Final Model - readmission_1year

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Global parameters

```
k <- 5 # Number of folds for cross validation
grid_size <- 30 # Number of parameter combination to tune on each model
max_auc_loss <- 0.01 # Max accepted loss of AUC for reducing num of features
```

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)
library(pROC)
library(caret)
library(themis)

source("aux_functions.R")

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', '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))

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. 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. aortografia
84. arteriografia
85. cintilografia

86. ecocardiograma
87. endoscopia
88. flebografia
89. pet_ct
90. ultrassom
91. tomografia
92. ressonancia
93. exames_imagem_qtde
94. dieta_parenteral
95. bic
96. mpp
97. hospital_stay

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)))

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

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")

  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)

  cv_results <- collect_metrics(model_fit_rs) %>% filter(.metric == 'roc_auc')

  return(
    list(
      cv_auc =  cv_results$mean,
      cv_auc_std_err = cv_results$std_err,
      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
  )
)

hyperparameters$sample_size <- 1

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: 0.715"
```

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

```
## [1] "Full Model Test AUC: 0.714"
```

Features with zero importance on the initial model:

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

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

1. transplant
2. endocardites
3. renal_failure
4. hemodialysis
5. copd
6. dialysis_t0
7. antiplaquetario_ev
8. antiviral
9. antiretroviral
10. cec
11. transplante_cardiaco
12. cir_toracica
13. icp
14. intervencao_cv
15. angioplastia
16. cve_desf
17. transfusao
18. teste_esforco
19. espiro_ergoespiro
20. tilt_teste
21. citologia

22. biopsia
23. angio_rm
24. angio_tc
25. aortografia
26. arteriografia
27. endoscopia
28. flebografia
29. pet_ct
30. dieta_parenteral
31. mpp

```
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: 0.712"
```

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

```
## [1] "Trimmed Model Test AUC: 0.710"
```

```
selection_results <- tibble::tribble(
  ~`Number of Features`, ~`CV AUC`, ~`CV AUC Std Error`, ~`AUC Loss`, ~`Least Important Feature`,
  length(features), full_model$cv_auc, full_model$cv_auc_std_err, 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),
            `CV AUC` = current_model$cv_auc,
            `CV AUC Std Error` = current_model$cv_auc_std_err,
            `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),
            `CV AUC` = current_model$cv_auc,
            `CV AUC Std Error` = current_model$cv_auc_std_err,
            `AUC Loss` = current_auc_loss,
```

```
            `Least Important Feature` = current_least_important)

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

selection_results %>% niceFormatting(digits = 4, label = 1)
```

Table 1:

Number of Features	CV AUC	CV AUC Std Error	AUC Loss	Least Important Feature
97	0.7150	0.0068	0.0000	heart_disease
66	0.7123	0.0064	0.0026	af
65	0.7113	0.0059	0.0037	insulina
64	0.7126	0.0060	0.0024	race
63	0.7114	0.0060	0.0036	cintilografia
62	0.7115	0.0054	0.0035	antifungico
61	0.7121	0.0055	0.0028	cateter_venoso_central
60	0.7099	0.0059	0.0051	tomografia
59	0.7103	0.0049	0.0047	eletrofisiologia
58	0.7100	0.0057	0.0050	interconsulta
57	0.7098	0.0051	0.0051	procedure_type_1
56	0.7079	0.0051	0.0071	cateterismo
55	0.7089	0.0050	0.0060	diabetes
54	0.7090	0.0050	0.0060	ultrassom
53	0.7071	0.0051	0.0079	bic
52	0.7066	0.0054	0.0084	ecocardiograma
51	0.7034	0.0054	0.0116	underlying_heart_disease

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

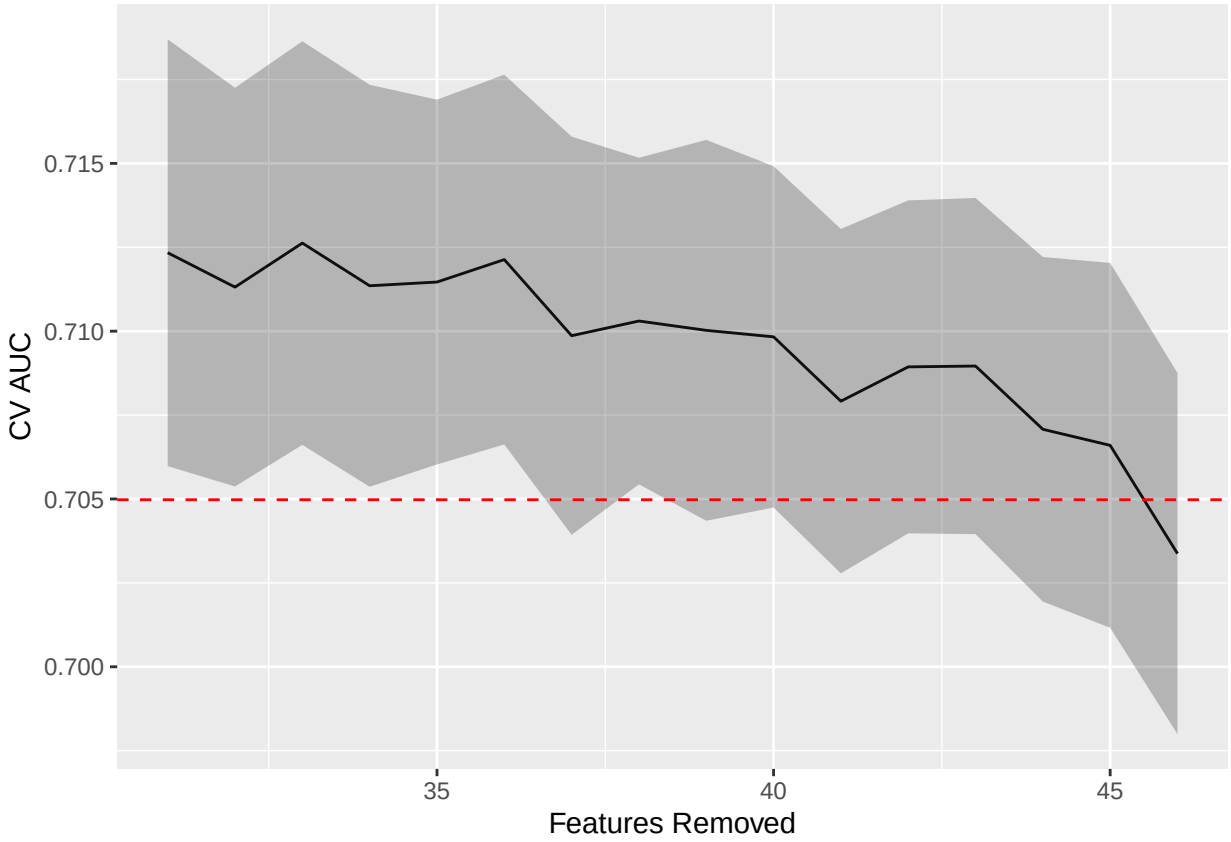
```
## [1] "Selected Model CV Train AUC: 0.703"
```

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

```
## [1] "Selected Model Test AUC: 0.706"
```

```
 selection_results <- selection_results %>%
  filter(`Number of Features` < length(features)) %>%
  mutate(`Features Removed` = length(features) - `Number of Features`,
         `CV AUC Low` = `CV AUC` - `CV AUC Std Error`,
         `CV AUC High` = `CV AUC` + `CV AUC Std Error`)

selection_results %>%
  ggplot(aes(x = `Features Removed`, y = `CV AUC`,
             ymin = `CV AUC Low`, ymax = `CV AUC High`)) +
  geom_line() +
  geom_ribbon(alpha = .3) +
```

```
  geom_hline(yintercept = full_model$cv_auc - max_auc_loss,
             linetype = "dashed", color = "red")
```




```
# 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. hospital_stay
2. admission_pre_t0_count
3. meds_cardiovasc_qtde
4. vasodilatador
5. admission_pre_t0_180d
6. icu_t0
7. classe_meds_qtde
8. diuretico
9. year_adm_t0
10. antiarritmico
11. cied_final_1
12. equipe_multiprof
13. age
14. metodos_graficos_qtde
15. reop_type_1
16. admission_t0_emergency
17. ieca_bra
18. insuf_cardiaca

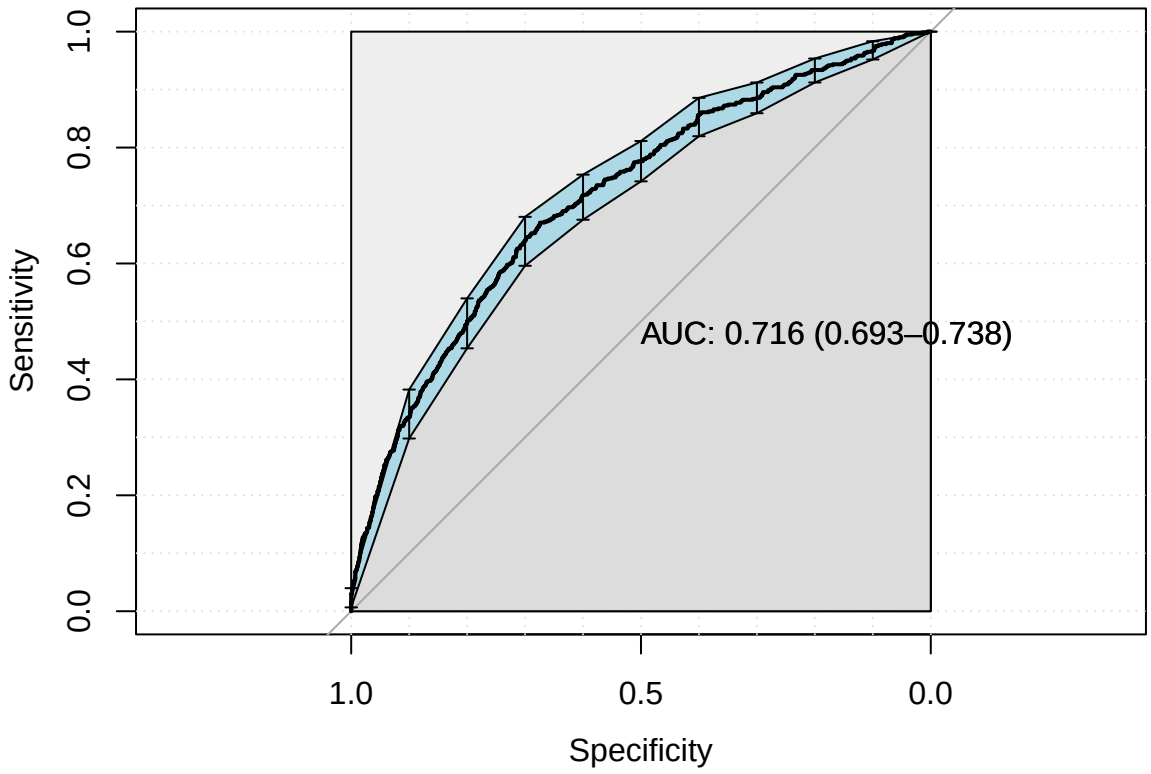
19. espironolactona
20. laboratorio
21. bloq_calcio
22. meds_antimicrobianos
23. cied_final_group_1
24. procedure_type_new
25. estatina
26. dva
27. education_level
28. psicofarmacos
29. analises_clinicas_qtde
30. exames_imagem_qtde
31. proced_invasivos_qtde
32. sex
33. heart_failure
34. patient_state
35. aco
36. digoxina
37. cultura
38. comorbidities_count
39. holter
40. betabloqueador
41. nyha_basal
42. prior_mi
43. valvopathy
44. histopatologia_qtde
45. underlying_heart_disease
46. outros_proced_cirurgicos
47. ressonancia
48. cardiac_arrest
49. ventilacao_mecanica
50. anticonvulsivante
51. heart_disease

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())

lightgbm_smote_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()) %>%
  step_impute_mean(all_numeric_predictors()) %>%
  step_smote(!!sym(outcome_column))

lightgbm_upsample_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()) %>%
```

```
  step_upsample(!!sym(outcome_column))

lightgbm_tuning <- function(recipe) {

  lightgbm_spec <- boost_tree(
    mtry = tune(),
    trees = tune(),
    min_n = tune(),
    tree_depth = tune(),
    learn_rate = tune(),
    loss_reduction = tune(),
    sample_size = 1.0
  ) %>%
    set_engine("lightgbm") %>%
    set_mode("classification")

  lightgbm_grid <- grid_latin_hypercube(
    mtry(range = c(1L, length(selected_features))),
    trees(range = c(100L, 300L)),
    min_n(),
    tree_depth(),
    learn_rate(),
    loss_reduction(),
    size = grid_size
  )

  lightgbm_workflow <-
    workflow() %>%
    add_recipe(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, label = 4)

  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)

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

  return(list(auc = as.numeric(lightgbm_auc$auc),
              auc_lower = lightgbm_auc$ci[1],
              auc_upper = lightgbm_auc$ci[3],
              parameters = lightgbm_parameters,
              fit = final_lightgbm_fit))
}

standard_results <- lightgbm_tuning(lightgbm_recipe)
```



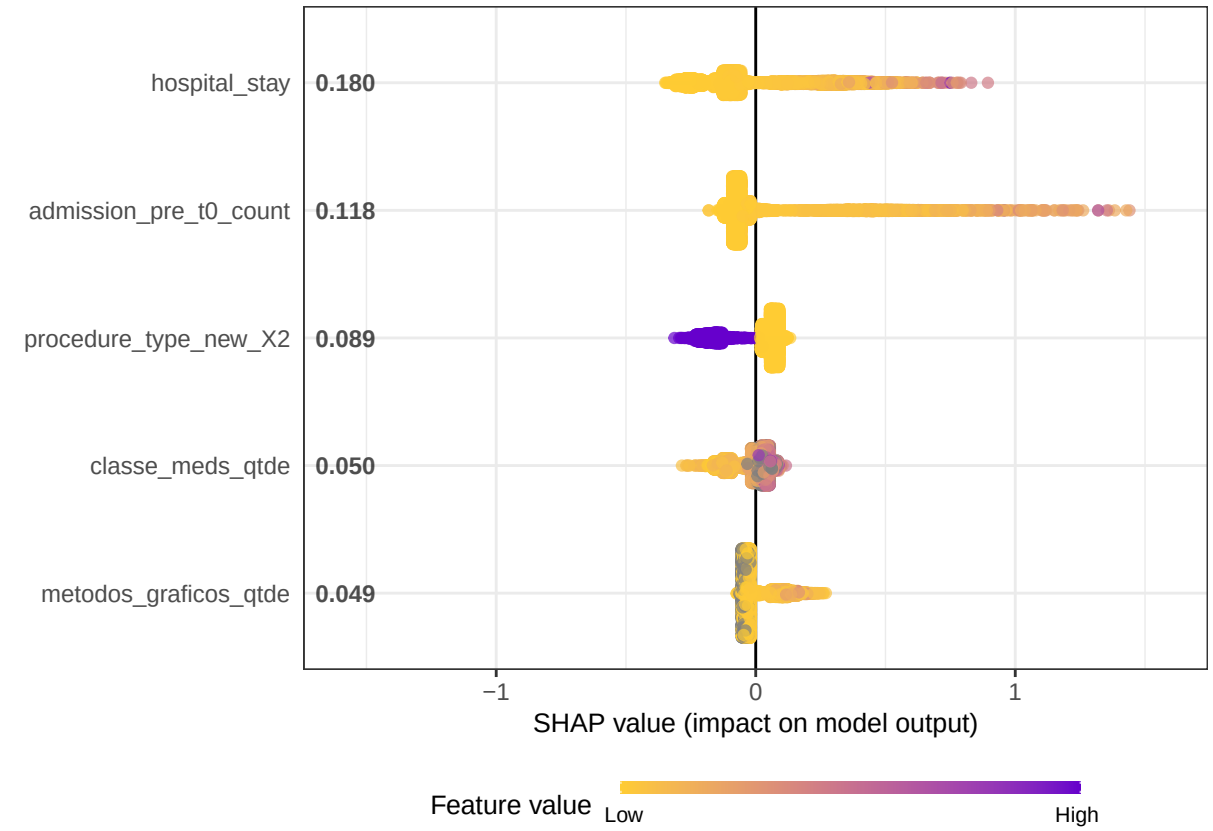

```
## [1] "Optimal Threshold: 0.11"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 2783  199
##    1 1344  405
##
##                Accuracy : 0.6739
##                  95% CI : (0.6603, 0.6872)
##     No Information Rate : 0.8723
##     P-Value [Acc > NIR] : 1
```

```
##
##                   Kappa : 0.1906
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.6743
##             Specificity : 0.6705
##          Pos Pred Value : 0.9333
##          Neg Pred Value : 0.2316
##              Prevalence : 0.8723
##          Detection Rate : 0.5882
##    Detection Prevalence : 0.6303
##       Balanced Accuracy : 0.6724
##
##        'Positive' Class : 0
##
```

```r
# smote_results <- lightgbm_tuning(lightgbm_smote_recipe)
# upsample_results <- lightgbm_tuning(lightgbm_upsample_recipe)

final_lightgbm_fit <- standard_results$fit
lightgbm_parameters <- standard_results$parameters

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

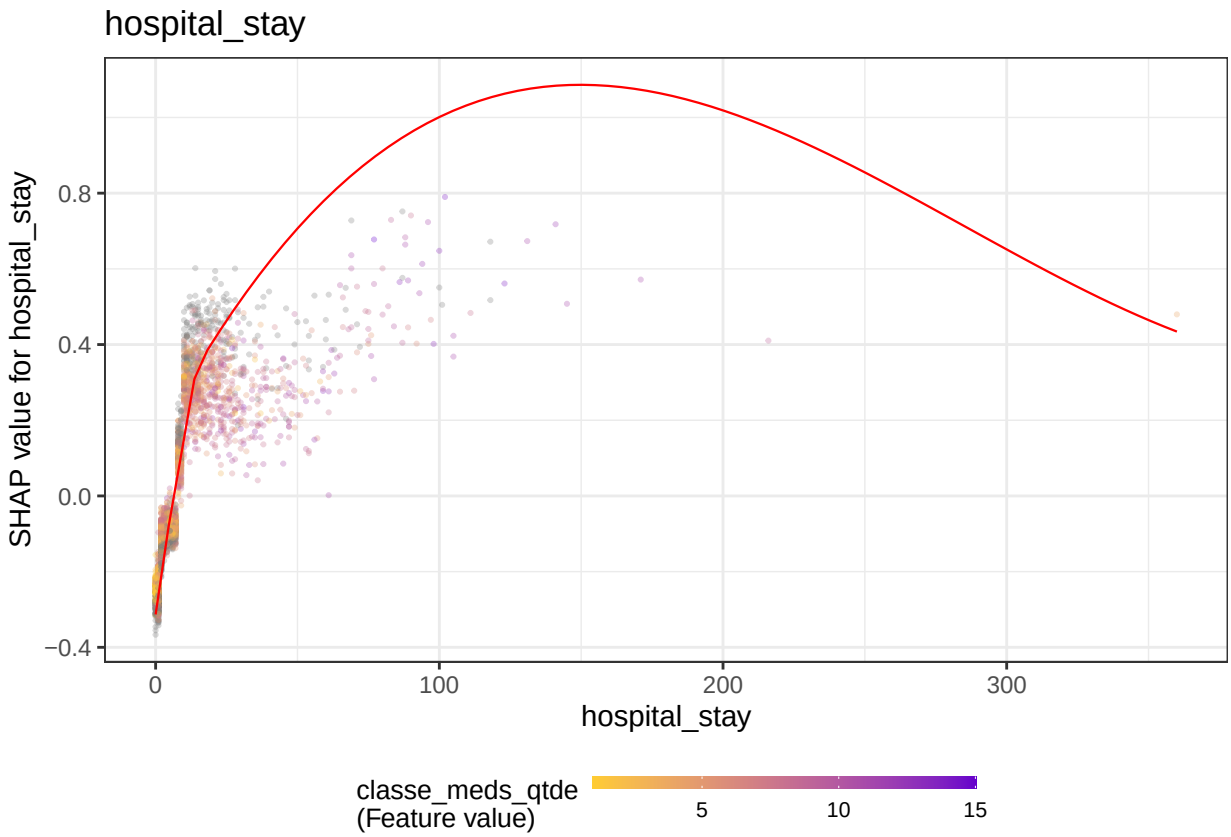
SHAP values

```r
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)))

n_plots <- min(5, length(selected_features))

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

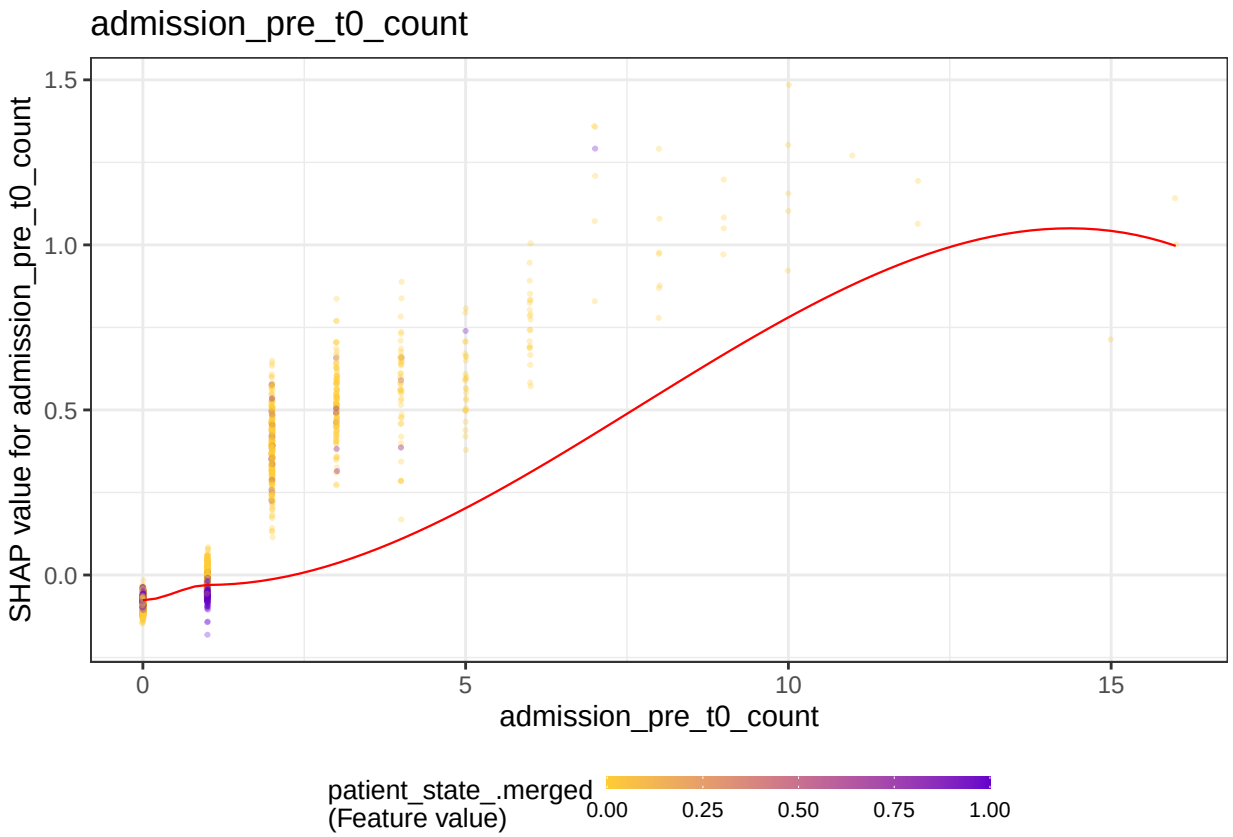



```
shap <- shap.prep(lightgbm_model, X_train = matrix_test)

for (x in shap.importance(shap, names_only = TRUE)[1:n_plots]) {
  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'
```




```
## `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
```



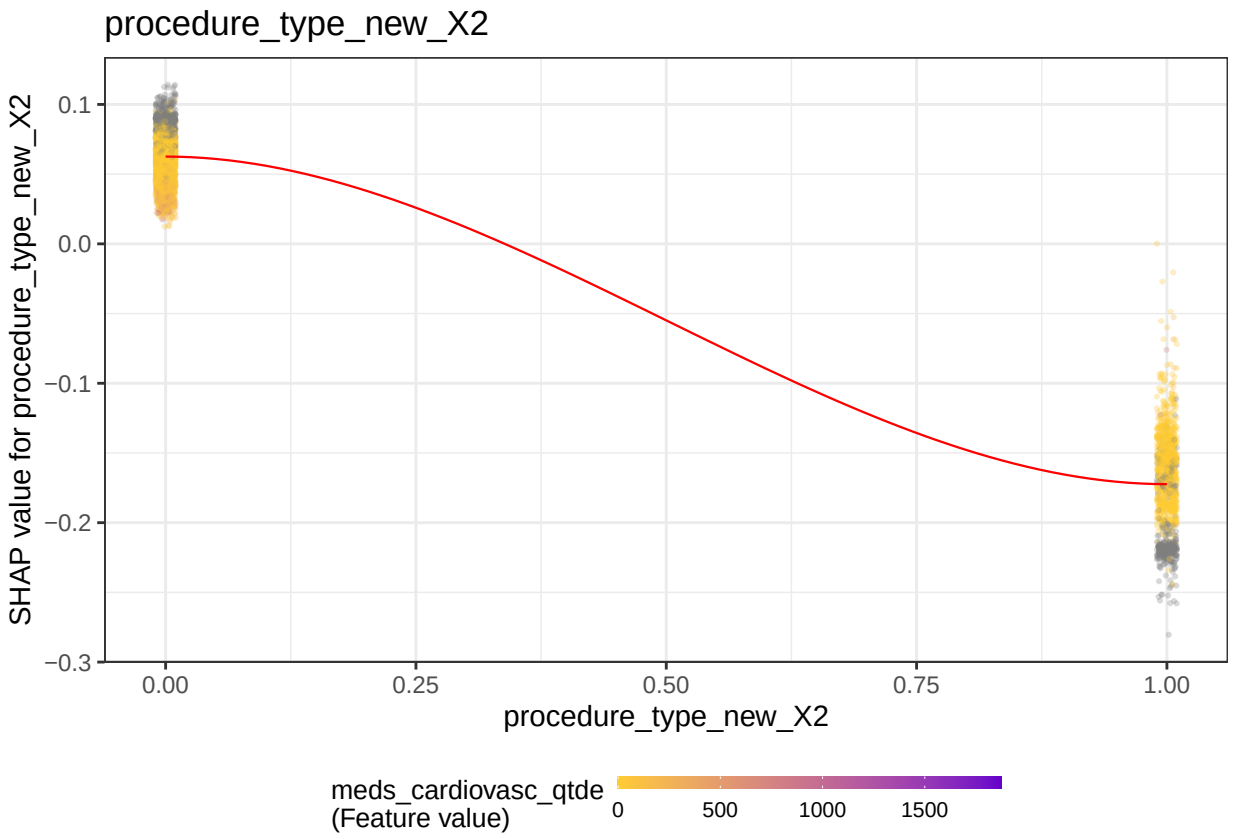

```
## `geom_smooth()` using formula 'y ~ x'
```

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

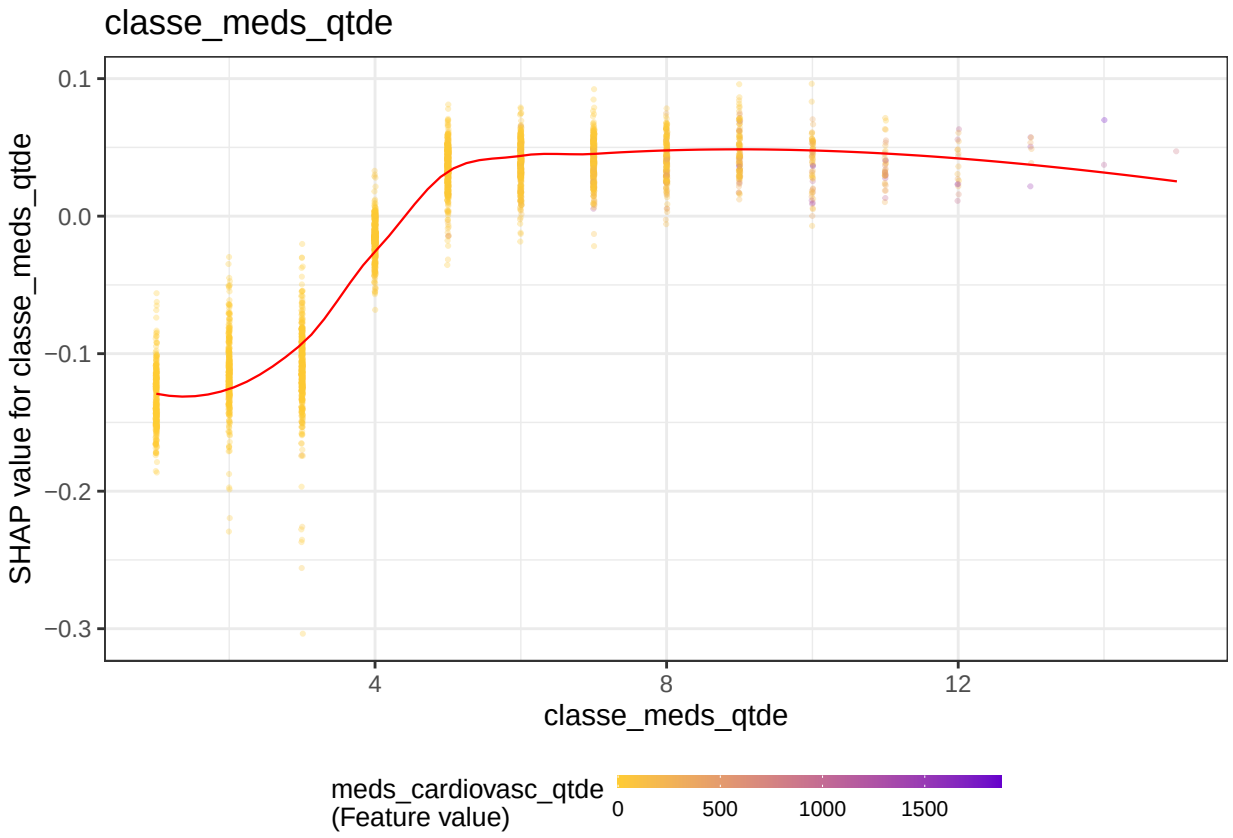
```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, : neighborhood radius
## 1.005
```

```
## 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
```

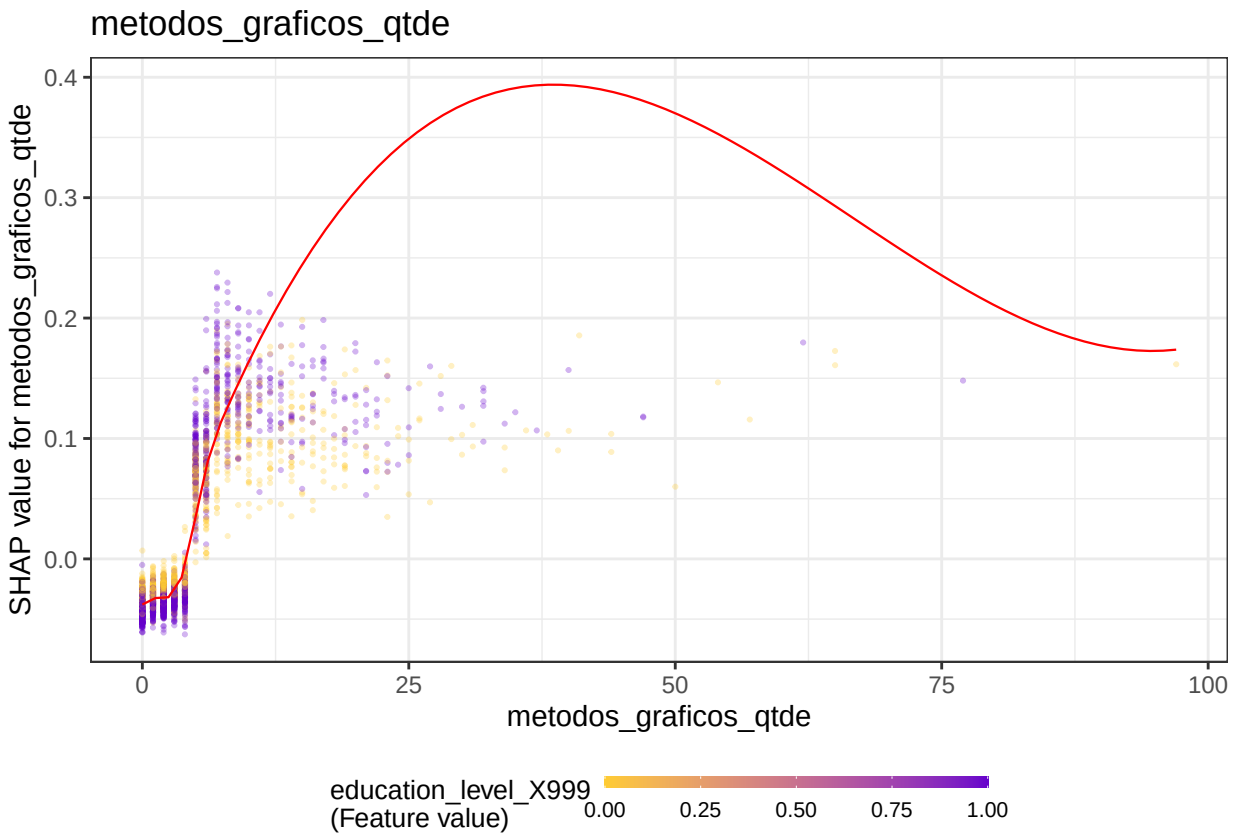



```
## `geom_smooth()` using formula 'y ~ x'
## Warning: Removed 1507 rows containing non-finite values (stat_smooth).
## Warning: Removed 1507 rows containing missing values (geom_point).
```



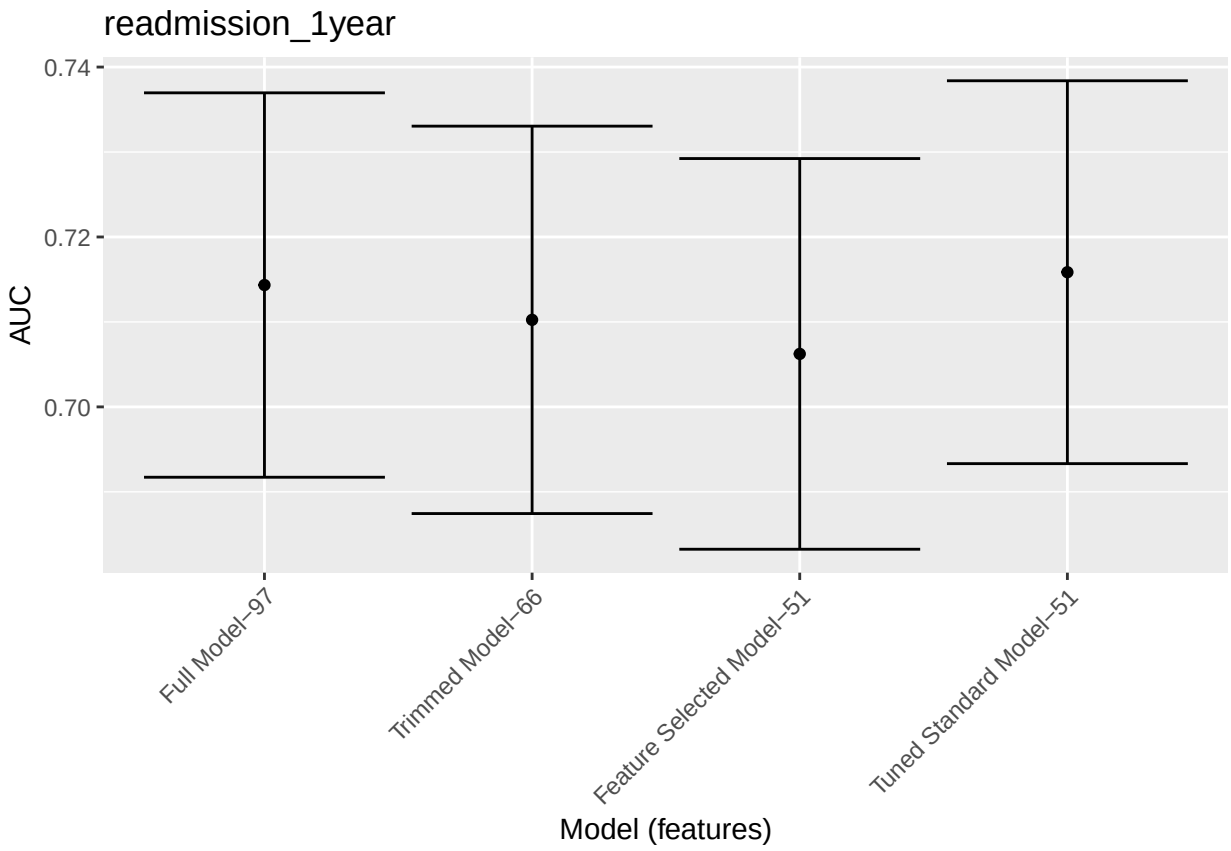

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning: Removed 810 rows containing non-finite values (stat_smooth).
## Warning: Removed 810 rows containing missing values (geom_point).
```



Models Comparison

```
df_auc <- tibble::tribble(
  ~Model, ~`AUC`, ~`Lower Limit`, ~`Upper Limit`, ~`Features`,
  'Full Model', full_model$auc, full_model$auc_lower, full_model$auc_upper, length(features),
  'Trimmed Model', trimmed_model$auc, trimmed_model$auc_lower, trimmed_model$auc_upper, length(trimmed_features)
  'Feature Selected Model', feature_selected_model$auc, feature_selected_model$auc_lower, feature_selected_model
  'Tuned Standard Model', standard_results$auc, standard_results$auc_lower, standard_results$auc_upper, length(s
  # 'Tuned Smote Model', smote_results$auc, smote_results$auc_lower, smote_results$auc_upper, length(selected_fe
  # 'Tuned Upsample Model', upsample_results$auc, upsample_results$auc_lower, upsample_results$auc_upper, length
) %>%
  mutate(Target = outcome_column,
         `Model (features)` = fct_reorder(paste0(Model, "-", Features), -Features))

df_auc %>%
  ggplot(aes(
    x = `Model (features)`,
    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))
```