Final Model - readmission_60d

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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. age
2. education_level
3. underlying_heart_disease
4. heart_disease
5. nyha_basal
6. prior_mi
7. heart_failure
8. af
9. cardiac_arrest
10. transplant
11. valvopathy
12. diabetes
13. hemodialysis
14. comorbidities_count
15. procedure_type_1
16. reop_type_1
17. procedure_type_new
18. cied_final_1
19. cied_final_group_1
20. admission_pre_t0_count
21. admission_pre_t0_180d
22. icu_t0
23. dialysis_t0
24. admission_t0_emergency

25. aco
26. antiarritmico
27. betabloqueador
28. ieca_bra
29. dva
30. digoxina
31. estatina
32. diuretico
33. vasodilatador
34. insuf_cardiaca
35. espironolactona
36. bloq_calcio
37. antiplaquetario_ev
38. insulina
39. anticonvulsivante
40. psicofarmacos
41. antifungico
42. antiviral
43. classe_meds_qtde
44. meds_cardiovasc_qtde
45. meds_antimicrobianos
46. ventilacao_mecanica
47. cec
48. transplante_cardiaco
49. cir_toracica
50. outros_proced_cirurgicos
51. icp
52. angioplastia
53. cateterismo
54. eletrofisiologia
55. cateter_venoso_central
56. proced_invasivos_qtde
57. cve_desf
58. transfusao
59. interconsulta
60. equipe_multiprof
61. holter
62. teste_esforco
63. espiro_ergoespiro
64. tilt_teste
65. metodos_graficos_qtde
66. laboratorio
67. cultura
68. analises_clinicas_qtde
69. citologia
70. biopsia
71. histopatologia_qtde
72. angio_rm
73. angio_tc
74. arteriografia
75. cintilografia
76. ecocardiograma
77. endoscopia
78. pet_ct
79. ultrassom
80. tomografia
81. ressonancia
82. exames_imagem_qtde
83. bic
84. 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: 0.706"
```

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

```
## [1] "Full Model Test AUC: 0.681"
```

Features with zero importance on the initial model:

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

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

1. education_level
2. underlying_heart_disease
3. heart_disease
4. transplant
5. hemodialysis
6. dialysis_t0
7. antiplaquetario_ev
8. insulina
9. antiviral
10. cec
11. transplante_cardiaco
12. cir_toracica
13. icp
14. angioplastia
15. cateter_venoso_central
16. teste_esforco
17. espiro_ergoespiro
18. tilt_teste
19. biopsia
20. angio_rm
21. arteriografia
22. 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: 0.685"
```

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

```
## [1] "Trimmed Model Test AUC: 0.663"
```

```r
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
84	0.7064	0.0162	0.0000	nyha_basal
83	0.7068	0.0167	-0.0004	education_level
82	0.7056	0.0169	0.0008	angio_tc
81	0.7055	0.0165	0.0009	cateter_venoso_central
80	0.7061	0.0165	0.0003	transfusao
79	0.7064	0.0171	-0.0001	cardiac_arrest
78	0.7045	0.0163	0.0019	diabetes
77	0.7045	0.0163	0.0019	outros_proced_cirurgicos
76	0.7046	0.0157	0.0018	citologia
75	0.7036	0.0154	0.0027	cied_final_1

Table 1: *(continued)*

Number of Features	CV AUC	CV AUC Std Error	AUC Loss	Least Important Feature
74	0.7053	0.0159	0.0011	digoxina
73	0.7012	0.0154	0.0051	cve_desf
72	0.7027	0.0156	0.0037	eletrofisiologia
71	0.7014	0.0162	0.0050	tomografia
70	0.7001	0.0161	0.0063	valvopathy
69	0.6993	0.0157	0.0071	antifungico
68	0.6988	0.0154	0.0076	ressonancia
67	0.6978	0.0146	0.0086	ventilacao_mecanica
66	0.6983	0.0153	0.0081	interconsulta
65	0.6951	0.0143	0.0113	histopatologia_qtde

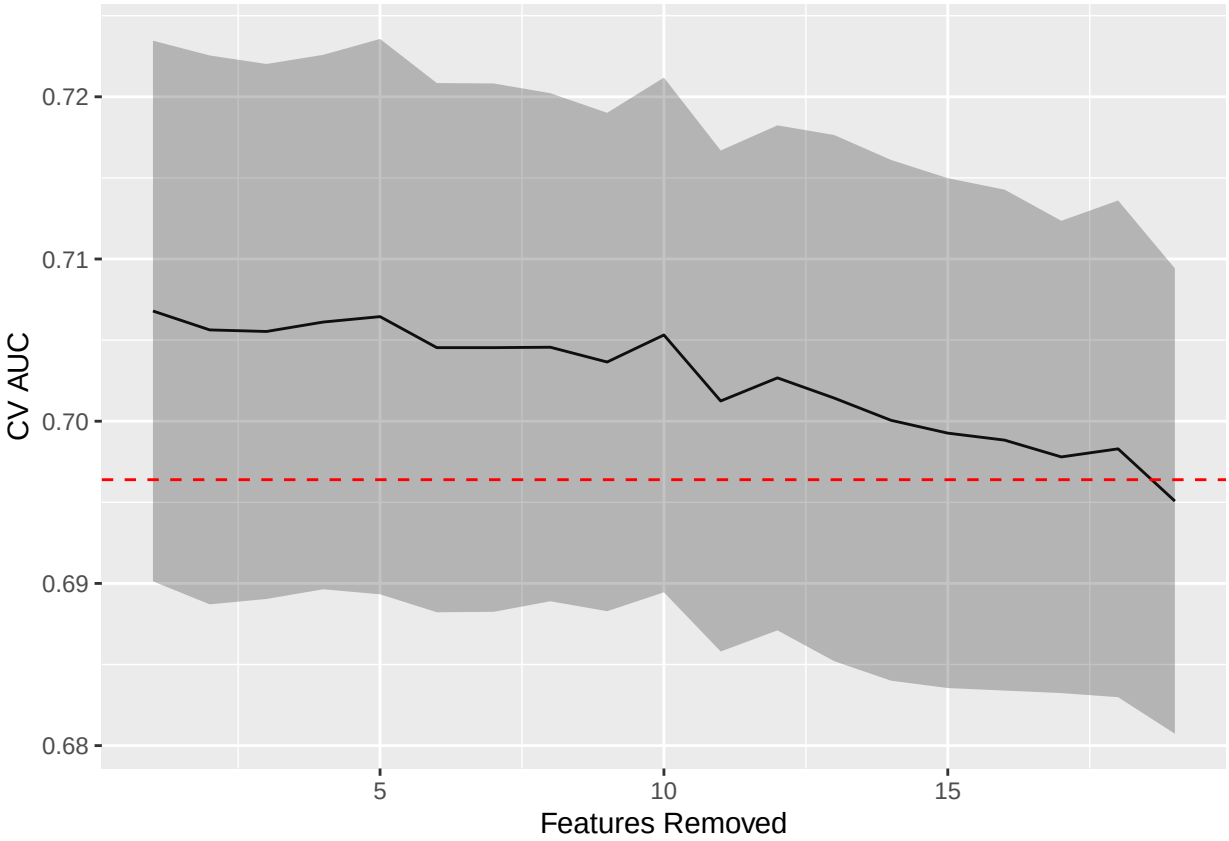
```
if (exists('last_feature_dropped')) {
  selected_features <- c(current_features, last_feature_droped)
} else {
  selected_features <- current_features
}

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: 0.695"
```

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

```
## [1] "Selected Model Test AUC: 0.674"
```

```
 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. age
2. underlying_heart_disease
3. heart_disease
4. prior_mi
5. heart_failure
6. af
7. transplant
8. hemodialysis
9. comorbidities_count
10. procedure_type_1
11. reop_type_1
12. procedure_type_new
13. cied_final_group_1
14. admission_pre_t0_count
15. admission_pre_t0_180d
16. icu_t0
17. dialysis_t0
18. admission_t0_emergency
19. aco
20. antiarritmico
21. betabloqueador

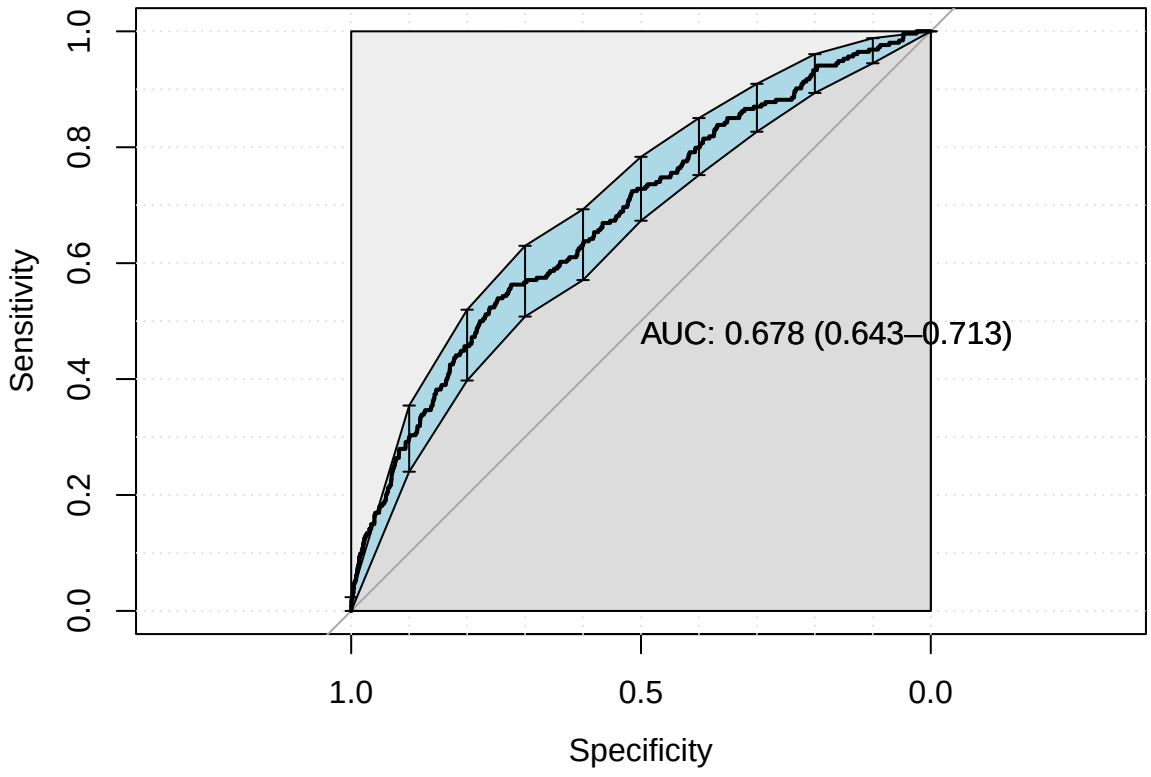
22. ieca_bra
23. dva
24. estatina
25. diuretico
26. vasodilatador
27. insuf_cardiaca
28. espironolactona
29. bloq_calcio
30. antiplaquetario_ev
31. insulina
32. anticonvulsivante
33. psicofarmacos
34. antiviral
35. classe_meds_qtde
36. meds_cardiovasc_qtde
37. meds_antimicrobianos
38. cec
39. transplante_cardiaco
40. cir_toracica
41. icp
42. angioplastia
43. cateterismo
44. proced_invasivos_qtde
45. equipe_multiprof
46. holter
47. teste_esforco
48. espiro_ergoespiro
49. tilt_teste
50. metodos_graficos_qtde
51. laboratorio
52. cultura
53. analises_clinicas_qtde
54. biopsia
55. histopatologia_qtde
56. angio_rm
57. arteriografia
58. cintilografia
59. ecocardiograma
60. endoscopia
61. pet_ct
62. ultrassom
63. exames_imagem_qtde
64. bic
65. hospital_stay

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"
```

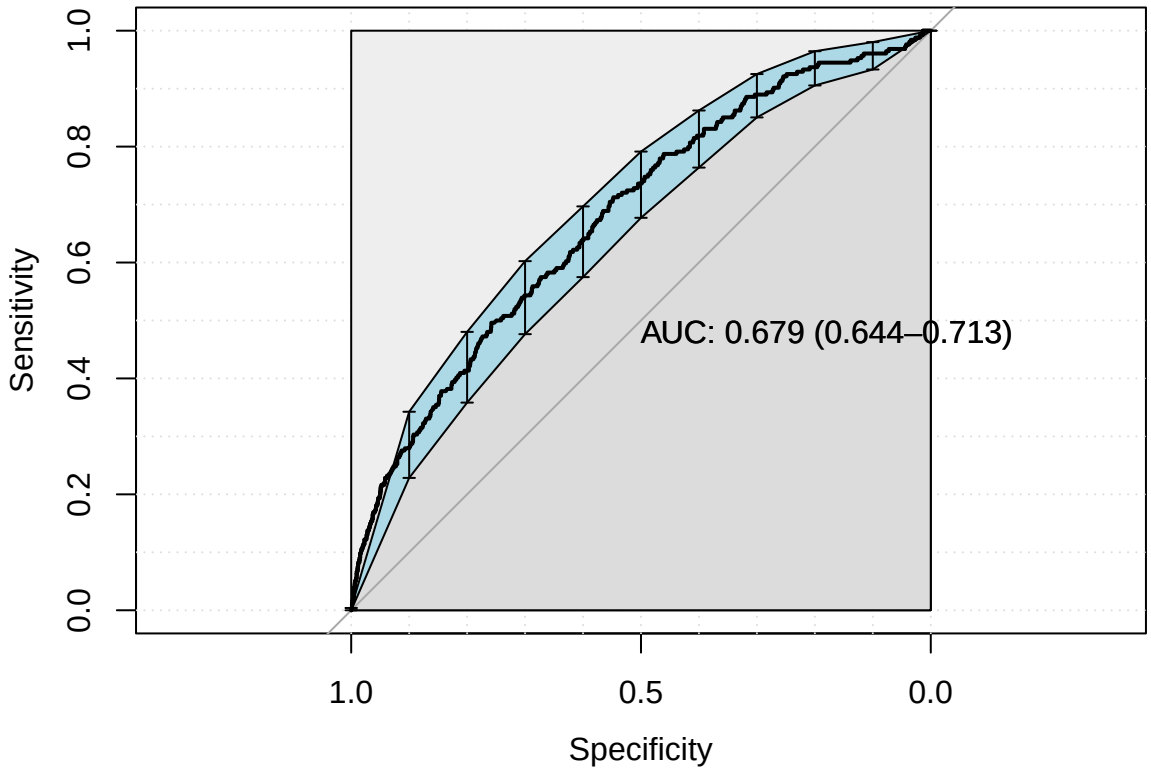
```
    ) %>%
    ggplot(aes(value, mean, color = parameter)) +
    geom_point(alpha = 0.8, show.legend = FALSE) +
    facet_wrap(~parameter, scales = "free_x") +
    labs(x = NULL, y = "AUC")

  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: 0.06"
```

```
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3241  111
##    1 1235  143
##
##                Accuracy : 0.7154
##                  95% CI : (0.7023, 0.7283)
##     No Information Rate : 0.9463
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.093
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.7241
##             Specificity : 0.5630
##          Pos Pred Value : 0.9669
##          Neg Pred Value : 0.1038
##              Prevalence : 0.9463
##          Detection Rate : 0.6852
##    Detection Prevalence : 0.7087
##       Balanced Accuracy : 0.6435
##
##        'Positive' Class : 0
##
```

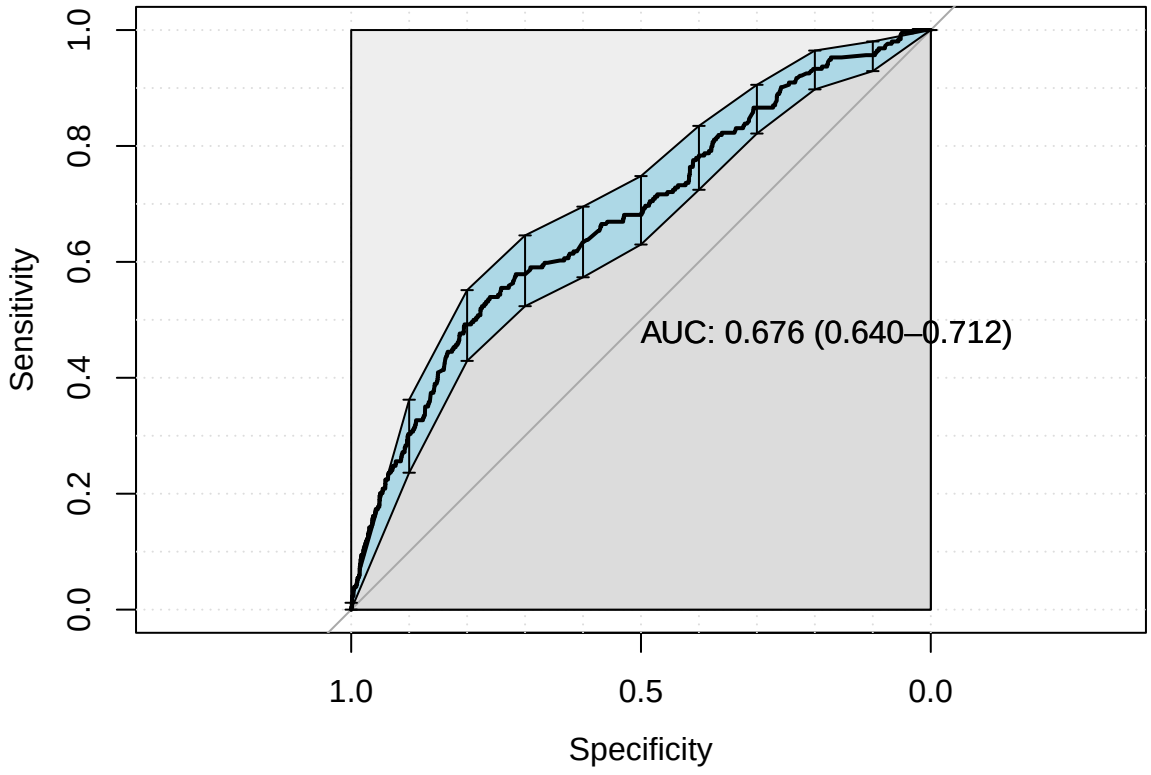
```
smote_results <- lightgbm_tuning(lightgbm_smote_recipe)
```




```
## [1] "Optimal Threshold: 0.37"
## Confusion Matrix and Statistics
##
##     reference
```

```
## data    0    1
##    0 2452   73
##    1 2024  181
##
##                Accuracy : 0.5567
##                  95% CI : (0.5424, 0.5709)
##     No Information Rate : 0.9463
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.0563
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.54781
##             Specificity : 0.71260
##          Pos Pred Value : 0.97109
##          Neg Pred Value : 0.08209
##              Prevalence : 0.94630
##          Detection Rate : 0.51839
##    Detection Prevalence : 0.53383
##       Balanced Accuracy : 0.63020
##
##        'Positive' Class : 0
##
```

```
upsample_results <- lightgbm_tuning(lightgbm_upsample_recipe)
```



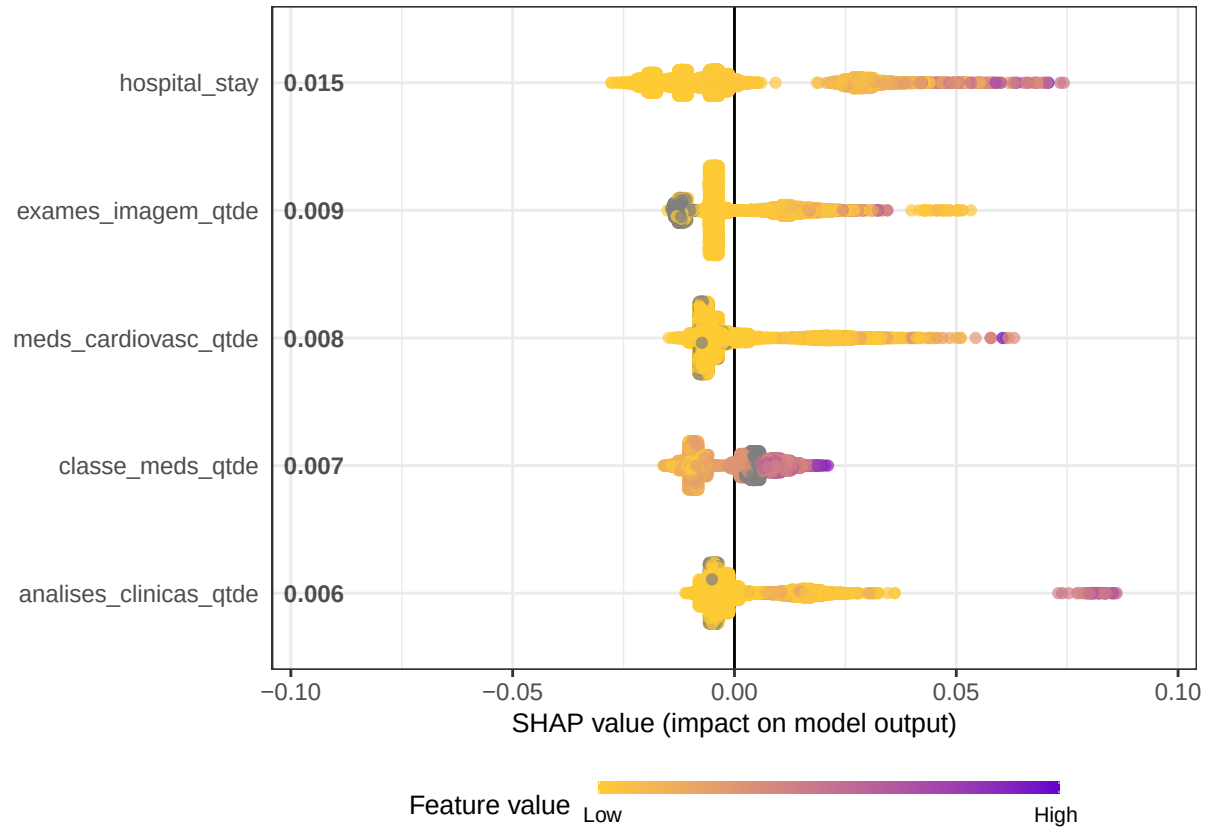

```
## [1] "Optimal Threshold: 0.51"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3405  117
##    1 1071  137
```

```
##
##                Accuracy : 0.7488
##                  95% CI : (0.7362, 0.7611)
##     No Information Rate : 0.9463
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.1083
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.7607
##             Specificity : 0.5394
##          Pos Pred Value : 0.9668
##          Neg Pred Value : 0.1134
##              Prevalence : 0.9463
##          Detection Rate : 0.7199
##    Detection Prevalence : 0.7446
##       Balanced Accuracy : 0.6500
##
##        'Positive' Class : 0
##
```

```
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
#   )
# )
```

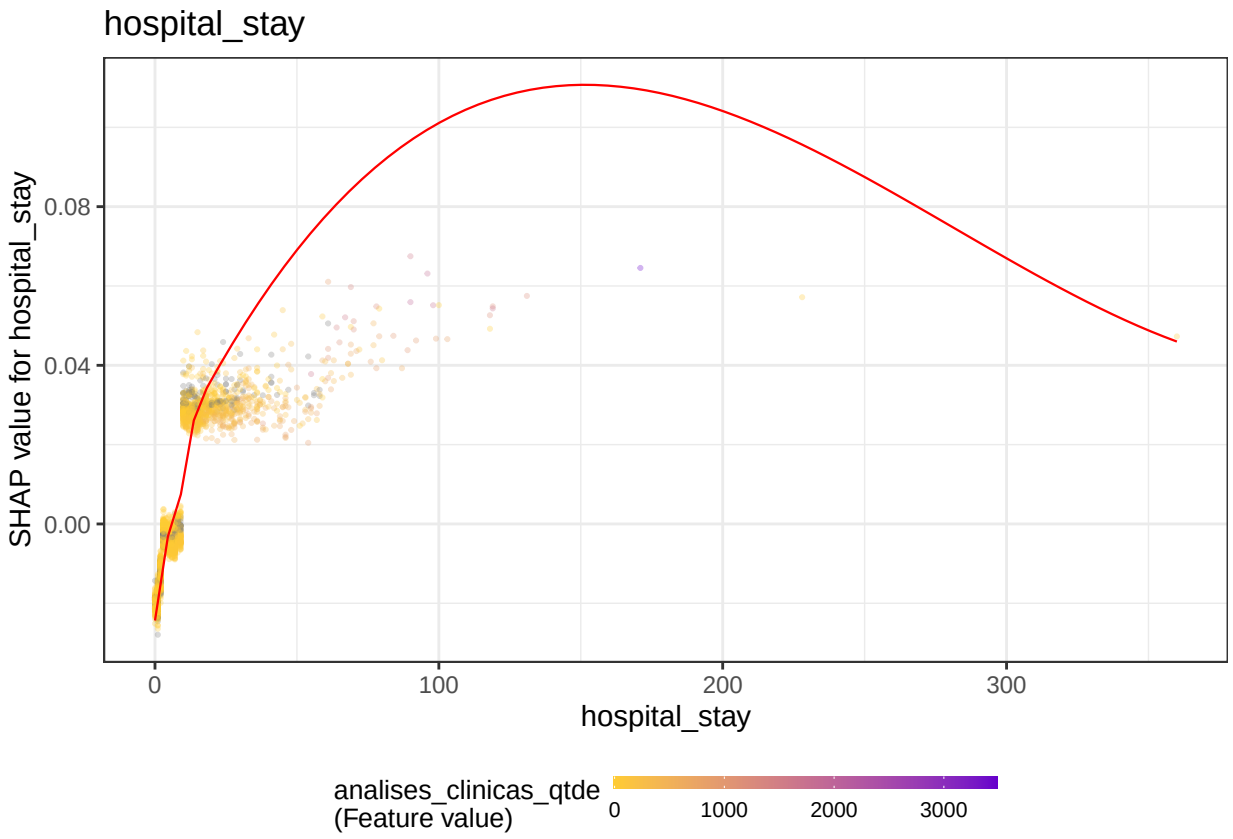
SHAP values

```
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)
```

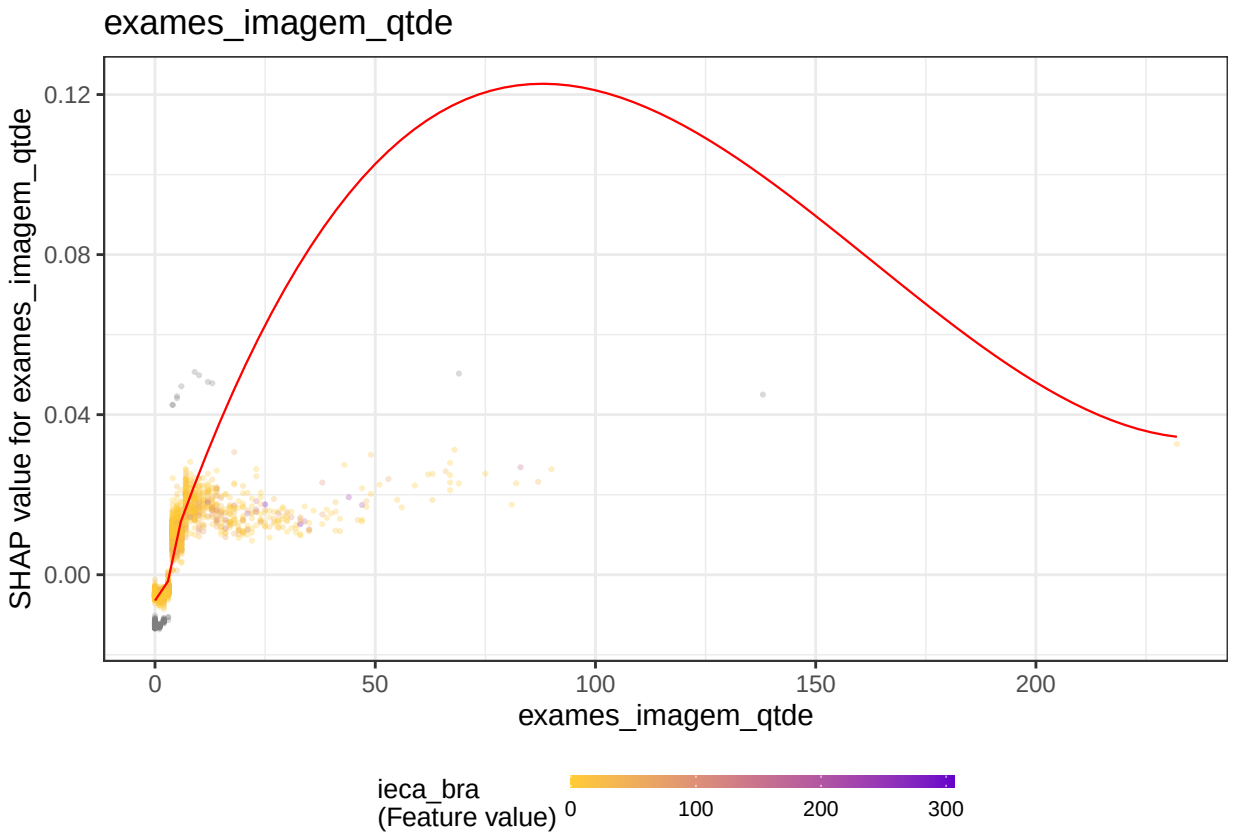



```
shap <- shap.prep(lightgbm_model, X_train = matrix_test)

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'
```

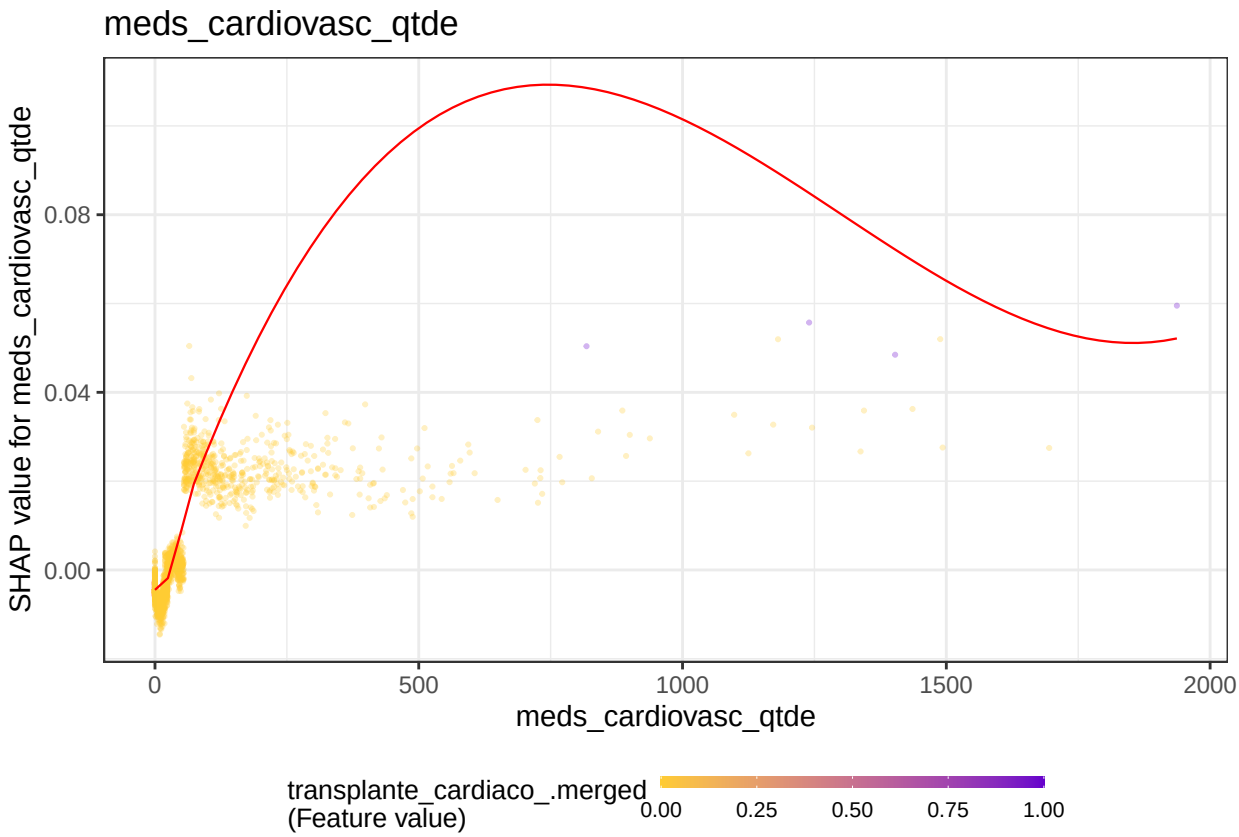



```
## `geom_smooth()` using formula 'y ~ x'
## Warning: Removed 802 rows containing non-finite values (stat_smooth).
## Warning: Removed 802 rows containing missing values (geom_point).
```

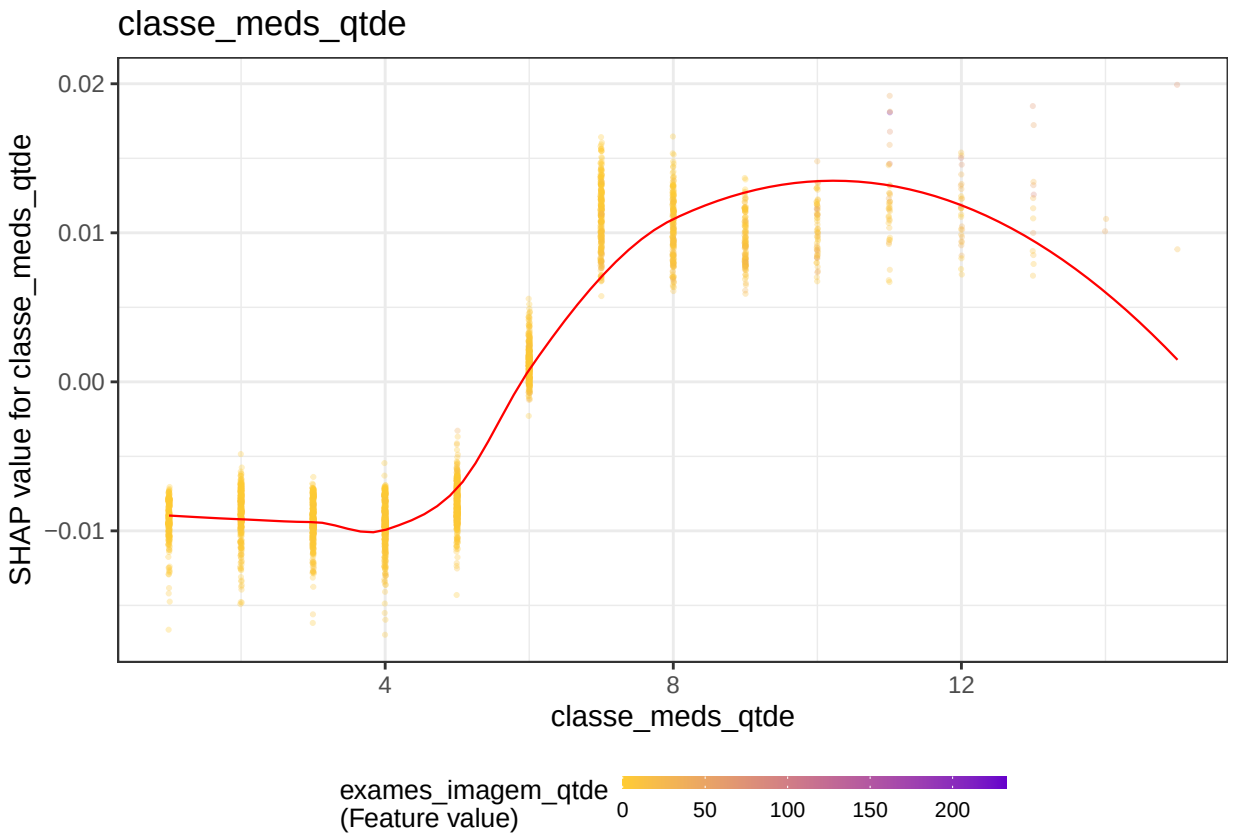



```
## `geom_smooth()` using formula 'y ~ x'
```

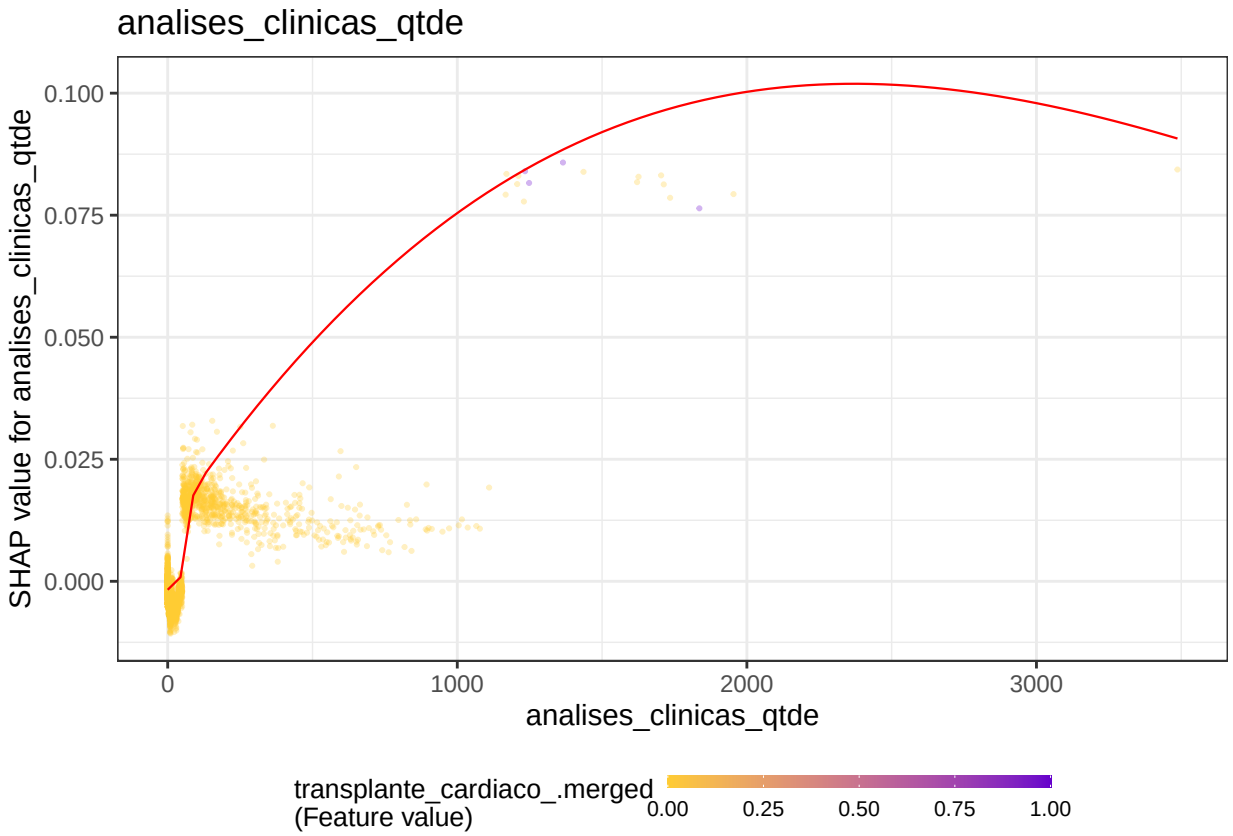
```
## Warning: Removed 1041 rows containing non-finite values (stat_smooth).
## Warning: Removed 1041 rows containing missing values (geom_point).
```




```
## `geom_smooth()` using formula 'y ~ x'
## Warning: Removed 1455 rows containing non-finite values (stat_smooth).
## Warning: Removed 1455 rows containing missing values (geom_point).
```

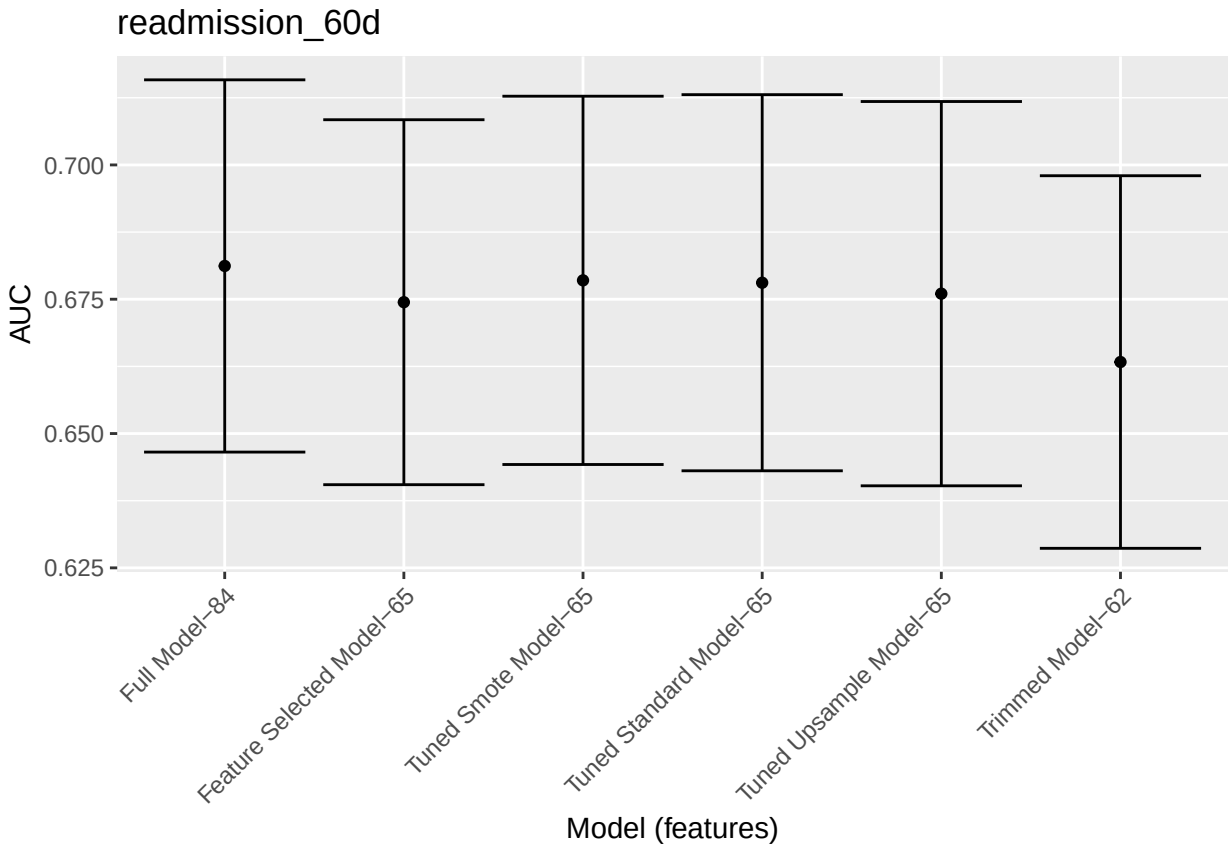



```
## `geom_smooth()` using formula 'y ~ x'
## Warning: Removed 802 rows containing non-finite values (stat_smooth).
## Warning: Removed 802 rows containing missing values (geom_point).
```



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_feat
  'Tuned Upsample Model', upsample_results$auc, upsample_results$auc_lower, upsample_results$auc_upper, length(s
) %>%
  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))
```