Final Model - readmission_1year

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Imports

```
library(tidyverse)
library(yaml)
library(tidymodels)
library(usemodels)
library(vip)
library(kableExtra)

library(SHAPforxgboost)
library(xgboost)
library(Matrix)
library(mltools)
library(bonsai)
library(lightgbm)

select <- dplyr::select
```

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[columns_list$outcome_columns] <- lapply(df[columns_list$outcome_columns], factor)
df <- mutate(df, across(where(is.character), as.factor))
```

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

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

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

Eligible features

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

```
exception_columns <- c('death_intraop', 'death_intraop_1')

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
                        )

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

if (is.null(features_list)) {
  features = eligible_features
} else {
  features = base::intersect(eligible_features, features_list)
}
```

Starting features:

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

1. sex
2. age
3. race
4. education_level
5. patient_state
6. underlying_heart_disease
7. heart_disease
8. nyha_basal
9. prior_mi
10. heart_failure
11. af
12. cardiac_arrest
13. transplant
14. valvopathy
15. endocardites
16. diabetes
17. renal_failure
18. hemodialysis
19. copd
20. comorbidities_count
21. procedure_type_1
22. reop_type_1
23. procedure_type_new
24. cied_final_1
25. cied_final_group_1
26. admission_pre_t0_count
27. admission_pre_t0_180d
28. year_adm_t0
29. icu_t0
30. dialysis_t0
31. admission_t0_emergency
32. aco
33. antiarritmico
34. betabloqueador
35. ieca_bra
36. dva
37. digoxina

38. estatina
39. diuretico
40. vasodilatador
41. insuf_cardiaca
42. espironolactona
43. bloq_calcio
44. antiplaquetario_ev
45. insulina
46. anticonvulsivante
47. psicofarmacos
48. antifungico
49. antiviral
50. antiretroviral
51. classe_meds_qtde
52. meds_cardiovasc_qtde
53. meds_antimicrobianos
54. cec
55. transplante_cardiaco
56. cir_toracica
57. outros_proced_cirurgicos
58. icp
59. intervencao_cv
60. angioplastia
61. cateterismo
62. eletrofisiologia
63. cateter_venoso_central
64. proced_invasivos_qtde
65. cve_desf
66. transfusao
67. interconsulta
68. equipe_multiprof
69. ecg
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. aortografia
84. arteriografia
85. cintilografia
86. ecocardiograma
87. endoscopia
88. flebografia
89. pet_ct
90. ultrassom
91. tomografia
92. radiografia
93. ressonancia
94. exames_imagem_qtde
95. bic
96. mpp

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) %>% select(all_of(c(features, outcome_column)))
df_test <- testing(df_split) %>% select(all_of(c(features, outcome_column)))
```

Global parameters

```
k <- 5 # Number of folds for cross validation
grid_size <- 50 # Number of parameter combination to tune on each model

set.seed(234)
df_folds <- vfold_cv(df_train, v = k,
                     strata = all_of(outcome_column))

max_auc_loss <- 0.01
```

Functions

```
niceFormatting <- function(df, caption="", digits = 2, font_size = NULL){
  df %>%
    kbl(booktabs = T, longtable = T, caption = caption,
        digits = digits, format = "latex") %>%
    kable_styling(font_size = font_size,
                  latex_options = c("striped", "HOLD_position", "repeat_header"))
}
```

```
validation = function(model_fit, new_data, plot=TRUE) {
  library(pROC)
  library(caret)

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

  pROC_obj <- roc(
    new_data[[outcome_column]],
    test_predictions_prob,
    direction = "<",
    levels = c(0, 1),
    smoothed = TRUE,
    ci = TRUE,
    ci.alpha = 0.9,
    stratified = FALSE,
    plot = plot,
    auc.polygon = TRUE,
    max.auc.polygon = TRUE,
    grid = TRUE,
    print.auc = TRUE,
    show.thres = TRUE
  )
```

```
  test_predictions_class <-
    predict(model_fit, new_data = new_data, type = "class") %>%
    rename_at(vars(starts_with(".pred_")), ~ str_remove(., ".pred_")) %>%
    .$class

  conf_matrix <- table(test_predictions_class, new_data[[outcome_column]])

  if (plot) {
    sens.ci <- ci.se(pROC_obj)
    plot(sens.ci, type = "shape", col = "lightblue")
    plot(sens.ci, type = "bars")

    confusionMatrix(conf_matrix) %>% print
  }

  return(pROC_obj)
}
```

Feature Selection

```
model_fit_wf <- function(df_train, features, outcome_column, hyperparameters){
  model_recipe <-
    recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula,
           data = df_train %>% select(all_of(c(features, outcome_column)))) %>%
    step_novel(all_nominal_predictors()) %>%
    step_unknown(all_nominal_predictors()) %>%
    step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
    step_impute_mean(all_numeric_predictors()) %>%
    step_zv(all_predictors())

  model_spec <-
    do.call(boost_tree, hyperparameters) %>%
    set_engine("lightgbm") %>%
    set_mode("classification")

  model_workflow <-
    workflow() %>%
    add_recipe(model_recipe) %>%
    add_model(model_spec)

  model_fit_rs <- model_workflow %>%
    fit_resamples(df_folds)

  model_fit <- model_workflow %>%
    fit(df_train)

  model_auc <- validation(model_fit, df_test, plot = F)

  raw_model <- parsnip::extract_fit_engine(model_fit)

  feature_importance <- lgb.importance(raw_model, percentage = TRUE)

  return(
    list(
      cv_auc = collect_metrics(model_fit_rs) %>% filter(.metric == 'roc_auc') %>% .$mean,
      importance = feature_importance,
      auc = as.numeric(model_auc$auc),
      auc_lower = model_auc$ci[1],
      auc_upper = model_auc$ci[3]
```

```
    )
  )
}
```

```
hyperparameters <- readRDS(
  sprintf(
    "./auxiliar/model_selection/hyperparameters/lightgbm_%s.rds",
    outcome_column
  )
)

full_model <- model_fit_wf(df_train, features, outcome_column, hyperparameters)

sprintf('Full Model CV Train AUC: %.3f' ,full_model$cv_auc)
```

```
## [1] "Full Model CV Train AUC: 0.716"
```

```
sprintf('Full Model Test AUC: %.3f' ,full_model$auc)
```

```
## [1] "Full Model Test AUC: 0.712"
```

Features with zero importance on the initial model:

```
unimportant_features <- setdiff(features, full_model$importance$Feature)

unimportant_features %>%
  gluedown::md_order()
```

1. antiretroviral
2. transplante_cardiaco
3. cir_toracica
4. angioplastia
5. tilt_teste
6. angio_rm
7. aortografia
8. pet_ct

```
trimmed_features <- full_model$importance$Feature
hyperparameters$mtry <- min(hyperparameters$mtry, length(trimmed_features))
trimmed_model <- model_fit_wf(df_train, trimmed_features,
                              outcome_column, hyperparameters)

sprintf('Trimmed Model CV Train AUC: %.3f' ,trimmed_model$cv_auc)
```

```
## [1] "Trimmed Model CV Train AUC: 0.716"
```

```
sprintf('Trimmed Model Test AUC: %.3f' ,trimmed_model$auc)
```

```
## [1] "Trimmed Model Test AUC: 0.712"
```

```
selection_results <- tibble::tribble(
  ~`Number of Features`, ~`AUC Loss`, ~`Least Important Feature`,
  length(features), 0, tail(full_model$importance$Feature, 1)
)

if (full_model$cv_auc - trimmed_model$cv_auc < max_auc_loss) {
  current_features <- trimmed_features
  current_model <- trimmed_model
  current_least_important <- tail(current_model$importance$Feature, 1)
  current_auc_loss <- full_model$cv_auc - current_model$cv_auc

  selection_results <- selection_results %>%
    add_row(`Number of Features` = length(trimmed_features),
            `AUC Loss` = current_auc_loss,
            `Least Important Feature` = current_least_important)
```

```
} else {
  current_features <- features
  current_model <- full_model
  current_least_important <- tail(current_model$importance$Feature, 1)
  current_auc_loss <- 0
}

while (current_auc_loss < max_auc_loss) {
  last_feature_droped <- current_least_important

  current_features <- setdiff(current_features, current_least_important)
  hyperparameters$mtry = min(hyperparameters$mtry, length(current_features))
  current_model <- model_fit_wf(df_train, current_features, outcome_column, hyperparameters)
  current_least_important <- tail(current_model$importance$Feature, 1)

  current_auc_loss <- full_model$cv_auc - current_model$cv_auc

  selection_results <- selection_results %>%
    add_row(`Number of Features` = length(current_features),
            `AUC Loss` = current_auc_loss,
            `Least Important Feature` = current_least_important)

  # print(c(length(current_features), current_auc_loss))
}

selection_results %>% niceFormatting(digits = 4)
```

Table 1:

Number of Features	AUC Loss	Least Important Feature
96	0.0000	transfusao
88	0.0000	antiviral
87	0.0016	cec
86	0.0019	intervencao_cv
85	0.0024	citologia
84	0.0022	transfusao
83	0.0020	dialysis_t0
82	-0.0008	mpp
81	-0.0019	teste_esforco
80	-0.0030	transplant
79	0.0016	cve_desf
78	0.0031	heart_disease
77	0.0013	renal_failure
76	0.0007	angio_tc
75	0.0026	antiplaquetario_ev
74	0.0035	copd
73	-0.0007	espiro_ergoespiro
72	0.0014	arteriografia
71	0.0042	eletrofisiologia
70	0.0005	af
69	0.0006	hemodialysis
68	0.0029	icp
67	0.0004	antifungico
66	0.0027	anticonvulsivante
65	0.0024	biopsia
64	-0.0002	cardiac_arrest
63	0.0007	tomografia
62	-0.0009	holter

Table 1: *(continued)*

Number of Features	AUC Loss	Least Important Feature
61	-0.0006	procedure_type_1
60	0.0037	outros_proced_cirurgicos
59	0.0040	cateter_venoso_central
58	0.0017	flebografia
57	-0.0004	cateterismo
56	-0.0008	ressonancia
55	0.0026	diabetes
54	0.0027	aco
53	0.0037	valvopathy
52	0.0030	cultura
51	0.0015	endoscopia
50	0.0027	cintilografia
49	0.0024	heart_failure
48	0.0044	bic
47	0.0015	prior_mi
46	0.0014	cied_final_group_1
45	0.0042	endocardites
44	0.0028	procedure_type_new
43	0.0029	insulina
42	0.0070	sex
41	0.0027	interconsulta
40	0.0029	ecocardiograma
39	0.0041	analises_clinicas_qtde
38	0.0039	histopatologia_qtde
37	0.0039	proced_invasivos_qtde
36	0.0038	race
35	0.0062	ultrassom
34	0.0061	underlying_heart_disease
33	0.0071	betabloqueador
32	0.0059	ecg
31	0.0057	education_level
30	0.0032	bloq_calcio
29	0.0039	dva
28	0.0039	nyha_basal
27	0.0067	digoxina
26	0.0060	patient_state
25	0.0078	admission_t0_emergency
24	0.0073	radiografia
23	0.0087	insuf_cardiaca
22	0.0066	admission_pre_t0_180d
21	0.0084	psicofarmacos
20	0.0066	comorbidities_count
19	0.0067	exames_imagem_qtde
18	0.0071	espironolactona
17	0.0085	cied_final_1
16	0.0120	equipe_multiprof

```r
if (exists('last_feature_dropped')) {
  selected_features <- c(current_features, last_feature_droped)
} else {
  selected_features <- current_features
}
```

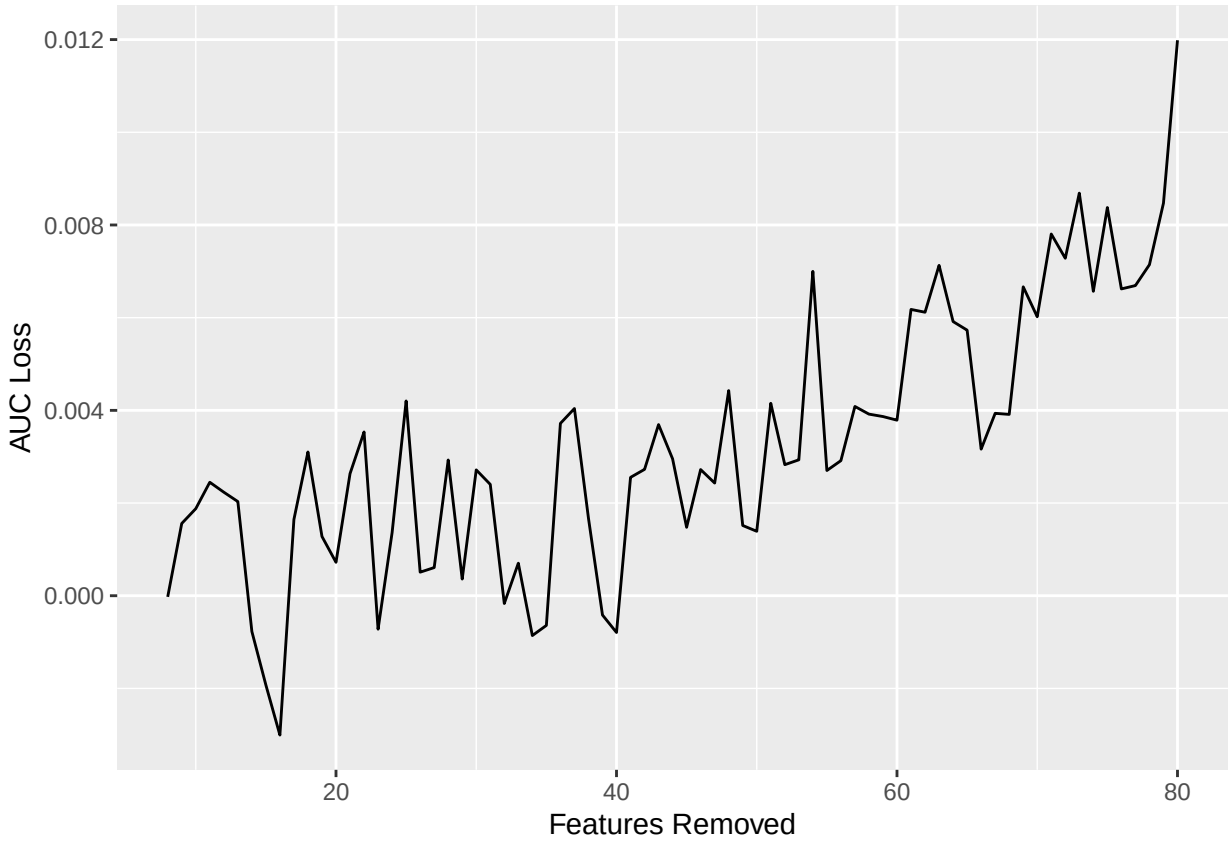
```
con <- file(sprintf('./auxiliar/final_model/selected_features/%s.yaml', outcome_column), "w")
write_yaml(selected_features, con)
close(con)

feature_selected_model <- model_fit_wf(df_train, selected_features,
                                       outcome_column, hyperparameters)

sprintf('Trimmed Model CV Train AUC: %.3f', feature_selected_model$cv_auc)
```

```
## [1] "Trimmed Model CV Train AUC: 0.704"
```

```
sprintf('Trimmed Model Test AUC: %.3f', feature_selected_model$auc)
```

```
## [1] "Trimmed Model Test AUC: 0.693"
```

```
selection_results %>%
  filter(`Number of Features` < length(features)) %>%
  mutate(`Features Removed` = length(features) - `Number of Features`) %>%
  ggplot(aes(x = `Features Removed`, y = `AUC Loss`)) +
  geom_line()
```



Hyperparameter tuning

Selected features:

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

1. admission_pre_t0_count
2. age
3. meds_cardiovasc_qtde
4. icu_t0
5. year_adm_t0
6. classe_meds_qtde
7. metodos_graficos_qtde

8. laboratorio
9. diuretico
10. antiarritmico
11. meds_antimicrobianos
12. vasodilatador
13. estatina
14. reop_type_1
15. ieca_bra
16. equipe_multiprof

```
# doParallel::registerDoParallel(8)
```

Smote

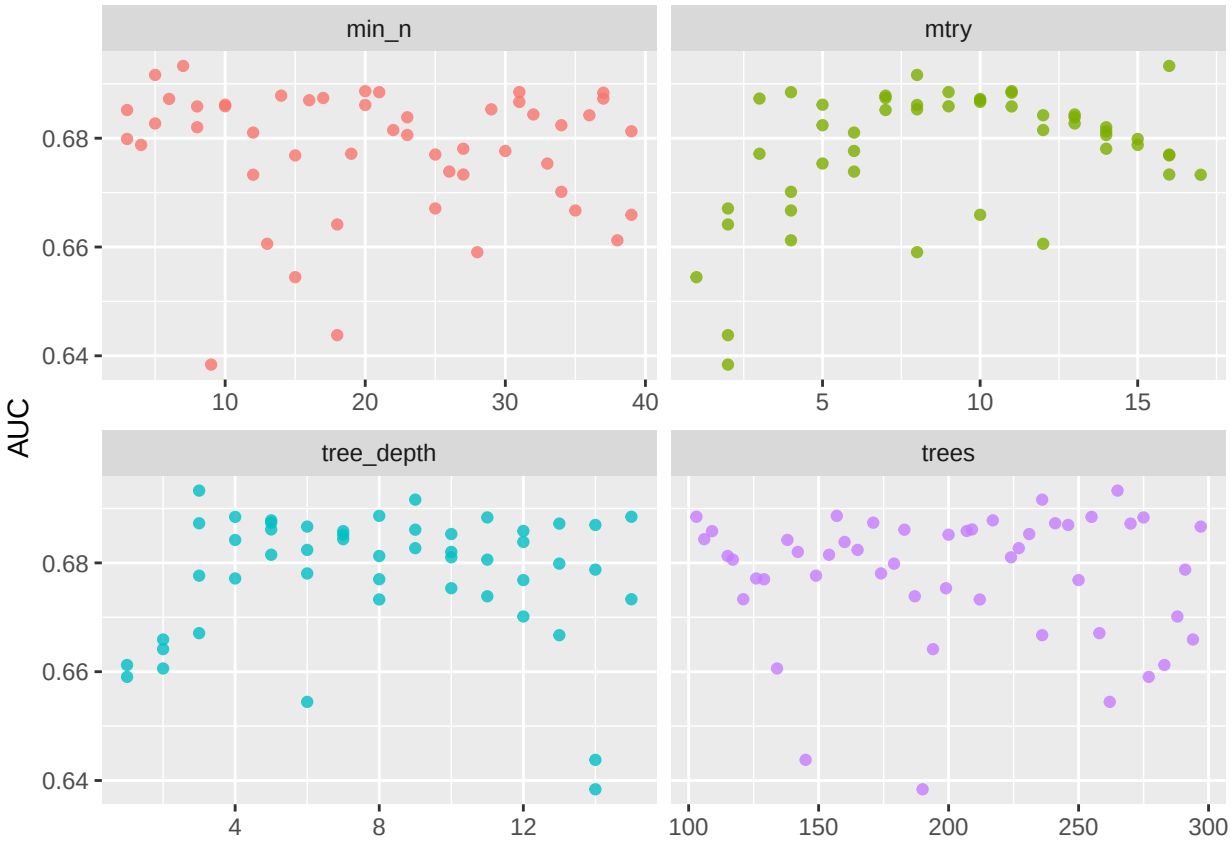
```
library(themis)

lightgbm_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula,
         data = df_train %>% select(all_of(c(selected_features, outcome_column)))) %>%
  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(), one_hot = TRUE) %>%
  step_impute_mean(all_numeric_predictors()) %>%
  step_zv(all_predictors()) %>%
  step_smote(!!sym(outcome_column))

lightgbm_spec <- boost_tree(
  mtry = tune(),
  trees = tune(),
  min_n = tune(),
  tree_depth = tune(),
  learn_rate = tune(),
  loss_reduction = tune()
) %>%
  set_engine("lightgbm") %>%
  set_mode("classification")

lightgbm_grid <- grid_latin_hypercube(
  finalize(mtry(),
           df_train %>% dplyr::select(all_of(c(selected_features, outcome_column)))),
  dials::trees(range = c(100L, 300L)),
  min_n(),
  tree_depth(),
  learn_rate(),
  loss_reduction(),
  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") %>%
```

```
  niceFormatting(digits = 5)
```

Table 2:

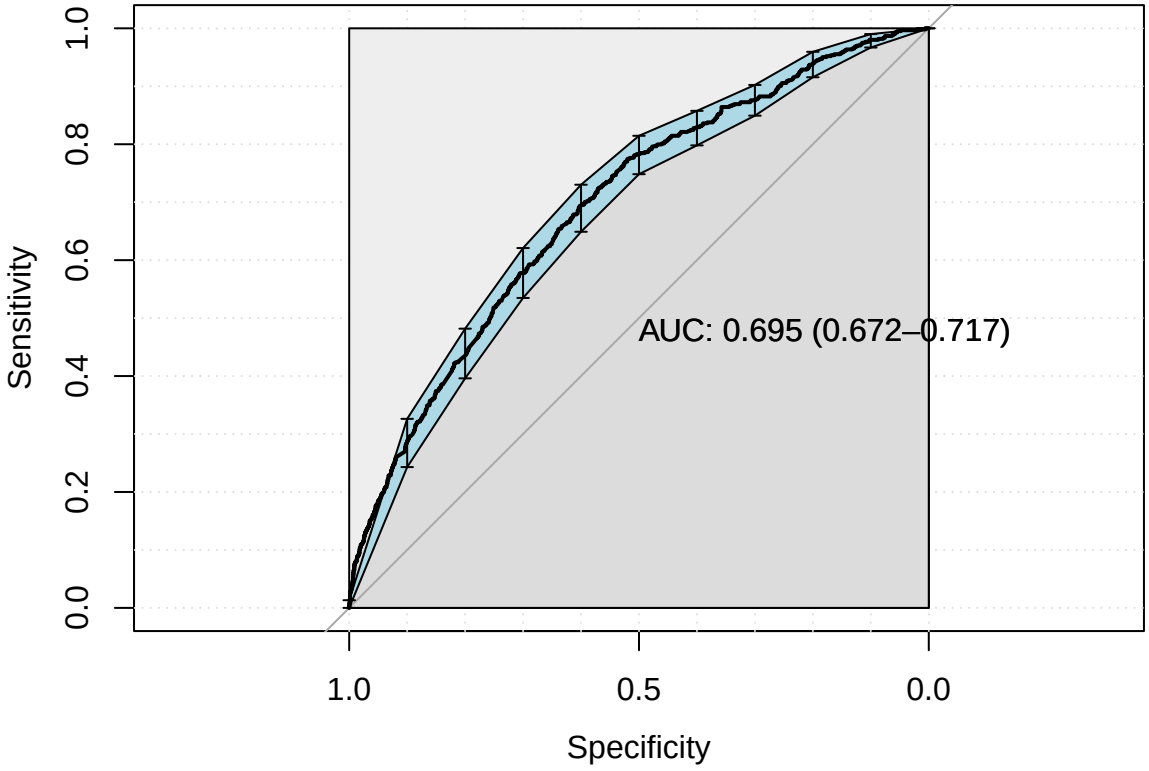
mtry	trees	min_n	tree_depth	learn_rate	loss_reduction	.metric	.estimator	mean	n	std_err	.config
16	265	7	3	0.04205	0.00004	roc_auc	binary	0.69329	5	0.00696	Preprocessor1_
8	236	5	9	0.04614	0.00795	roc_auc	binary	0.69163	5	0.00485	Preprocessor1_
11	157	20	8	0.00421	0.00000	roc_auc	binary	0.68865	5	0.00661	Preprocessor1_
9	103	31	15	0.00000	0.00001	roc_auc	binary	0.68849	5	0.00508	Preprocessor1_
4	255	21	4	0.01551	0.03460	roc_auc	binary	0.68846	5	0.00657	Preprocessor1_

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

lightgbm_tune %>%
  collect_metrics() %>%
  filter(.metric == "roc_auc") %>%
  select(mean, mtry:tree_depth) %>%
  pivot_longer(mtry:tree_depth,
               values_to = "value",
               names_to = "parameter"
  ) %>%
  ggplot(aes(value, mean, color = parameter)) +
  geom_point(alpha = 0.8, show.legend = FALSE) +
  facet_wrap(~parameter, scales = "free_x") +
  labs(x = NULL, y = "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_smote_auc <- validation(final_lightgbm_fit, df_test)
```




```
## Confusion Matrix and Statistics
##
##
## test_predictions_class    0    1
##                      0 3870  479
##                      1  257  125
##
##                Accuracy : 0.8444
##                  95% CI : (0.8338, 0.8546)
##     No Information Rate : 0.8723
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1716
##
##  Mcnemar's Test P-Value : 3.756e-16
##
##             Sensitivity : 0.9377
##             Specificity : 0.2070
##          Pos Pred Value : 0.8899
##          Neg Pred Value : 0.3272
##              Prevalence : 0.8723
##          Detection Rate : 0.8180
##    Detection Prevalence : 0.9193
##       Balanced Accuracy : 0.5723
##
##        'Positive' Class : 0
```

```
##
lightgbm_parameters <- lightgbm_tune %>%
  show_best("roc_auc", n = 1) %>%
  select(trees, mtry, min_n, tree_depth, learn_rate, loss_reduction) %>%
  as.list

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

Upsample

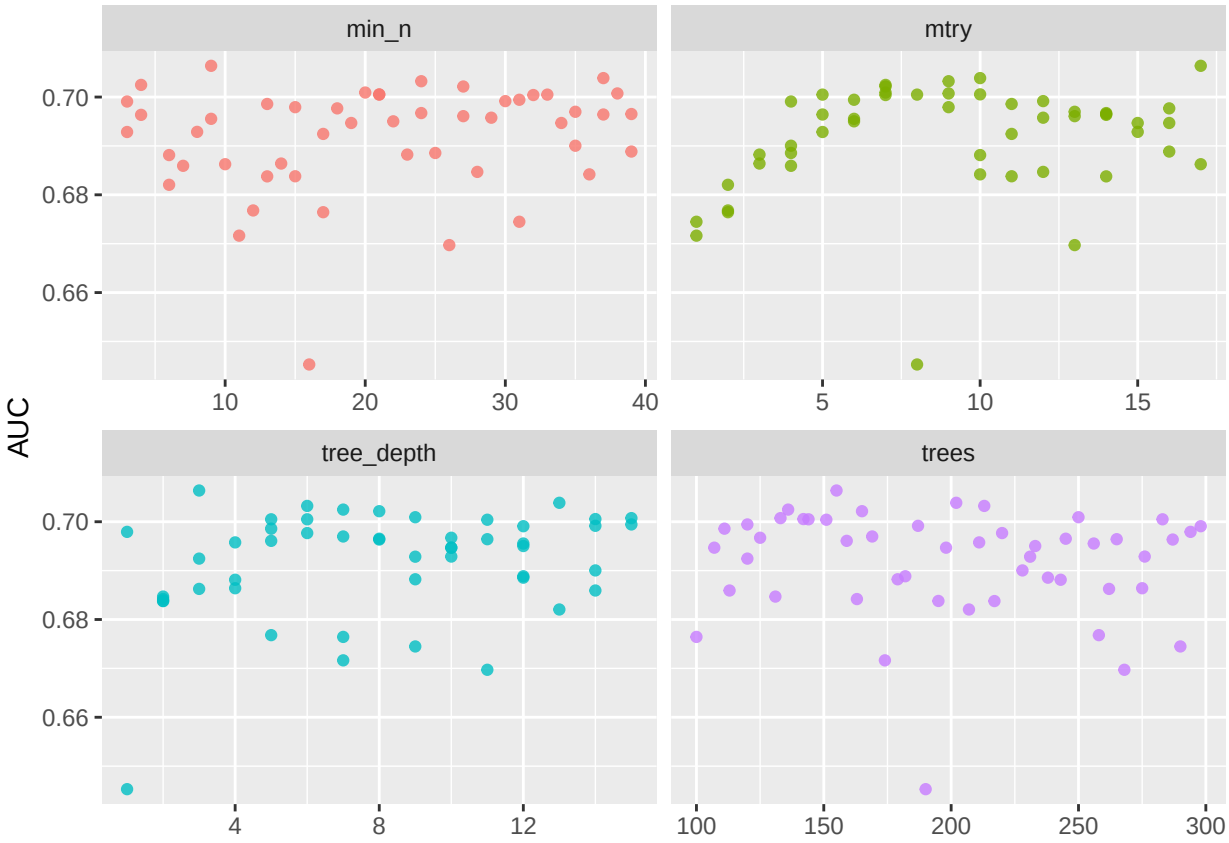
```
lightgbm_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula,
         data = df_train %>% select(all_of(c(selected_features, outcome_column)))) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(), threshold = 0.05, other = ".merged") %>%
  step_dummy(all_nominal_predictors(), one_hot = TRUE) %>%
  step_impute_mean(all_numeric_predictors()) %>%
  step_zv(all_predictors()) %>%
  step_upsample(!!sym(outcome_column))

lightgbm_spec <- boost_tree(
  mtry = tune(),
  trees = tune(),
  min_n = tune(),
  tree_depth = tune(),
  learn_rate = tune(),
  loss_reduction = tune()
) %>%
  set_engine("lightgbm") %>%
  set_mode("classification")

lightgbm_grid <- grid_latin_hypercube(
  finalize(mtry(),
           df_train %>% dplyr::select(all_of(c(selected_features, outcome_column)))),
  dials::trees(range = c(100L, 300L)),
  min_n(),
  tree_depth(),
  learn_rate(),
  loss_reduction(),
  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") %>%
  niceFormatting(digits = 5)
```

Table 3:

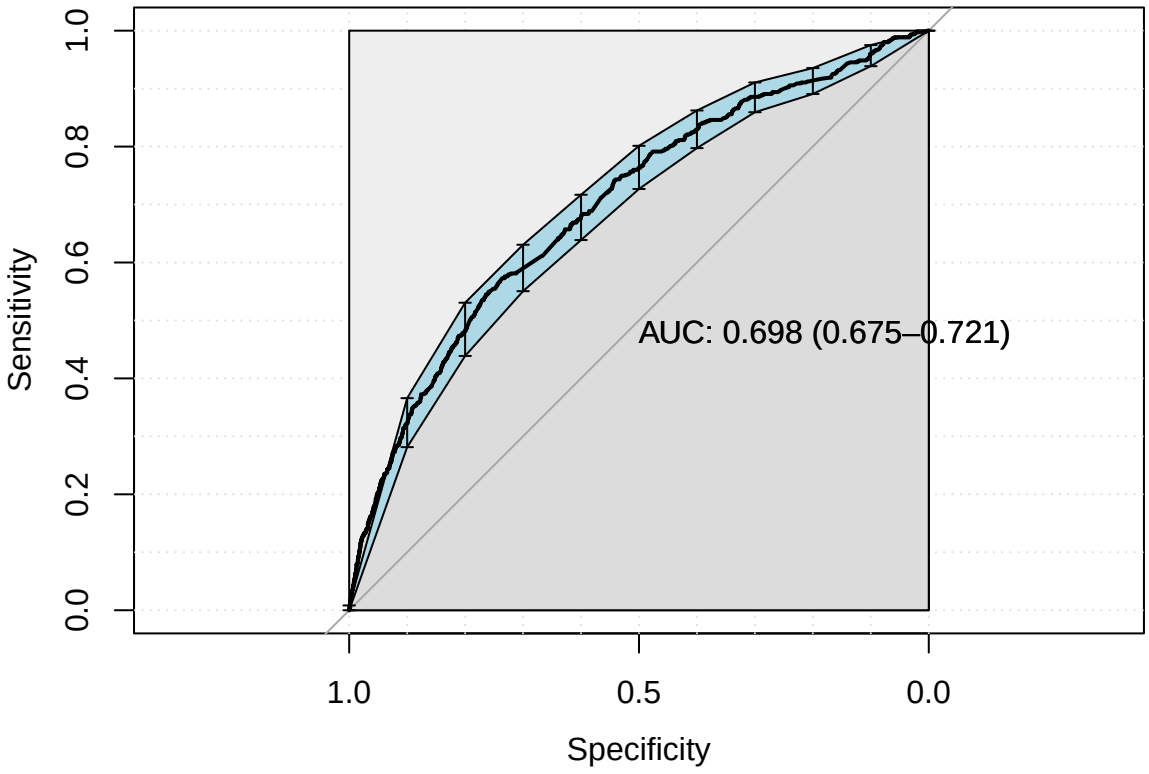
mtry	trees	min_n	tree_depth	learn_rate	loss_reduction	.metric	.estimator	mean	n	std_err	.config
17	155	9	3	0.02081	0.00000	roc_auc	binary	0.70639	5	0.00637	Preprocessor1_
10	202	37	13	0.00095	0.00000	roc_auc	binary	0.70388	5	0.00538	Preprocessor1_
9	213	24	6	0.00000	0.00011	roc_auc	binary	0.70324	5	0.00525	Preprocessor1_
7	136	4	7	0.00000	0.00094	roc_auc	binary	0.70248	5	0.00468	Preprocessor1_
7	165	27	8	0.00000	0.00376	roc_auc	binary	0.70216	5	0.00466	Preprocessor1_

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

lightgbm_tune %>%
  collect_metrics() %>%
  filter(.metric == "roc_auc") %>%
  select(mean, mtry:tree_depth) %>%
  pivot_longer(mtry:tree_depth,
               values_to = "value",
               names_to = "parameter"
  ) %>%
  ggplot(aes(value, mean, color = parameter)) +
  geom_point(alpha = 0.8, show.legend = FALSE) +
  facet_wrap(~parameter, scales = "free_x") +
  labs(x = NULL, y = "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_upsample_auc <- validation(final_lightgbm_fit, df_test)
```




```
## Confusion Matrix and Statistics
##
##
## test_predictions_class    0    1
##                      0 3138  274
##                      1  989  330
##
##                Accuracy : 0.733
##                  95% CI : (0.7202, 0.7456)
##     No Information Rate : 0.8723
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2038
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.7604
##             Specificity : 0.5464
##          Pos Pred Value : 0.9197
##          Neg Pred Value : 0.2502
##              Prevalence : 0.8723
##          Detection Rate : 0.6633
##    Detection Prevalence : 0.7212
##       Balanced Accuracy : 0.6534
##
```

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

```
lightgbm_parameters <- lightgbm_tune %>%
  show_best("roc_auc", n = 1) %>%
  select(trees, mtry, min_n, tree_depth, learn_rate, loss_reduction) %>%
  as.list

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

Standard

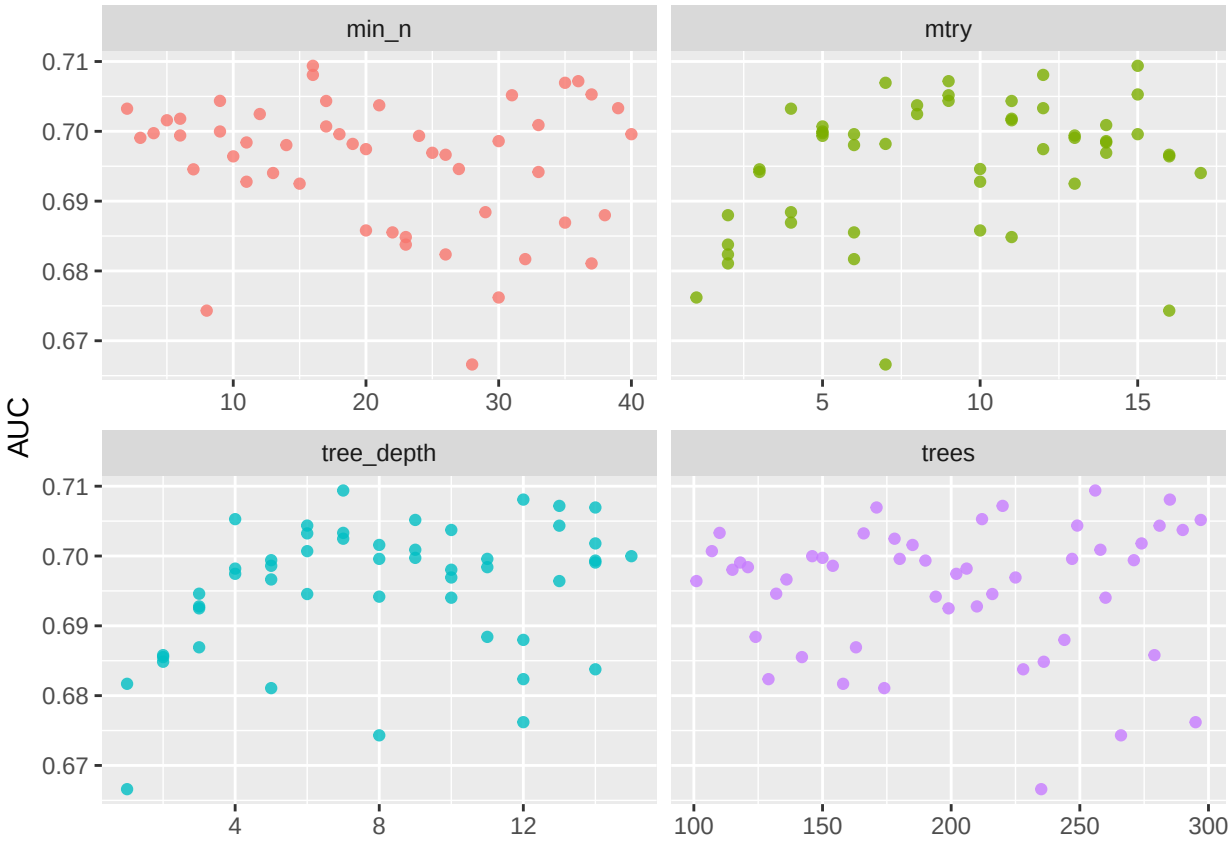
```
lightgbm_recipe <-
  recipe(formula = sprintf("%s ~ .", outcome_column) %>% as.formula,
         data = df_train %>% select(all_of(c(selected_features, outcome_column)))) %>%
  step_novel(all_nominal_predictors()) %>%
  step_unknown(all_nominal_predictors()) %>%
  step_other(all_nominal_predictors(),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

lightgbm_spec <- boost_tree(
  mtry = tune(),
  trees = tune(),
  min_n = tune(),
  tree_depth = tune(),
  learn_rate = tune(),
  loss_reduction = tune()
) %>%
  set_engine("lightgbm") %>%
  set_mode("classification")

lightgbm_grid <- grid_latin_hypercube(
  finalize(mtry(),
           df_train %>% dplyr::select(all_of(c(selected_features, outcome_column)))),
  dials::trees(range = c(100L, 300L)),
  min_n(),
  tree_depth(),
  learn_rate(),
  loss_reduction(),
  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") %>%
  niceFormatting(digits = 5)
```

Table 4:

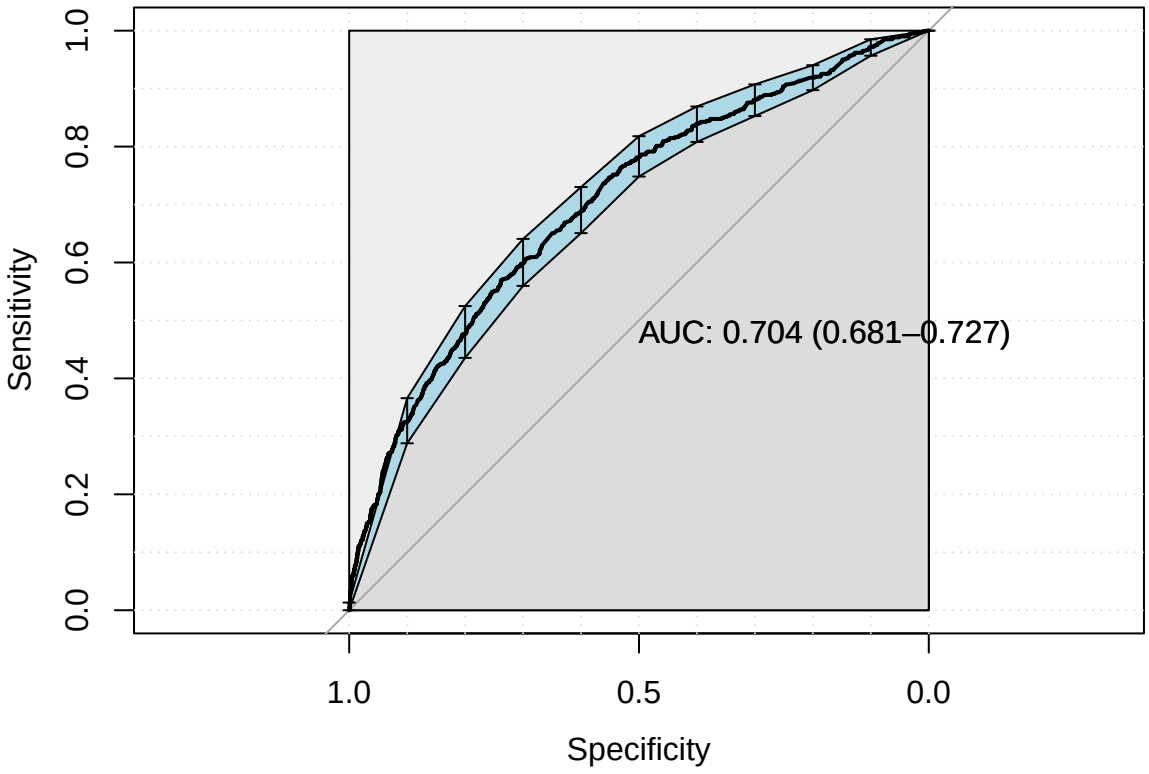
mtry	trees	min_n	tree_depth	learn_rate	loss_reduction	.metric	.estimator	mean	n	std_err	.config
15	256	16	7	0.02070	3.56344	roc_auc	binary	0.70938	5	0.00587	Preprocessor1_
12	285	16	12	0.01239	0.00000	roc_auc	binary	0.70808	5	0.00623	Preprocessor1_
9	220	36	13	0.00208	0.00000	roc_auc	binary	0.70718	5	0.00454	Preprocessor1_
7	171	35	14	0.00423	0.00000	roc_auc	binary	0.70695	5	0.00396	Preprocessor1_
15	212	37	4	0.05221	0.00000	roc_auc	binary	0.70528	5	0.00769	Preprocessor1_

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

lightgbm_tune %>%
  collect_metrics() %>%
  filter(.metric == "roc_auc") %>%
  select(mean, mtry:tree_depth) %>%
  pivot_longer(mtry:tree_depth,
               values_to = "value",
               names_to = "parameter"
  ) %>%
  ggplot(aes(value, mean, color = parameter)) +
  geom_point(alpha = 0.8, show.legend = FALSE) +
  facet_wrap(~parameter, scales = "free_x") +
  labs(x = NULL, y = "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)
```



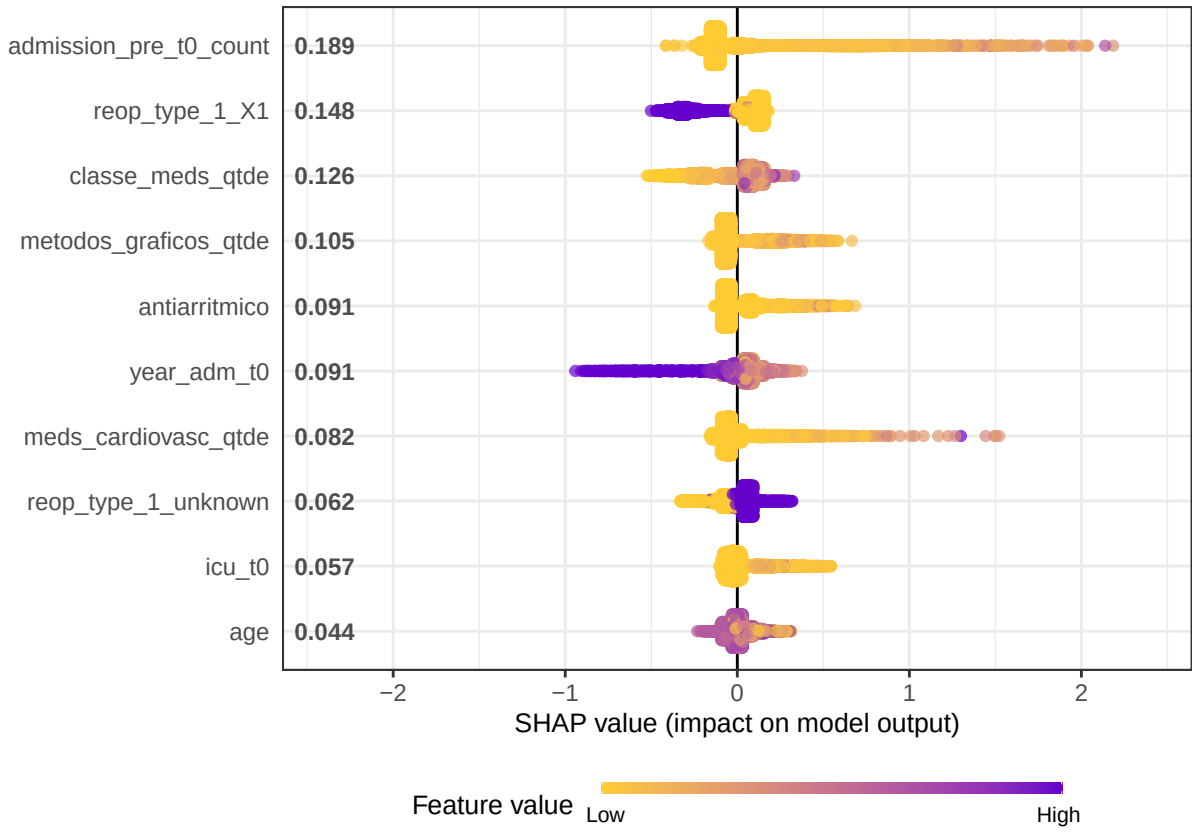

```
## Confusion Matrix and Statistics
##
##
## test_predictions_class    0    1
##                      0 4108  577
##                      1   19   27
##
##                Accuracy : 0.874
##                  95% CI : (0.8642, 0.8834)
##     No Information Rate : 0.8723
##     P-Value [Acc > NIR] : 0.3738
##
##                   Kappa : 0.0662
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.9954
##             Specificity : 0.0447
##          Pos Pred Value : 0.8768
##          Neg Pred Value : 0.5870
##              Prevalence : 0.8723
##          Detection Rate : 0.8683
##    Detection Prevalence : 0.9903
##       Balanced Accuracy : 0.5200
##
```

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

```
lightgbm_parameters <- lightgbm_tune %>%
  show_best("roc_auc", n = 1) %>%
  select(trees, mtry, min_n, tree_depth, learn_rate, loss_reduction) %>%
  as.list

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

SHAP values

```
lightgbm_model <- parsnip::extract_fit_engine(final_lightgbm_fit)

trained_rec <- prep(lightgbm_recipe, training = df_train)

df_train_baked <- bake(trained_rec, new_data = df_train)
df_test_baked <- bake(trained_rec, new_data = df_test)

matrix_train <- as.matrix(df_train_baked %>% select(-all_of(outcome_column)))
matrix_test <- as.matrix(df_test_baked %>% select(-all_of(outcome_column)))

shap.plot.summary.wrap1(model = lightgbm_model, X = matrix_train, top_n = 10, dilute = F)
```




```
# Crunch SHAP values
shap <- shap.prep(lightgbm_model, X_train = matrix_test)
```

```r
for (x in shap.importance(shap, names_only = TRUE)[1:5]) {
  p <- shap.plot.dependence(
    shap,
    x = x,
    color_feature = "auto",
    smooth = TRUE,
    jitter_width = 0.01,
    alpha = 0.3
  ) +
    labs(title = x)
  print(p)
}
```

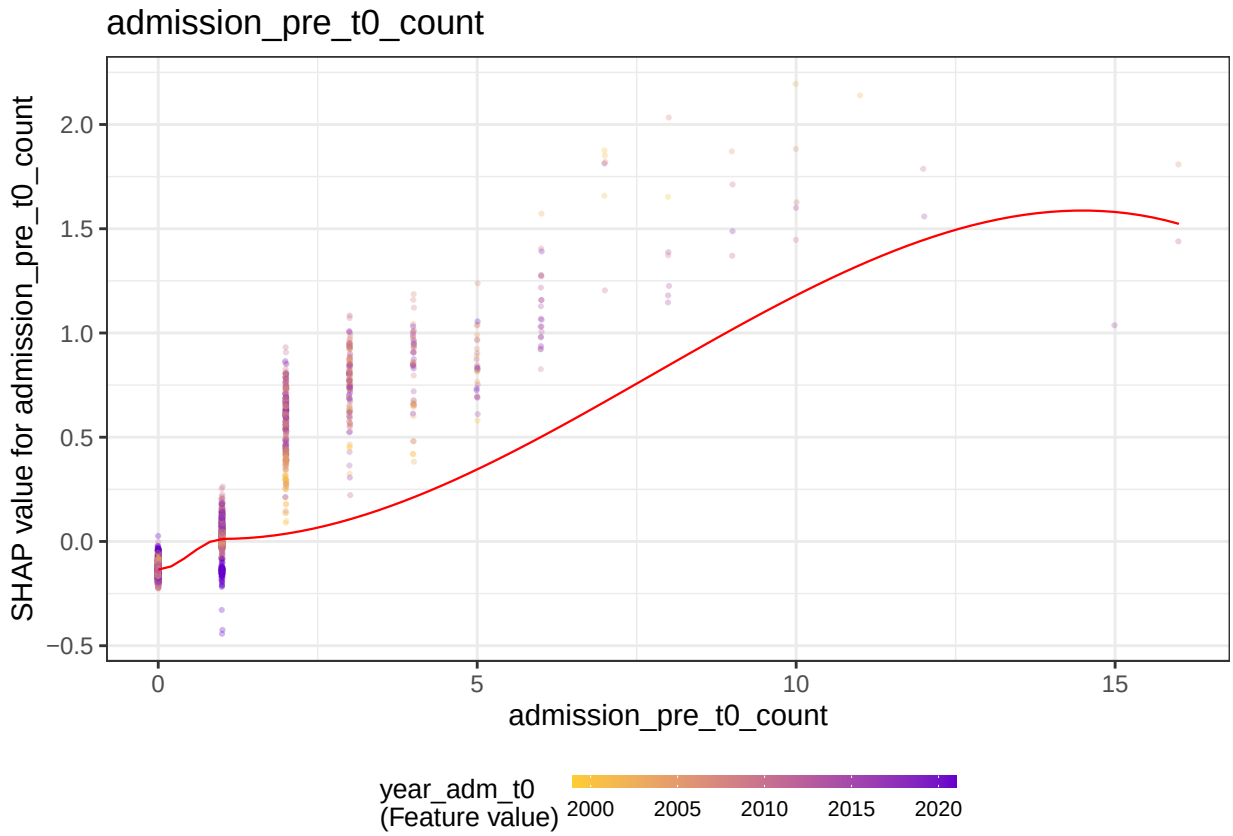
```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : pseudoinverse
## used at -0.08
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : neighborhood
## radius 1.08
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : reciprocal
## condition number 4.7124e-29
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : There are
## other near singularities as well. 1
```



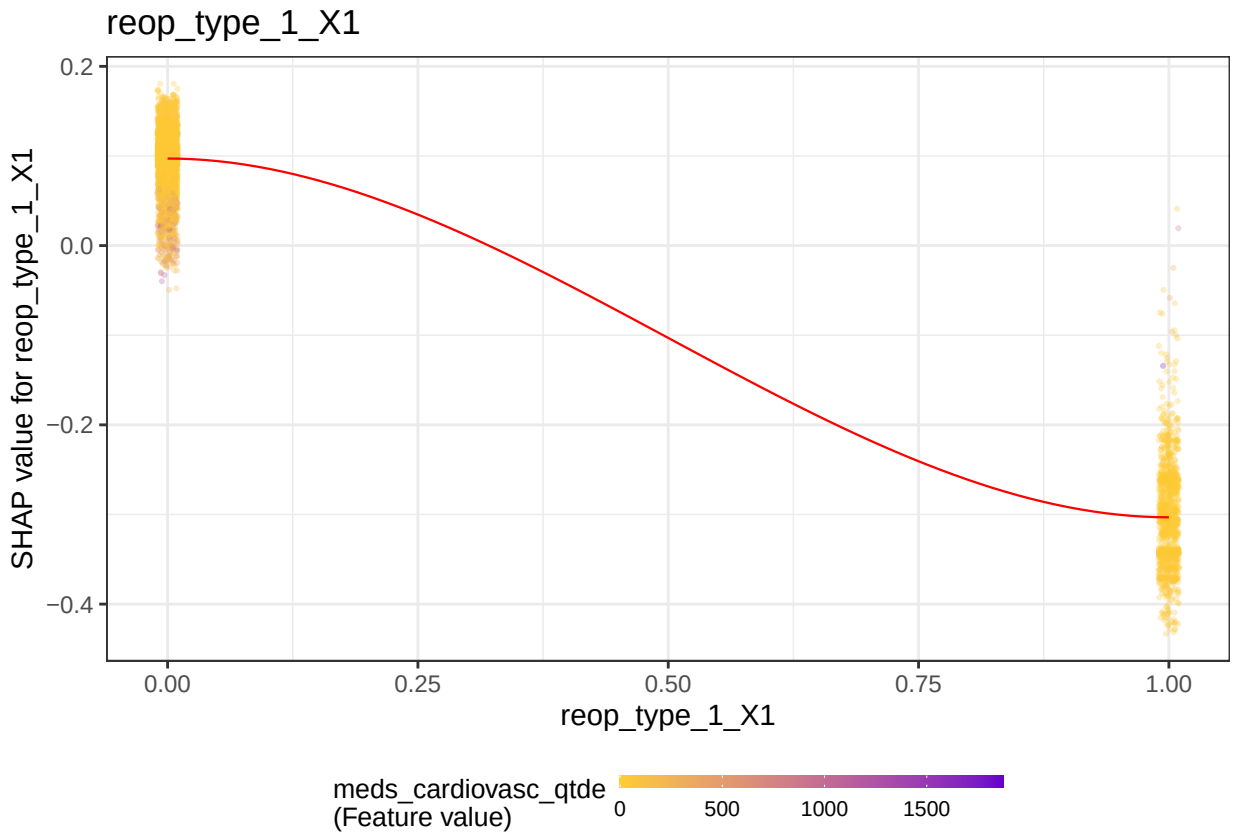

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : pseudoinverse
## used at -0.005
```

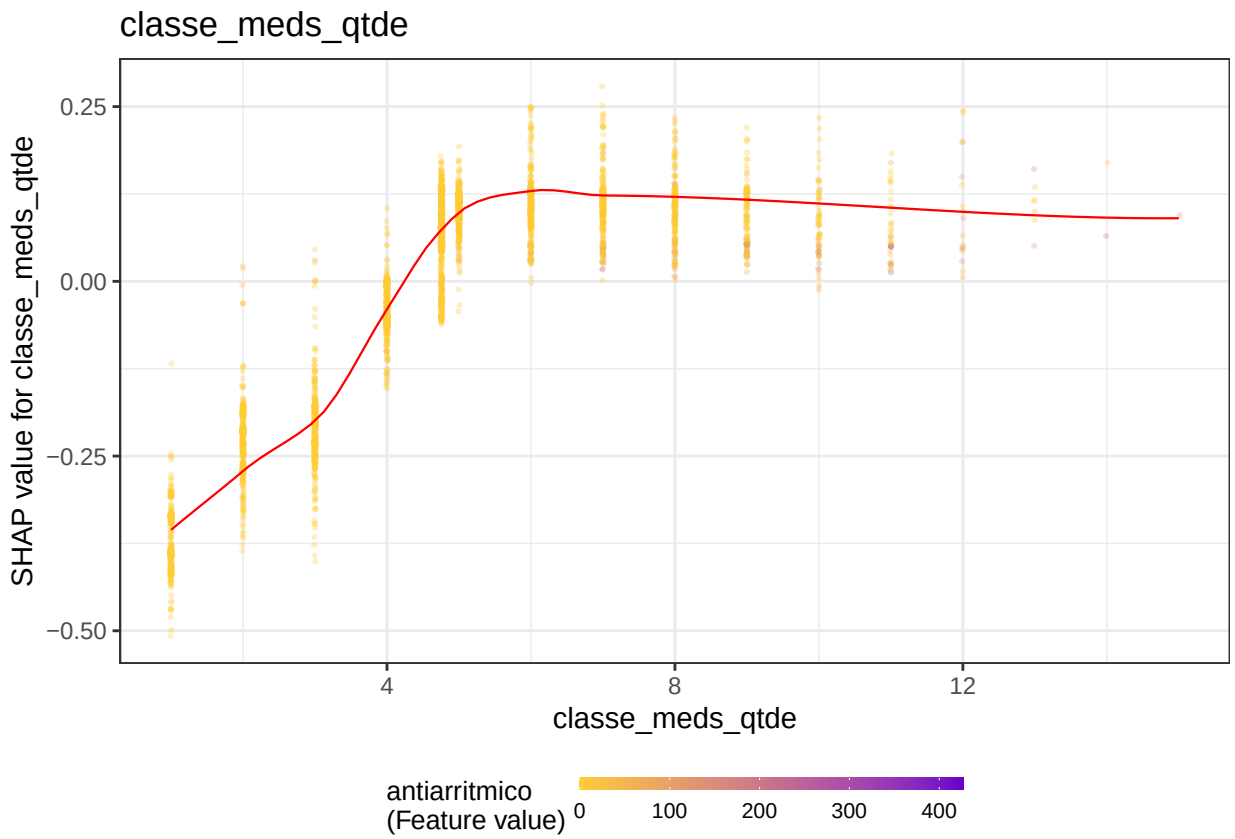
```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : neighborhood
## radius 1.005
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : reciprocal
## condition number 1.1644e-28
```

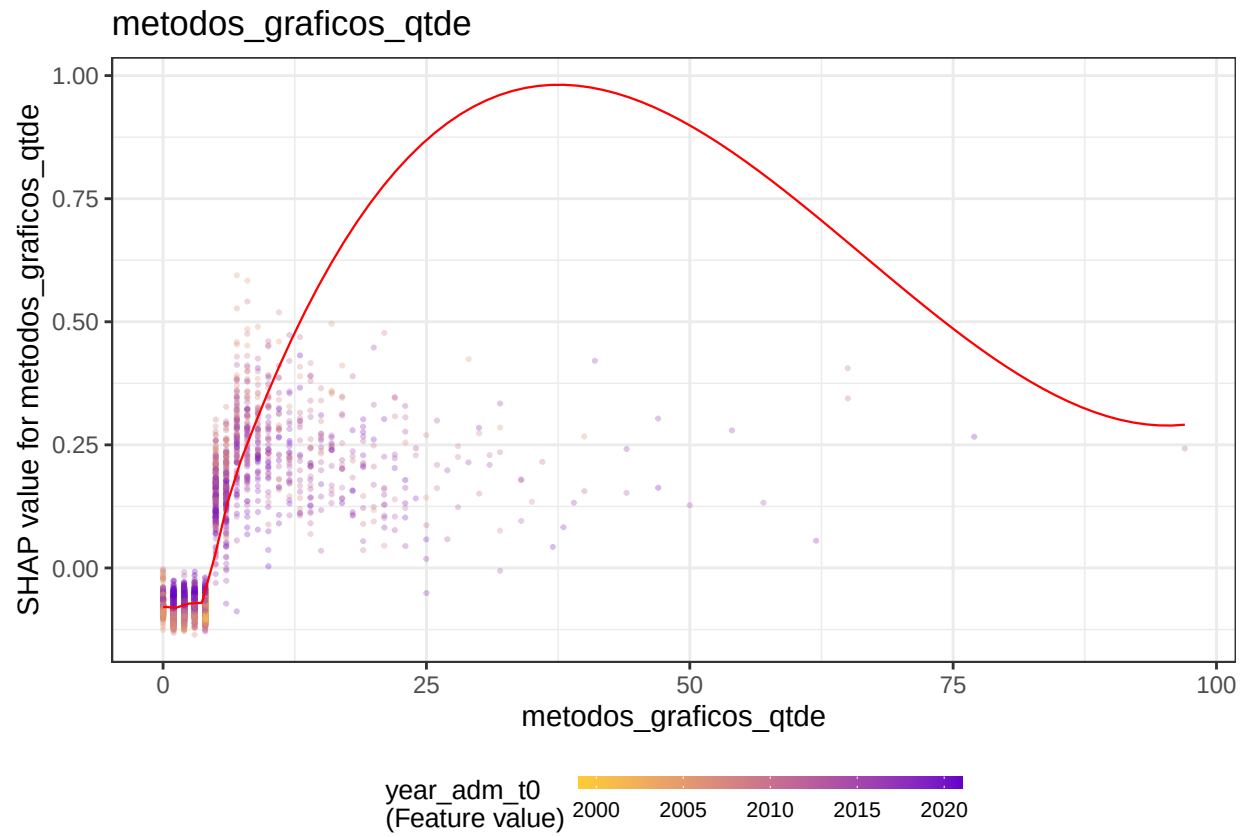
```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : There are
## other near singularities as well. 1.01
```



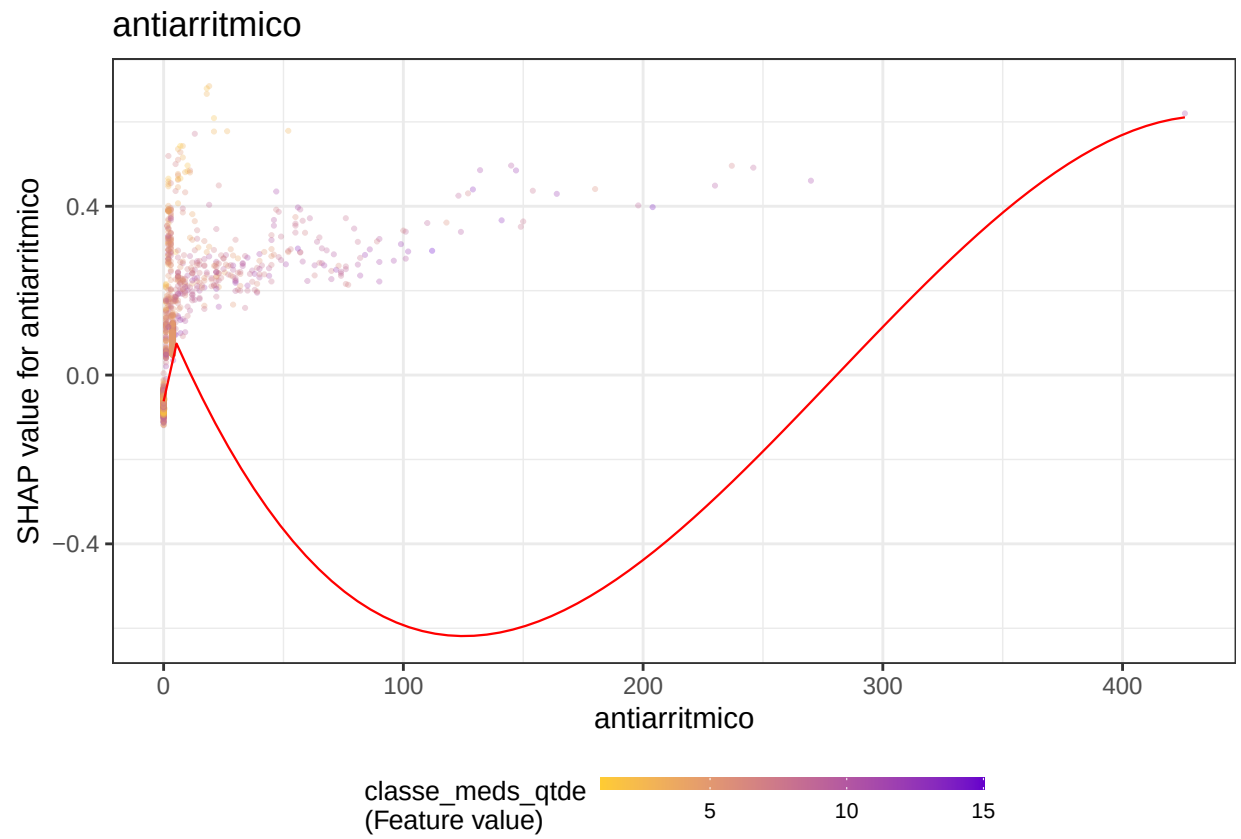

```
## `geom_smooth()` using formula 'y ~ x'
```




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

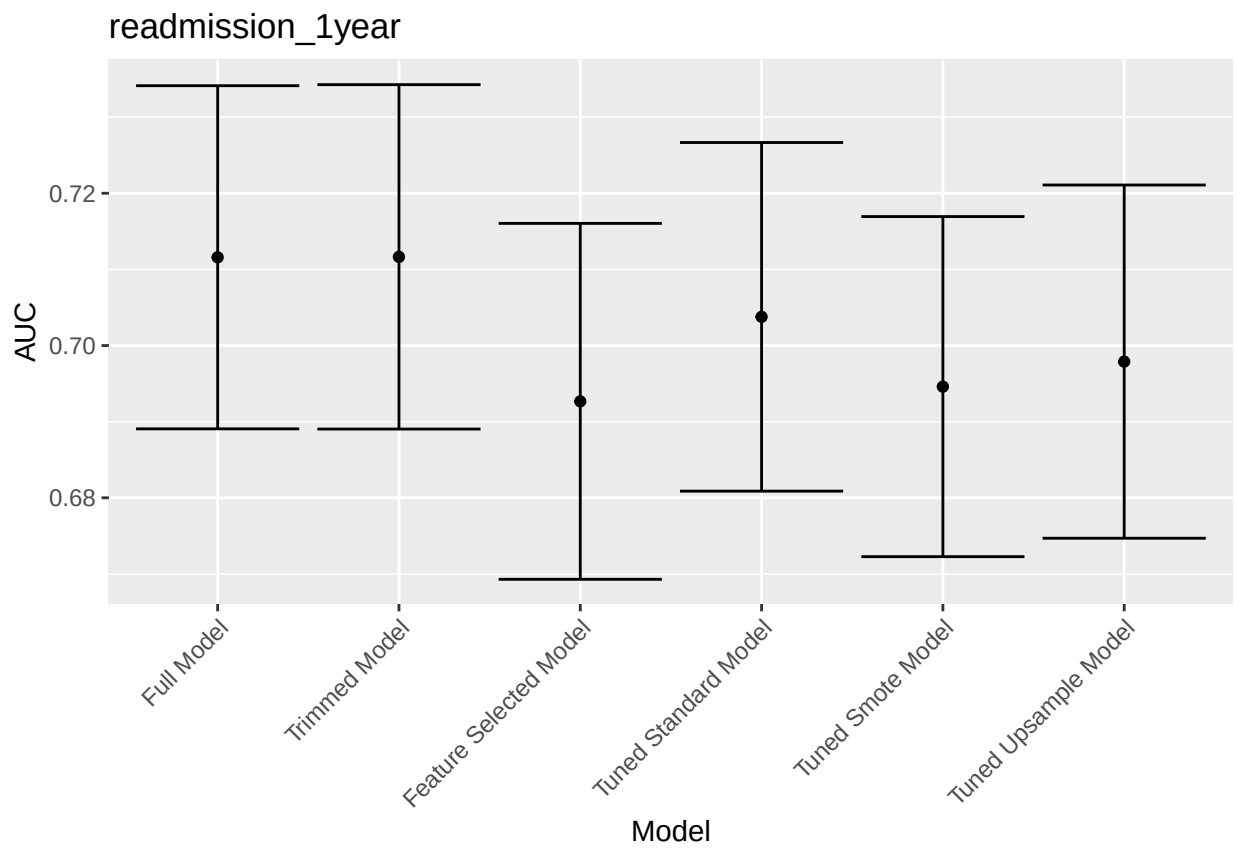



```
## `geom_smooth()` using formula 'y ~ x'
```



Models Comparison

```
df_auc <- tibble::tribble(
  ~Model, ~`AUC`, ~`Lower Limit`, ~`Upper Limit`,
  'Full Model', full_model$auc, full_model$auc_lower, full_model$auc_upper,
  'Trimmed Model', trimmed_model$auc, trimmed_model$auc_lower, trimmed_model$auc_upper,
  'Feature Selected Model', feature_selected_model$auc, feature_selected_model$auc_lower, feature_selected_model
  'Tuned Standard Model', as.numeric(lightgbm_auc$auc), lightgbm_auc$ci[1], lightgbm_auc$ci[3],
  'Tuned Smote Model', as.numeric(lightgbm_smote_auc$auc), lightgbm_smote_auc$ci[1], lightgbm_smote_auc$ci[3],
  'Tuned Upsample Model', as.numeric(lightgbm_upsample_auc$auc), lightgbm_upsample_auc$ci[1], lightgbm_upsample_

) %>%
  mutate(Target = outcome_column,
         Model = factor(Model,
                        levels = c('Full Model', 'Trimmed Model',
                                   'Feature Selected Model', 'Tuned Standard Model',
                                   'Tuned Smote Model', 'Tuned Upsample Model')))

df_auc %>%
  ggplot(aes(
    x = Model,
    y = AUC,
    ymin = `Lower Limit`,
    ymax = `Upper Limit`
  )) +
  geom_point() +
  geom_errorbar() +
  labs(title = outcome_column) +
  theme(axis.text.x = element_text(angle = 45, hjust=1))
```




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