.0291 roc_auc binary     0.709    10  0.0139 Prepro~
```

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

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

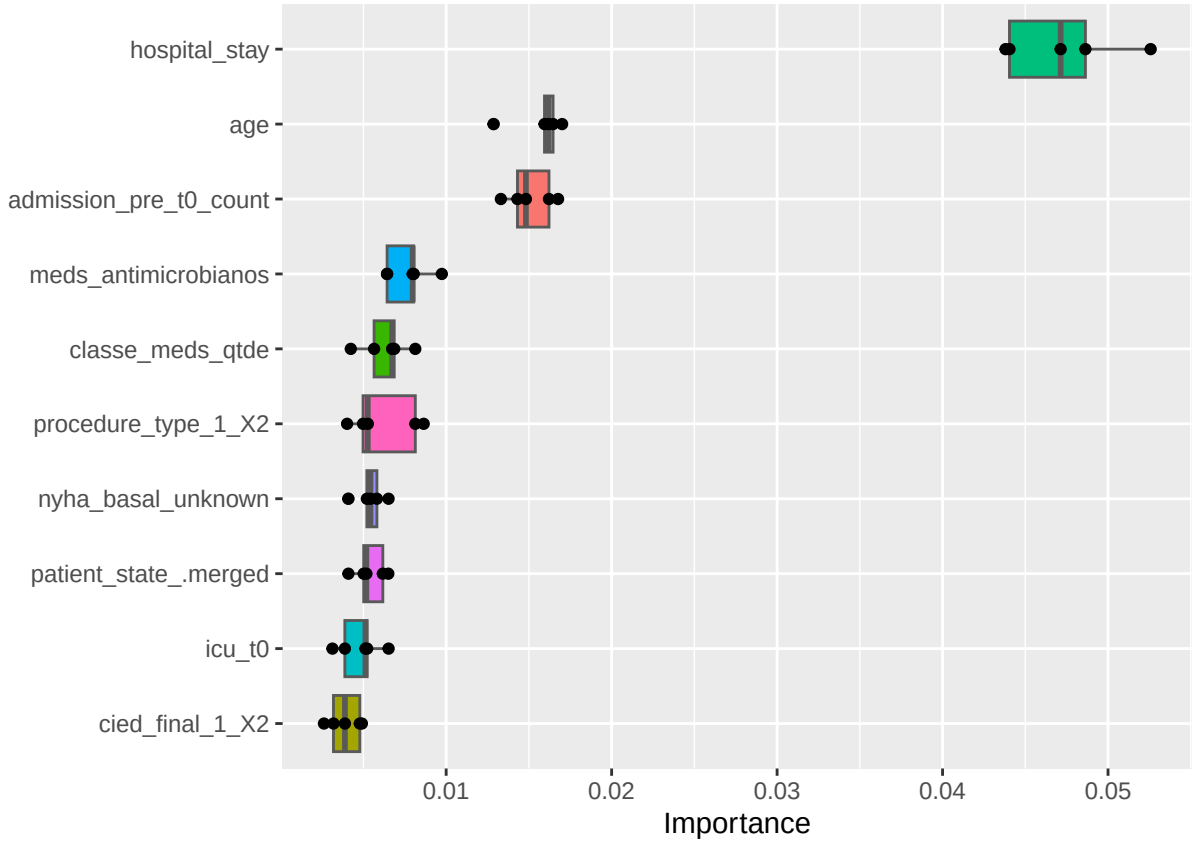



```
final_xgboost_workflow <-
  xgboost_workflow %>%
  finalize_workflow(best_xgboost)

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)
```




```
## [1] "Optimal Threshold: 0.10"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3118  193
##    1 1174  245
##
##                Accuracy : 0.711
##                  95% CI : (0.6978, 0.7239)
##     No Information Rate : 0.9074
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1425
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.7265
##             Specificity : 0.5594
##          Pos Pred Value : 0.9417
##          Neg Pred Value : 0.1727
##              Prevalence : 0.9074
##          Detection Rate : 0.6592
##    Detection Prevalence : 0.7000
##       Balanced Accuracy : 0.6429
##
##        'Positive' Class : 0
##
```

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




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

Minutes to run: 4.862

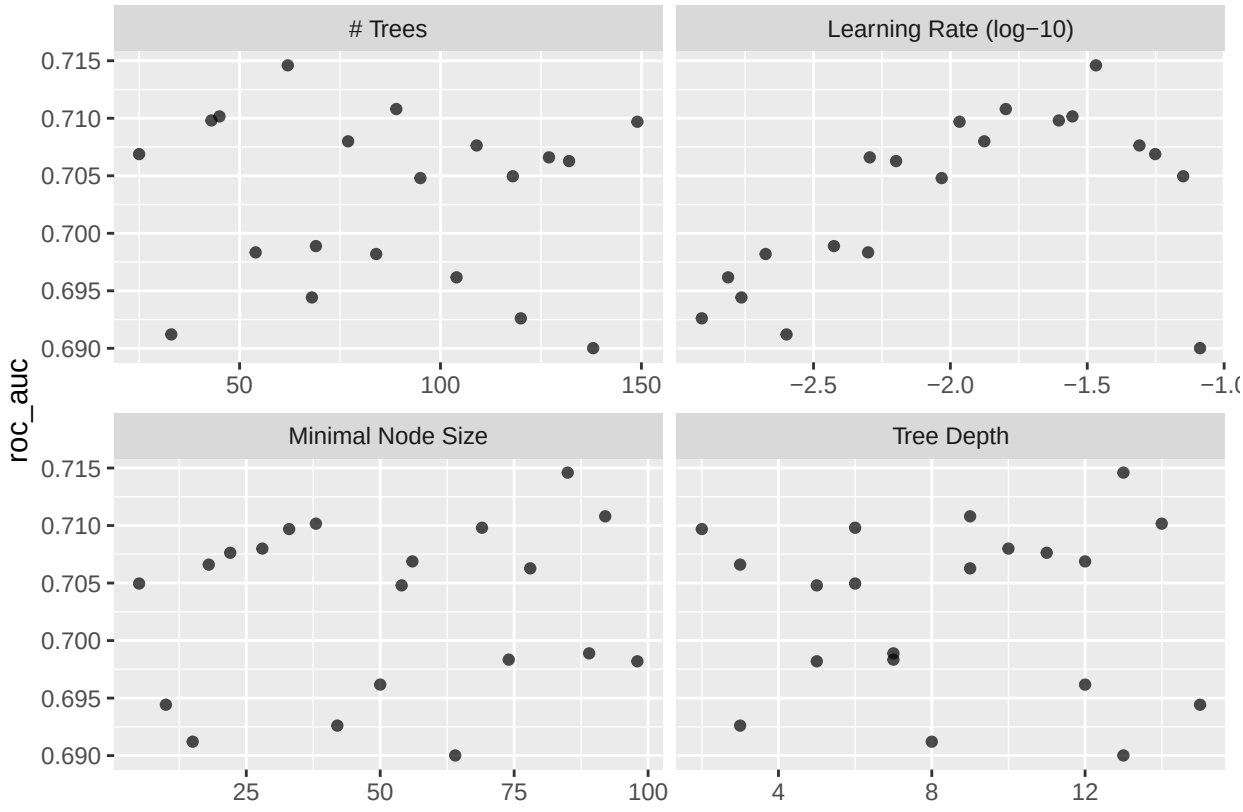
Boosted Tree (LightGBM)

```
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")
```

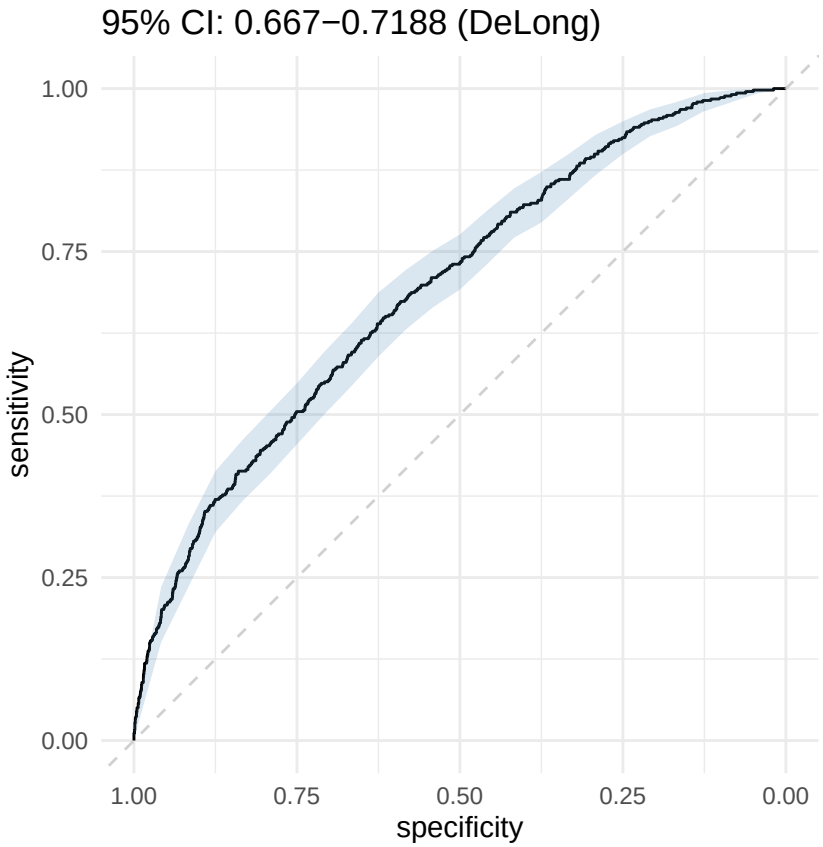
```
## # A tibble: 5 x 10
##   trees min_n tree_depth learn_rate .metric .estimator  mean     n std_err .config
##   <int> <int>      <int>      <dbl> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
## 1    62    85         13     0.0340 roc_auc binary     0.715    10  0.0116 Prepro~
## 2    89    92          9     0.0159 roc_auc binary     0.711    10  0.0119 Prepro~
## 3    45    38         14     0.0279 roc_auc binary     0.710    10  0.0117 Prepro~
## 4    43    69          6     0.0249 roc_auc binary     0.710    10  0.0114 Prepro~
## 5   149    33          2     0.0108 roc_auc binary     0.710    10  0.0102 Prepro~
```

```
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: 0.08"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 2651  154
##    1 1641  284
##
##                Accuracy : 0.6205
##                  95% CI : (0.6065, 0.6344)
##     No Information Rate : 0.9074
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1054
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.6177
##             Specificity : 0.6484
##          Pos Pred Value : 0.9451
##          Neg Pred Value : 0.1475
##              Prevalence : 0.9074
##          Detection Rate : 0.5605
##    Detection Prevalence : 0.5930
##       Balanced Accuracy : 0.6330
##
```

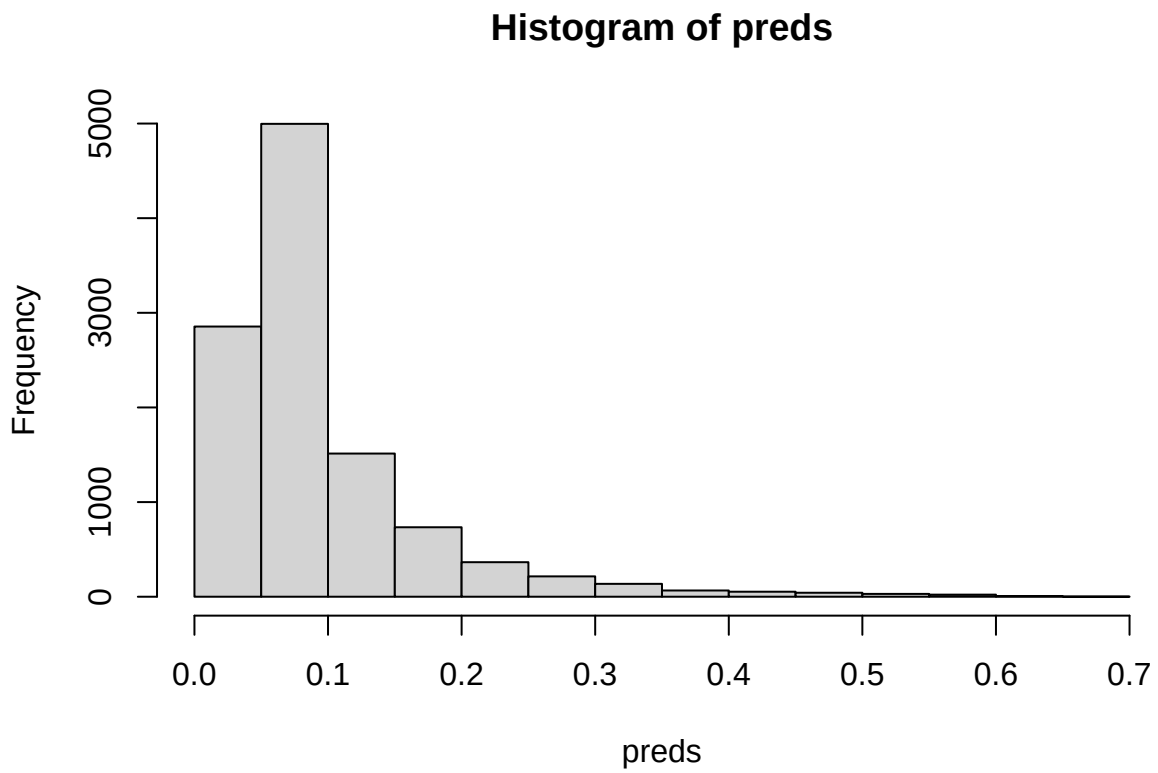
```
##        'Positive' Class : 0
##
```

```
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= 62
## .  min_n = integer 1= 85
## .  tree_depth = integer 1= 13
## .  learn_rate = double 1= 0.03403
```

```
con <- file(sprintf('./auxiliar/model_selection/hyperparameters/%s.yaml', outcome_column), "w")
write_yaml(lightgbm_parameters, con)
close(con)
```

Minutes to run: 3.184

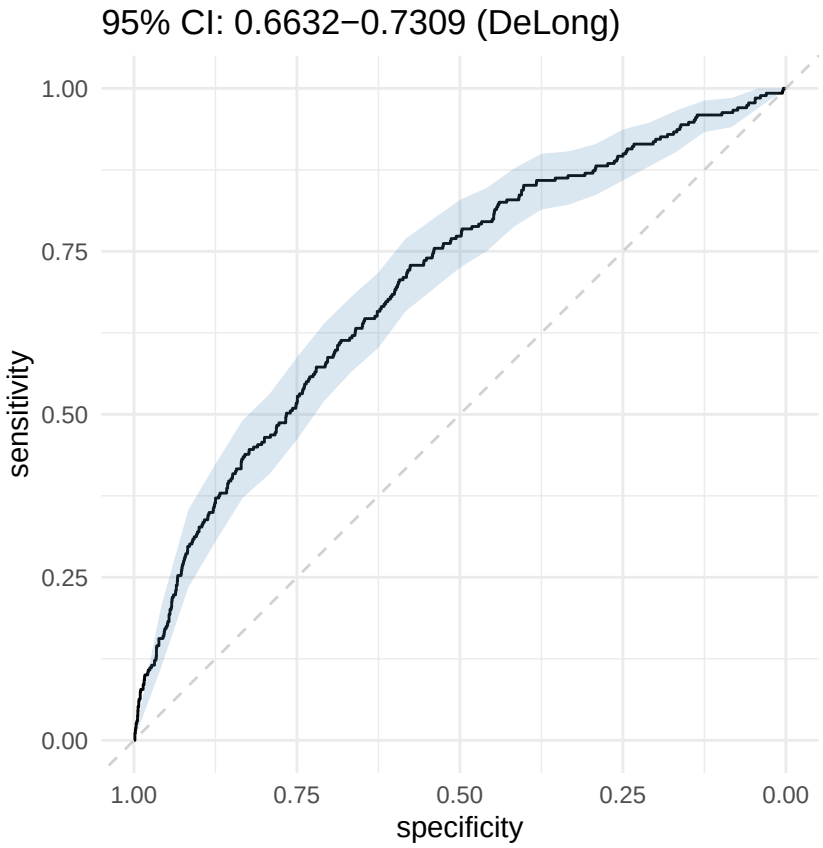


Minutes to run: 0.005

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())
```

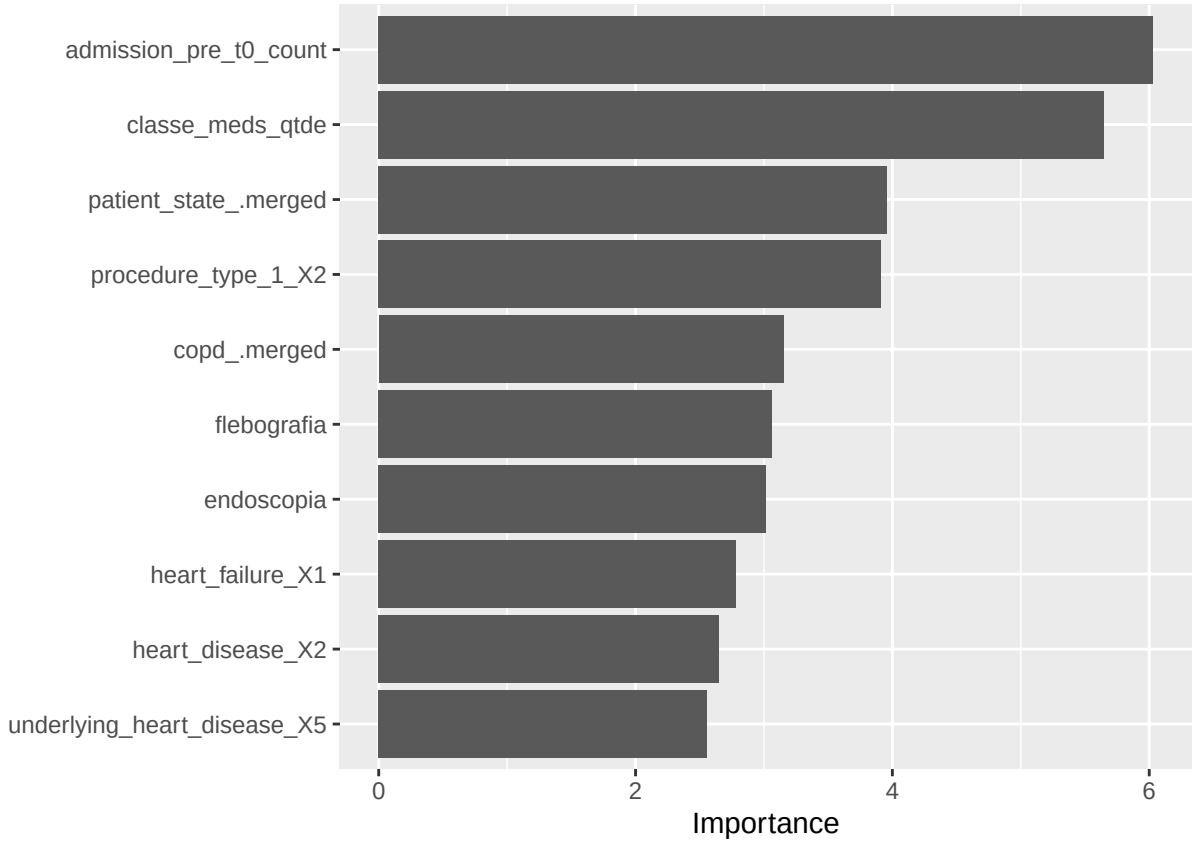
```r
glmnet_spec <-
  logistic_reg(penalty = 0) %>%
  set_mode("classification") %>%
  set_engine("glm")

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)
```




```
## [1] "Optimal Threshold: 0.07"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 1552   73
##    1 1141  196
##
##                Accuracy : 0.5901
##                  95% CI : (0.5722, 0.6079)
##     No Information Rate : 0.9092
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1094
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.5763
```

```
##             Specificity : 0.7286
##          Pos Pred Value : 0.9551
##          Neg Pred Value : 0.1466
##              Prevalence : 0.9092
##          Detection Rate : 0.5240
##    Detection Prevalence : 0.5486
##       Balanced Accuracy : 0.6525
##
##        'Positive' Class : 0
##
```

```
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')
```

Importance

Minutes to run: 0.217

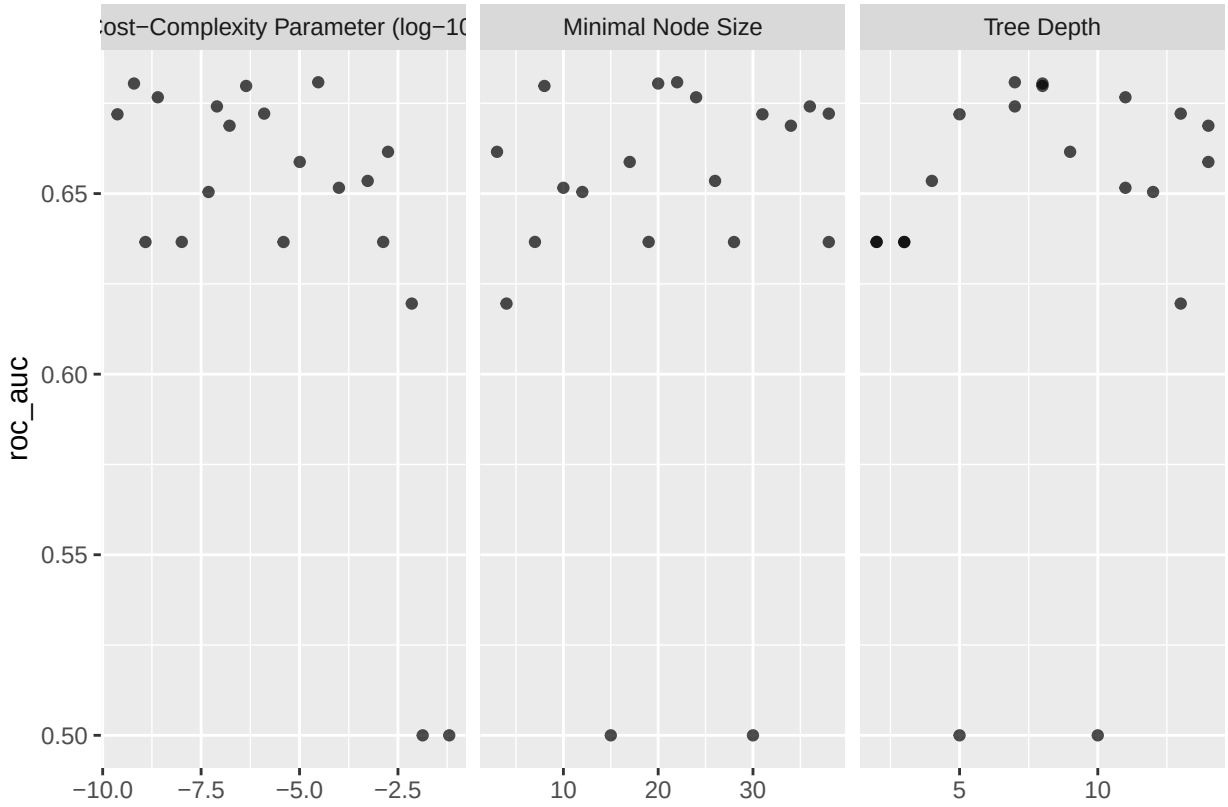
Decision Tree

```
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()
```

```
## # A tibble: 40 x 9
##    cost_complexity tree_depth min_n .metric .estimator  mean     n std_err .config
##              <dbl>      <int> <int> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
##  1        4.40e- 7          8     8 accura~ binary     0.898    10 0.00370 Prepro~
##  2        4.40e- 7          8     8 roc_auc binary     0.680    10 0.00996 Prepro~
##  3        3.92e- 6          3    38 accura~ binary     0.906    10 0.00288 Prepro~
##  4        3.92e- 6          3    38 roc_auc binary     0.637    10 0.00797 Prepro~
##  5        2.37e-10          5    31 accura~ binary     0.904    10 0.00288 Prepro~
##  6        2.37e-10          5    31 roc_auc binary     0.672    10 0.0123  Prepro~
##  7        6.35e- 2          5    30 accura~ binary     0.905    10 0.00282 Prepro~
##  8        6.35e- 2          5    30 roc_auc binary     0.5      10 0       Prepro~
##  9        2.99e- 5          7    22 accura~ binary     0.899    10 0.00307 Prepro~
## 10        2.99e- 5          7    22 roc_auc binary     0.681    10 0.00842 Prepro~
## # i 30 more rows
```

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

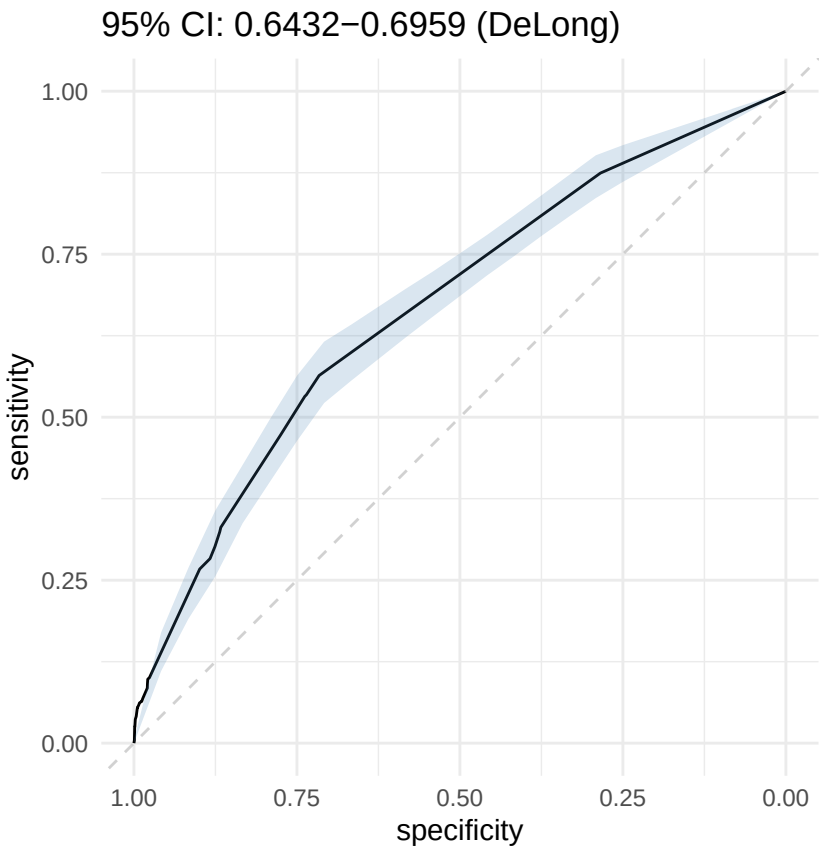



```
tree_tune %>%
  show_best("roc_auc")
```

```
## # A tibble: 5 x 9
##   cost_complexity tree_depth min_n .metric .estimator  mean     n std_err .config
##             <dbl>      <int> <int> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
## 1        2.99e- 5          7    22 roc_auc binary     0.681    10 0.00842 Preproc~
## 2        6.24e-10          8    20 roc_auc binary     0.680    10 0.00882 Preproc~
## 3        4.40e- 7          8     8 roc_auc binary     0.680    10 0.00996 Preproc~
## 4        2.52e- 9         11    24 roc_auc binary     0.677    10 0.00809 Preproc~
## 5        7.98e- 8          7    36 roc_auc binary     0.674    10 0.0117  Preproc~
```

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

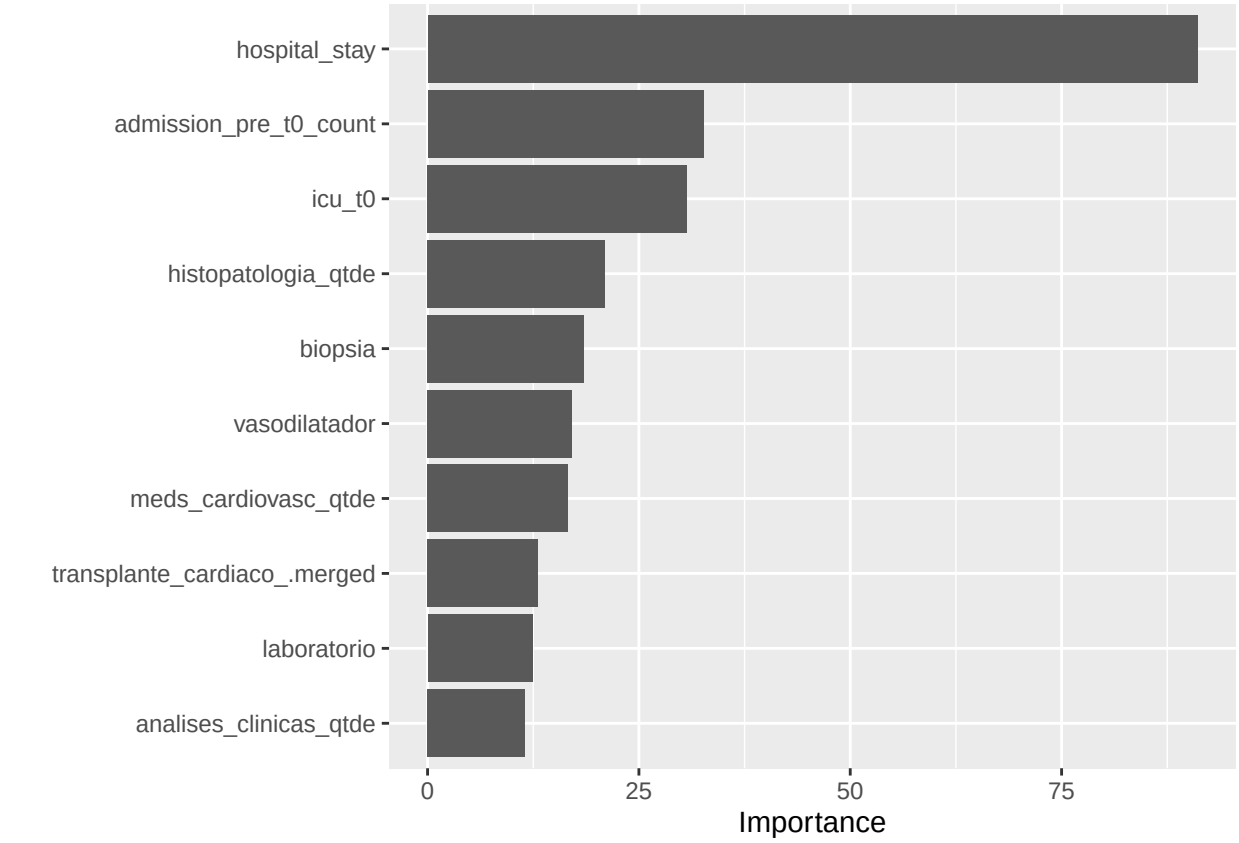
```r
final_tree_workflow <-
  tree_workflow %>%
  finalize_workflow(best_tree)

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)
```




```
## [1] "Optimal Threshold: 0.08"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3073  191
##    1 1219  247
##
##                Accuracy : 0.7019
##                  95% CI : (0.6886, 0.7149)
##     No Information Rate : 0.9074
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1363
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.7160
##             Specificity : 0.5639
##          Pos Pred Value : 0.9415
##          Neg Pred Value : 0.1685
```

```
##              Prevalence : 0.9074
##          Detection Rate : 0.6497
##    Detection Prevalence : 0.6901
##       Balanced Accuracy : 0.6400
##
##        'Positive' Class : 0
##
```

```
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: 4.815

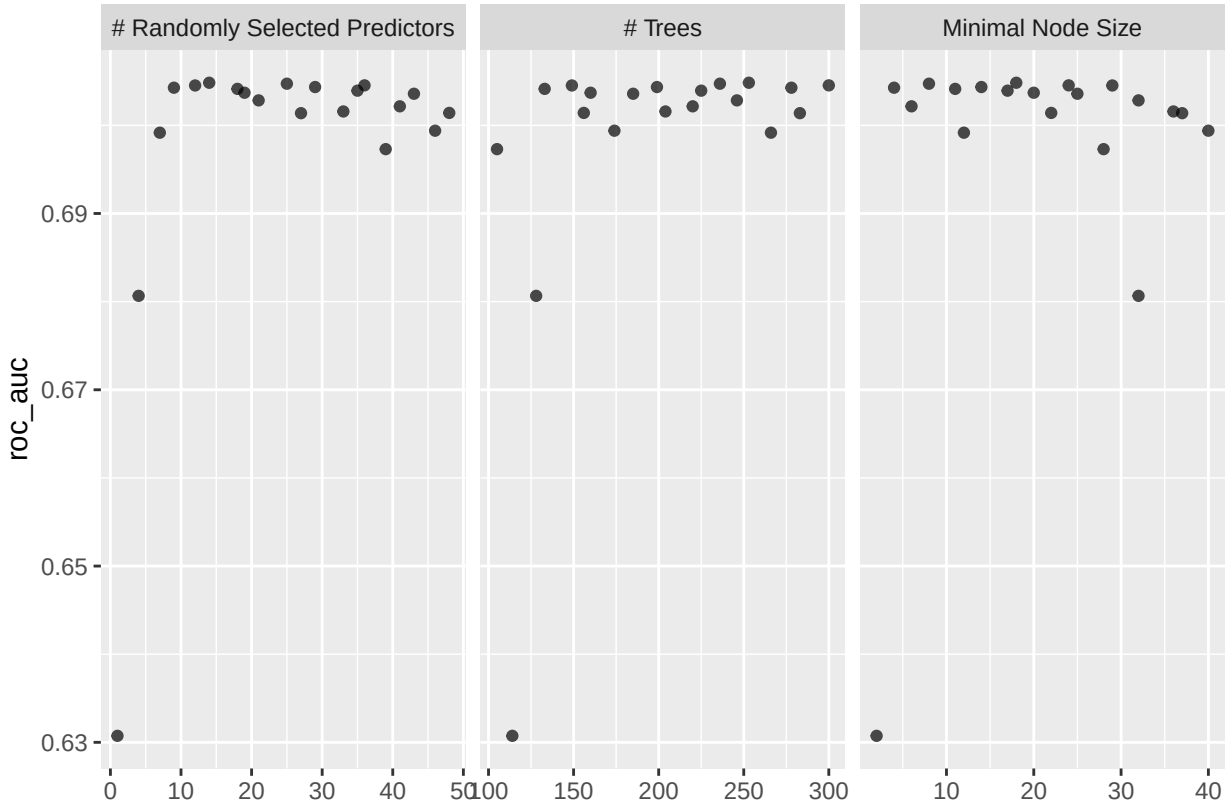
Random Forest

```
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()
```

```
## # A tibble: 40 x 9
##     mtry trees min_n .metric  .estimator  mean     n std_err .config
##    <int> <int> <int> <chr>    <chr>      <dbl> <int>   <dbl> <chr>
##  1     7   266    12 accuracy binary     0.906    10 0.00276 Preprocessor1_Model01
##  2     7   266    12 roc_auc  binary     0.699    10 0.0124  Preprocessor1_Model01
##  3    14   253    18 accuracy binary     0.906    10 0.00274 Preprocessor1_Model02
##  4    14   253    18 roc_auc  binary     0.705    10 0.0128  Preprocessor1_Model02
##  5     1   114     2 accuracy binary     0.905    10 0.00282 Preprocessor1_Model03
##  6     1   114     2 roc_auc  binary     0.631    10 0.0122  Preprocessor1_Model03
##  7    48   156    22 accuracy binary     0.906    10 0.00275 Preprocessor1_Model04
##  8    48   156    22 roc_auc  binary     0.701    10 0.0143  Preprocessor1_Model04
##  9     9   278     4 accuracy binary     0.905    10 0.00281 Preprocessor1_Model05
## 10     9   278     4 roc_auc  binary     0.704    10 0.0126  Preprocessor1_Model05
## # i 30 more rows
```

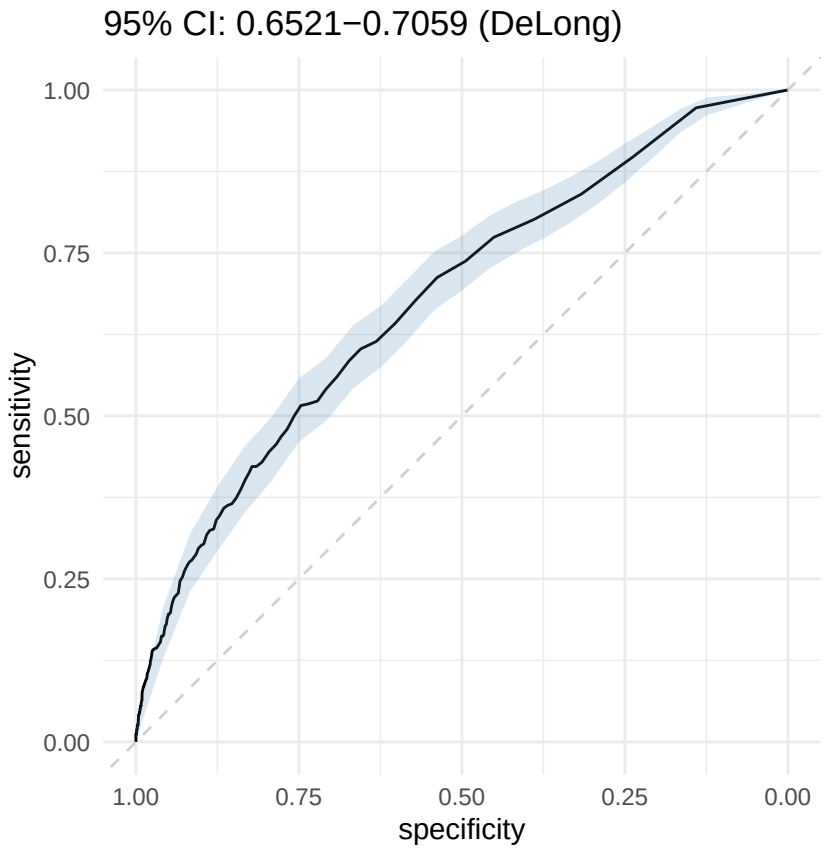
```
autoplot(rf_tune, metric = "roc_auc")
```




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

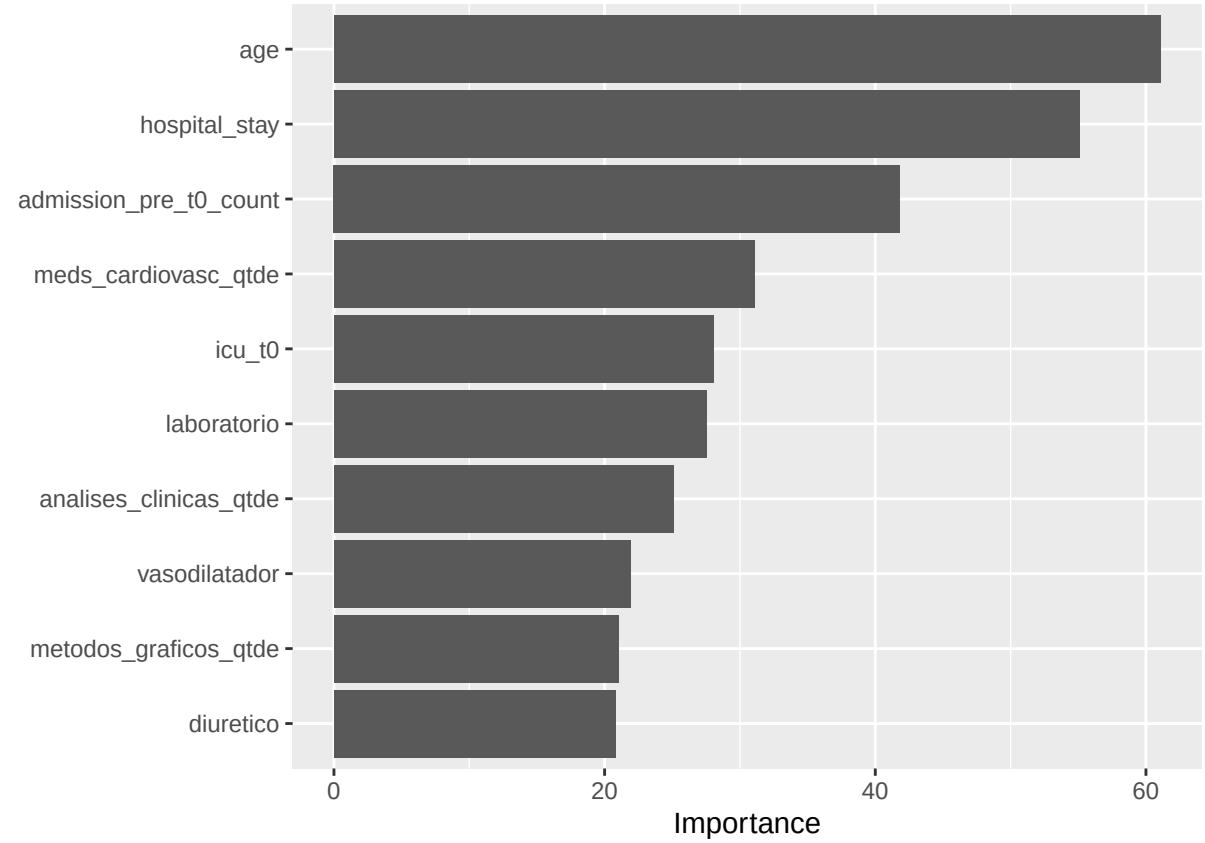
```
## # A tibble: 5 x 9
##    mtry trees min_n .metric .estimator  mean     n std_err .config
##   <int> <int> <int> <chr>   <chr>      <dbl> <int>   <dbl> <chr>
## 1    14   253    18 roc_auc binary     0.705    10  0.0128 Preprocessor1_Model02
## 2    25   236     8 roc_auc binary     0.705    10  0.0139 Preprocessor1_Model12
## 3    36   300    24 roc_auc binary     0.705    10  0.0125 Preprocessor1_Model19
## 4    12   149    29 roc_auc binary     0.705    10  0.0141 Preprocessor1_Model20
## 5    29   199    14 roc_auc binary     0.704    10  0.0124 Preprocessor1_Model14
```

```
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)
```




```
## [1] "Optimal Threshold: 0.07"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3206  212
##    1 1086  226
##
##                Accuracy : 0.7256
##                  95% CI : (0.7126, 0.7383)
##     No Information Rate : 0.9074
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1387
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.7470
##             Specificity : 0.5160
##          Pos Pred Value : 0.9380
##          Neg Pred Value : 0.1723
##              Prevalence : 0.9074
##          Detection Rate : 0.6778
##    Detection Prevalence : 0.7226
##       Balanced Accuracy : 0.6315
##
##        'Positive' Class : 0
##
```

```
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')
```

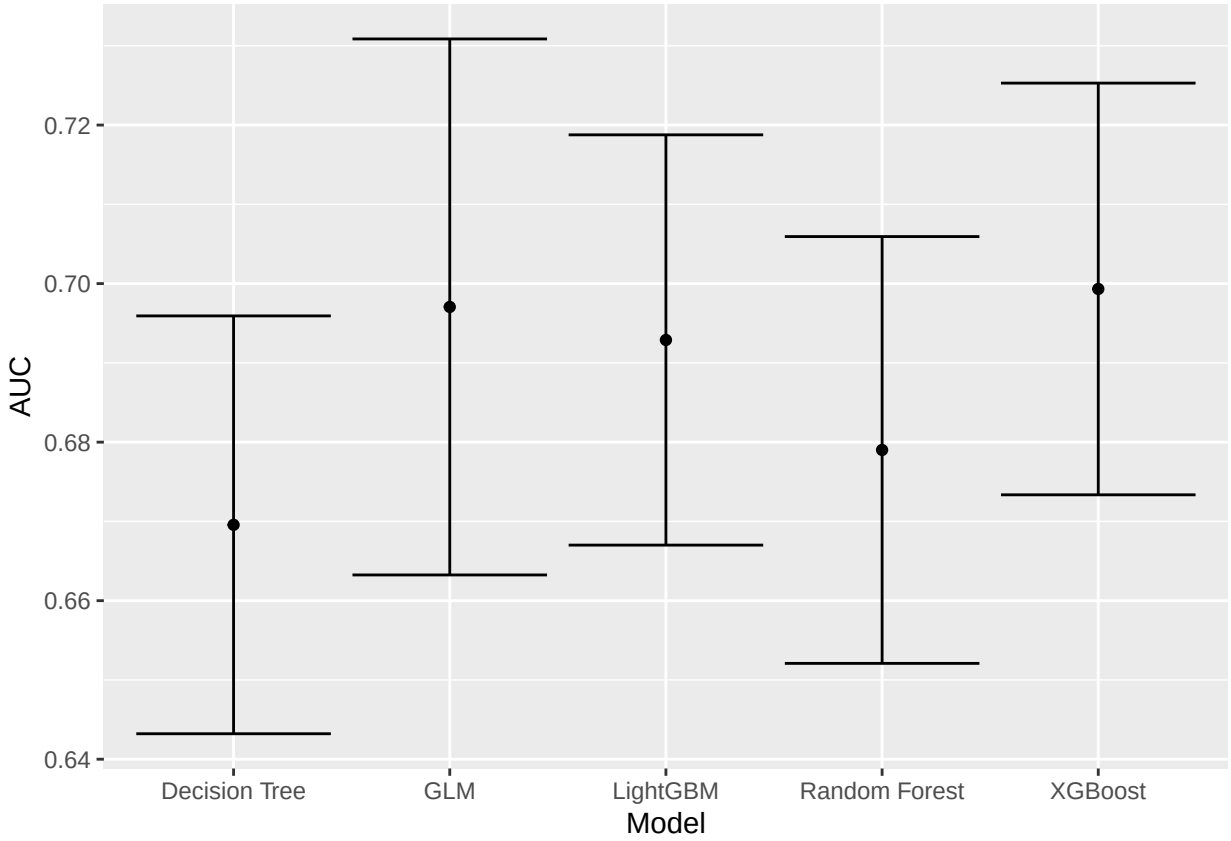



```
# extract_vip(final_rf_fit, pred_wrapper = predict,
#             reference_class = "1", use_matrix = FALSE,
#             method = 'permute')
```

Minutes to run: 70.045

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()
```




```
write_csv(df_auc, sprintf("./auxiliar/model_selection/performance/%s.csv", outcome_column))
```

Minutes to run: 0.002