Final Model - readmission_30d

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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
max_auc_loss <- params$max_auc_loss # Max accepted loss of AUC for reducing num of features
repeats <- params$repeats
Hmisc::list.tree(params)
```

```
##  params = list 5 (952 bytes)
## .  max_auc_loss = double 1= 0.01
## .  outcome_column = character 1= readmission_30d
## .  k = double 1= 10
## .  grid_size = double 1= 50
## .  repeats = double 1= 2
```

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)
```

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

```r
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

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

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

features_list = c(cat_features_list, num_features_list)
```

```r
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)
```

Starting features:

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

1. education_level
2. underlying_heart_disease
3. heart_disease
4. nyha_basal
5. prior_mi
6. heart_failure
7. transplant

8. endocardites
9. hemodialysis
10. comorbidities_count
11. procedure_type_1
12. reop_type_1
13. procedure_type_new
14. cied_final_1
15. cied_final_group_1
16. admission_pre_t0_count
17. admission_pre_t0_180d
18. icu_t0
19. dialysis_t0
20. admission_t0_emergency
21. aco
22. antiarritmico
23. betabloqueador
24. ieca_bra
25. dva
26. digoxina
27. estatina
28. diuretico
29. vasodilatador
30. insuf_cardiaca
31. espironolactona
32. bloq_calcio
33. antiplaquetario_ev
34. insulina
35. anticonvulsivante
36. psicofarmacos
37. antifungico
38. antiviral
39. classe_meds_qtde
40. meds_cardiovasc_qtde
41. meds_antimicrobianos
42. ventilacao_mecanica
43. cec
44. transplante_cardiaco
45. outros_proced_cirurgicos
46. icp
47. intervencao_cv
48. cateterismo
49. eletrofisiologia
50. cateter_venoso_central
51. proced_invasivos_qtde
52. cve_desf
53. transfusao
54. equipe_multiprof
55. holter
56. metodos_graficos_qtde
57. laboratorio
58. cultura
59. analises_clinicas_qtde
60. citologia
61. biopsia
62. histopatologia_qtde
63. angio_rm
64. angio_tc
65. cintilografia
66. ecocardiograma
67. endoscopia
68. flebografia

69. pet_ct
70. ultrassom
71. tomografia
72. ressonancia
73. exames_imagem_qtde
74. bic
75. mpp
76. 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),
                     repeats = repeats)
```

Feature Selection

```
custom_dummy_names <- function(var, lvl, ordinal = FALSE) {
  dummy_names(var, lvl, ordinal = FALSE, sep = "__")
}

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_dummy(all_nominal_predictors(), naming = custom_dummy_names)

  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) %>%
    separate(Feature, c("Feature","value"), "__", fill = 'right') %>%
    group_by(Feature) %>%
    summarise(Gain = sum(Gain),
              Cover = sum(Cover),
              Frequency = sum(Frequency)) %>%
    ungroup() %>%
    arrange(desc(Gain))

  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: 0.691"
```

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

```
## [1] "Full Model Test AUC: 0.703"
```

Features with zero importance on the initial model:

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

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

1. prior_mi
2. heart_failure
3. transplant
4. endocardites
5. hemodialysis
6. procedure_type_1
7. reop_type_1
8. dialysis_t0
9. antiplaquetario_ev
10. insulina
11. antiviral
12. cec

13. transplante_cardiaco
14. icp
15. intervencao_cv
16. cateterismo
17. eletrofisiologia
18. cateter_venoso_central
19. cve_desf
20. transfusao
21. citologia
22. biopsia
23. angio_rm
24. angio_tc
25. cintilografia
26. ecocardiograma
27. endoscopia
28. flebografia
29. pet_ct
30. tomografia
31. ressonancia

```
trimmed_features <- full_model$importance$Feature
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: 0.691"
```

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

```
## [1] "Trimmed Model Test AUC: 0.703"
```

```
selection_results <- tibble::tribble(
  ~`Tested Feature`, ~`Dropped`, ~`Number of Features`, ~`CV AUC`, ~`CV AUC Std Error`, ~`Total AUC Loss`, ~`Ins
  'None', TRUE, length(features), full_model$cv_auc, full_model$cv_auc_std_err, 0, 0
)

whitelist <- c()

if (full_model$cv_auc - trimmed_model$cv_auc < max_auc_loss) {
  current_features <- trimmed_features
  current_model <- trimmed_model
  current_auc_loss <- full_model$cv_auc - current_model$cv_auc
  instant_auc_loss <- full_model$cv_auc - current_model$cv_auc

  selection_results <- selection_results %>%
    add_row(`Tested Feature` = 'All unimportant',
            `Dropped` = TRUE,
            `Number of Features` = length(trimmed_features),
            `CV AUC` = current_model$cv_auc,
            `CV AUC Std Error` = current_model$cv_auc_std_err,
            `Total AUC Loss` = current_auc_loss,
            `Instant AUC Loss` = instant_auc_loss)
} else {
  current_features <- features
  current_model <- full_model
  current_auc_loss <- 0
}

while (current_auc_loss < max_auc_loss & mean(current_features %in% whitelist) < 1) {
  zero_importance_features <-
    setdiff(current_features, current_model$importance$Feature) %>%
    setdiff(whitelist)
```

```
  if (length(zero_importance_features) > 0) {
    current_least_important <- zero_importance_features[1]
  } else {
    current_least_important <-
      tail(setdiff(current_model$importance$Feature, whitelist), 1)
  }
  test_features <-
    setdiff(current_features, current_least_important)
  current_model <-
    model_fit_wf(df_train, test_features, outcome_column, hyperparameters)
  instant_auc_loss <-
    tail(selection_results %>% filter(Dropped) %>% .$`CV AUC`, n = 1) - current_model$cv_auc

  if (instant_auc_loss < max_auc_loss / 5 &
      current_auc_loss < max_auc_loss) {
    dropped <- TRUE
    current_features <- test_features
    current_auc_loss <- full_model$cv_auc - current_model$cv_auc
  } else {
    dropped <- FALSE
    whitelist <- c(whitelist, current_least_important)
  }

  selection_results <- selection_results %>%
    add_row(
      `Tested Feature` = current_least_important,
      `Dropped` = dropped,
      `Number of Features` = length(test_features),
      `CV AUC` = current_model$cv_auc,
      `CV AUC Std Error` = current_model$cv_auc_std_err,
      `Total AUC Loss` = current_auc_loss,
      `Instant AUC Loss` = instant_auc_loss
    )

  print(c(
    length(current_features),
    round(current_auc_loss, 4),
    round(instant_auc_loss, 4),
    current_least_important
  ))
}
```

```
## [1] "44"          "1e-04"       "0"           "antifungico"
## [1] "43"              "-1e-04"          "-2e-04"          "espironolactona"
## [1] "42"                  "-3e-04"              "-1e-04"
## [4] "histopatologia_qtde"
## [1] "41"                        "-7e-04"
## [3] "-4e-04"                    "outros_proced_cirurgicos"
## [1] "40"         "-0.0012"    "-5e-04"     "nyha_basal"
## [1] "39"      "-0.001"  "1e-04"   "cultura"
## [1] "38"                      "-0.0016"
## [3] "-6e-04"                  "admission_t0_emergency"
## [1] "37"        "-0.0017"   "0"         "ultrassom"
## [1] "36"             "-0.0014"        "2e-04"          "insuf_cardiaca"
## [1] "35"      "-0.0016" "-2e-04"  "mpp"
## [1] "34"                  "-0.002"             "-4e-04"
## [4] "exames_imagem_qtde"
## [1] "33"      "-0.0032" "-0.0011" "dva"
## [1] "32"      "-0.0028" "4e-04"   "holter"
## [1] "31"            "-0.003"        "-2e-04"        "heart_disease"
## [1] "30"                 "-0.003"             "0"
```

```
## [4] "cied_final_group_1"
## [1] "29"       "-0.0027" "2e-04"   "aco"
## [1] "28"        "-0.0028"  "-1e-04"   "ieca_bra"
## [1] "27"                    "-0.0039"               "-0.001"
## [4] "admission_pre_t0_180d"
## [1] "26"             "-0.0047"        "-8e-04"         "betabloqueador"
## [1] "25"        "-0.0059"  "-0.0012"  "estatina"
## [1] "24"           "-0.0067"     "-9e-04"      "bloq_calcio"
## [1] "23"                "-0.0069"          "-2e-04"
## [4] "equipe_multiprof"
## [1] "23"                  "-0.0069"            "0.0025"
## [4] "procedure_type_new"
## [1] "22"           "-0.008"      "-0.0011"     "laboratorio"
## [1] "21"                     "-0.0085"               "-5e-04"
## [4] "metodos_graficos_qtde"
## [1] "20"            "-0.0081"      "4e-04"        "cied_final_1"
## [1] "19"                    "-0.0094"              "-0.0013"
## [4] "meds_cardiovasc_qtde"
## [1] "18"                   "-0.0092"             "2e-04"
## [4] "ventilacao_mecanica"
## [1] "17"                 "-0.0084"           "8e-04"
## [4] "anticonvulsivante"
## [1] "16"             "-0.0085"       "-1e-04"        "psicofarmacos"
## [1] "15"                         "-0.0094"
## [3] "-9e-04"                     "underlying_heart_disease"
## [1] "14"                    "-0.0087"               "7e-04"
## [4] "proced_invasivos_qtde"
## [1] "13"             "-0.0097"       "-0.001"        "vasodilatador"
## [1] "12"                   "-0.009"              "8e-04"
## [4] "comorbidities_count"
## [1] "12"      "-0.009" "0.0022" "bic"
## [1] "12"       "-0.009"   "0.0035"   "digoxina"
## [1] "12"             "-0.009"        "0.0026"        "antiarritmico"
## [1] "12"      "-0.009" "0.0044" "icu_t0"
## [1] "11"        "-0.0099"   "-9e-04"    "diuretico"
## [1] "10"              "-0.0082"         "0.0017"          "education_level"
## [1] "9"                     "-0.0081"              "1e-04"
## [4] "meds_antimicrobianos"
## [1] "8"                 "-0.0128"          "-0.0046"
## [4] "classe_meds_qtde"
## [1] "7"                      "-0.0119"
## [3] "9e-04"                  "analises_clinicas_qtde"
## [1] "7"                      "-0.0119"
## [3] "0.0135"                 "admission_pre_t0_count"
## [1] "7"             "-0.0119"       "0.0415"        "hospital_stay"
```

```
selection_results %>%
  rename(Features = `Number of Features`) %>%
  niceFormatting(digits = 4, label = 1)
```

Table 1:

Tested Feature	Dropped	Features	CV AUC	CV AUC Std Error	Total AUC Loss	Instant AUC Loss
None	TRUE	76	0.6907	0.0082	0.0000	0.0000
All unimportant	TRUE	45	0.6905	0.0081	0.0001	0.0001
antifungico	TRUE	44	0.6906	0.0080	0.0001	0.0000
espironolactona	TRUE	43	0.6908	0.0081	-0.0001	-0.0002
histopatologia_qtde	TRUE	42	0.6910	0.0081	-0.0003	-0.0001
outros_proced_cirurgicos	TRUE	41	0.6914	0.0081	-0.0007	-0.0004
nyha_basal	TRUE	40	0.6918	0.0082	-0.0012	-0.0005
cultura	TRUE	39	0.6917	0.0083	-0.0010	0.0001

Table 1: *(continued)*

Tested Feature	Dropped	Features	CV AUC	CV AUC Std Error	Total AUC Loss	Instant AUC Loss
admission_t0_emergency	TRUE	38	0.6923	0.0083	-0.0016	-0.0006
ultrassom	TRUE	37	0.6923	0.0082	-0.0017	0.0000
insuf_cardiaca	TRUE	36	0.6921	0.0083	-0.0014	0.0002
mpp	TRUE	35	0.6923	0.0083	-0.0016	-0.0002
exames_imagem_qtde	TRUE	34	0.6927	0.0081	-0.0020	-0.0004
dva	TRUE	33	0.6938	0.0082	-0.0032	-0.0011
holter	TRUE	32	0.6934	0.0083	-0.0028	0.0004
heart_disease	TRUE	31	0.6937	0.0082	-0.0030	-0.0002
cied_final_group_1	TRUE	30	0.6936	0.0083	-0.0030	0.0000
aco	TRUE	29	0.6934	0.0085	-0.0027	0.0002
ieca_bra	TRUE	28	0.6935	0.0084	-0.0028	-0.0001
admission_pre_t0_180d	TRUE	27	0.6945	0.0084	-0.0039	-0.0010
betabloqueador	TRUE	26	0.6954	0.0086	-0.0047	-0.0008
estatina	TRUE	25	0.6966	0.0088	-0.0059	-0.0012
bloq_calcio	TRUE	24	0.6974	0.0088	-0.0067	-0.0009
equipe_multiprof	TRUE	23	0.6976	0.0086	-0.0069	-0.0002
procedure_type_new	FALSE	22	0.6951	0.0087	-0.0069	0.0025
laboratorio	TRUE	22	0.6987	0.0087	-0.0080	-0.0011
metodos_graficos_qtde	TRUE	21	0.6992	0.0084	-0.0085	-0.0005
cied_final_1	TRUE	20	0.6988	0.0086	-0.0081	0.0004
meds_cardiovasc_qtde	TRUE	19	0.7001	0.0085	-0.0094	-0.0013
ventilacao_mecanica	TRUE	18	0.6999	0.0083	-0.0092	0.0002
anticonvulsivante	TRUE	17	0.6991	0.0083	-0.0084	0.0008
psicofarmacos	TRUE	16	0.6992	0.0084	-0.0085	-0.0001
underlying_heart_disease	TRUE	15	0.7001	0.0084	-0.0094	-0.0009
proced_invasivos_qtde	TRUE	14	0.6994	0.0081	-0.0087	0.0007
vasodilatador	TRUE	13	0.7004	0.0088	-0.0097	-0.0010
comorbidities_count	TRUE	12	0.6996	0.0088	-0.0090	0.0008
bic	FALSE	11	0.6974	0.0085	-0.0090	0.0022
digoxina	FALSE	11	0.6961	0.0087	-0.0090	0.0035
antiarritmico	FALSE	11	0.6970	0.0091	-0.0090	0.0026
icu_t0	FALSE	11	0.6953	0.0088	-0.0090	0.0044
diuretico	TRUE	11	0.7006	0.0089	-0.0099	-0.0009
education_level	TRUE	10	0.6989	0.0090	-0.0082	0.0017
meds_antimicrobianos	TRUE	9	0.6988	0.0088	-0.0081	0.0001
classe_meds_qtde	TRUE	8	0.7034	0.0082	-0.0128	-0.0046
analises_clinicas_qtde	TRUE	7	0.7026	0.0087	-0.0119	0.0009
admission_pre_t0_count	FALSE	6	0.6891	0.0087	-0.0119	0.0135
hospital_stay	FALSE	6	0.6611	0.0078	-0.0119	0.0415

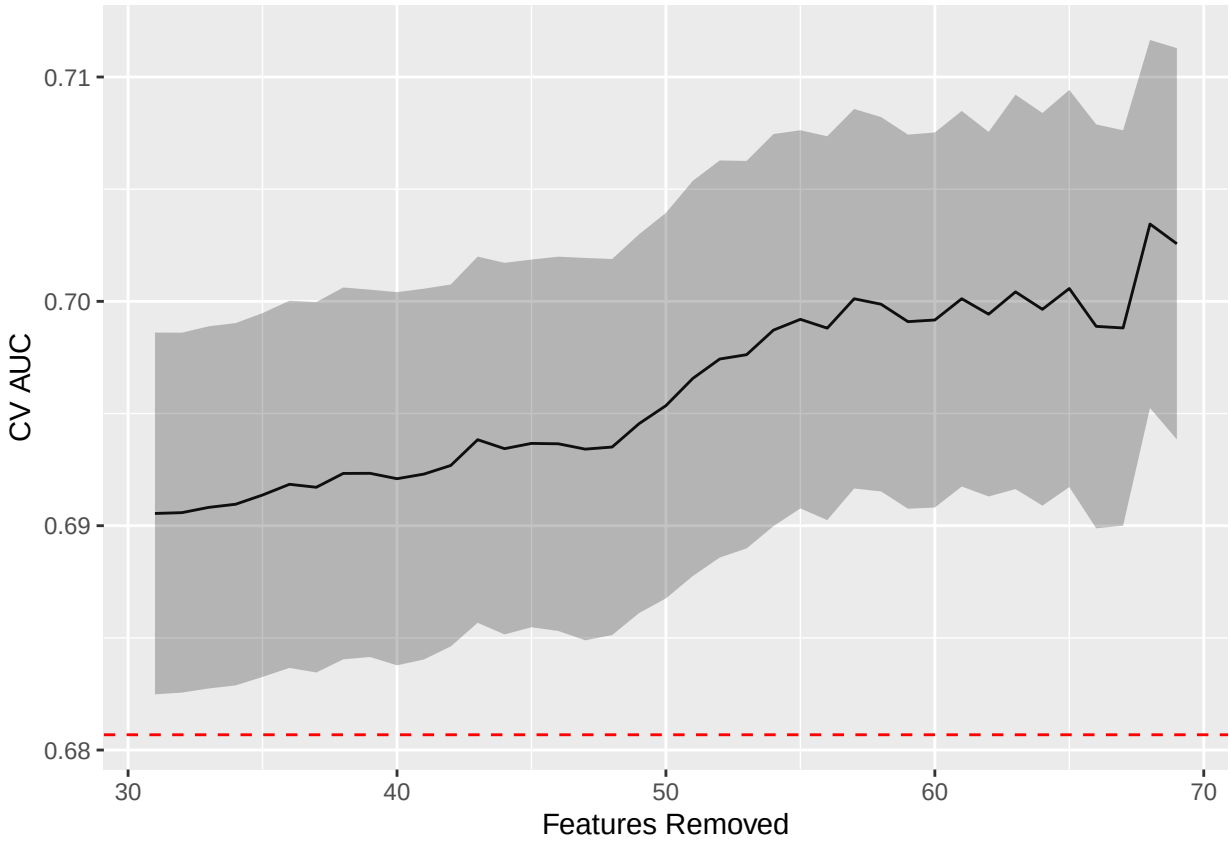
```
selected_features <- current_features

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: 0.692"
```

```
 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 %>%
  filter(Dropped) %>%
  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")
```



Hyperparameter tuning

Selected features:

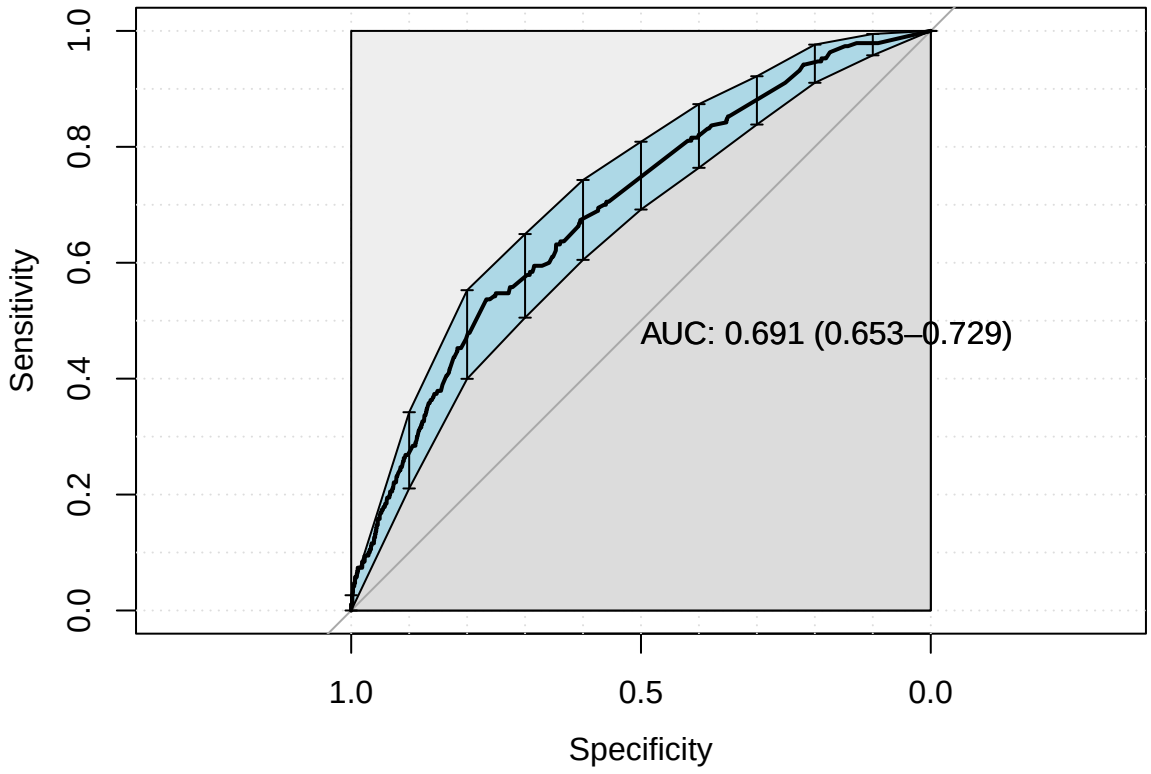
```
gluedown::md_order(selected_features, seq = TRUE, pad = TRUE)
```

1. hospital_stay
2. admission_pre_t0_count
3. antiarritmico
4. digoxina
5. bic
6. icu_t0
7. procedure_type_new

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_tuning <- function(recipe) {

  lightgbm_spec <- boost_tree(
    trees = tune(),
    min_n = tune(),
    tree_depth = tune(),
    learn_rate = tune(),
    sample_size = 1.0
  ) %>%
    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(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")

  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)
```

```
  lightgbm_parameters <- lightgbm_tune %>%
    show_best("roc_auc", n = 1) %>%
    select(trees, min_n, tree_depth, learn_rate) %>%
    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: 0.05"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3481   88
##    1 1059  102
##
##                Accuracy : 0.7575
##                  95% CI : (0.745, 0.7697)
##     No Information Rate : 0.9598
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.088
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.76674
##             Specificity : 0.53684
```

```
##          Pos Pred Value : 0.97534
##          Neg Pred Value : 0.08786
##              Prevalence : 0.95983
##          Detection Rate : 0.73594
##    Detection Prevalence : 0.75455
##       Balanced Accuracy : 0.65179
##
##        'Positive' Class : 0
##
```

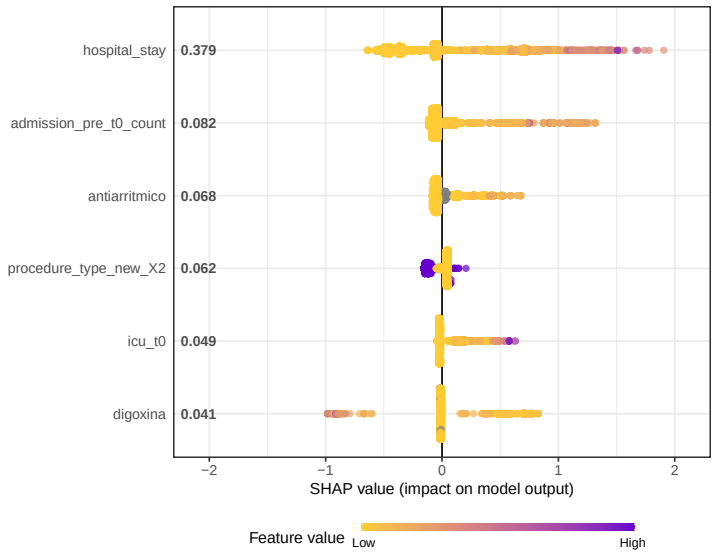
```r
final_lightgbm_fit <- standard_results$fit
lightgbm_parameters <- standard_results$parameters

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

# Save the final model. We need it for the calculator
lgb.save(
  parsnip::extract_fit_engine(final_lightgbm_fit),
  sprintf("./results/%s/final_model.txt", outcome_column)
)
saveRDS(final_lightgbm_fit,
        sprintf("./results/%s/final_model_wf.rds", outcome_column))
```

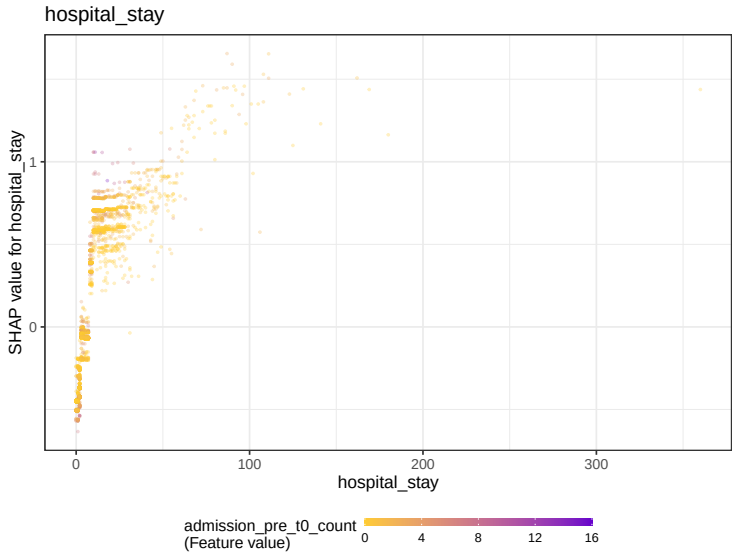
SHAP values

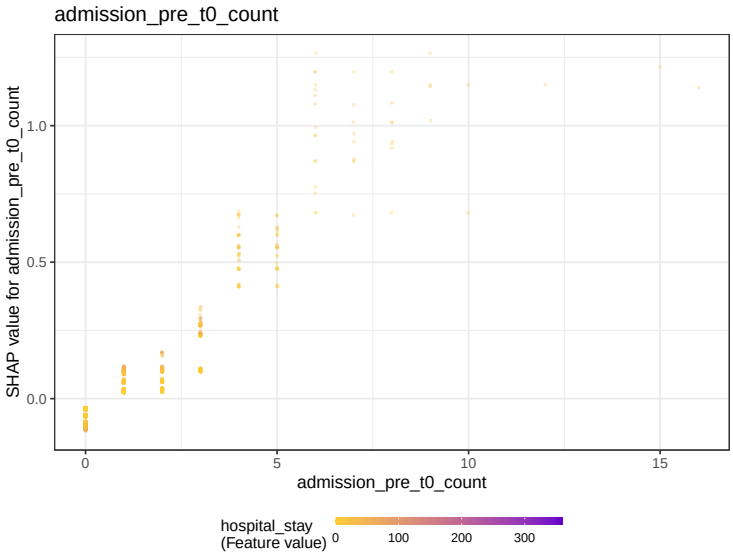
```r
lightgbm_model <- parsnip::extract_fit_engine(final_lightgbm_fit)

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(6, length(selected_features))
plotted <- 0

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)) {
  p <- shap.plot.dependence(
    shap,
    x = x,
    color_feature = "auto",
    smooth = FALSE,
    jitter_width = 0.01,
    alpha = 0.3
  ) +
    labs(title = x)
```

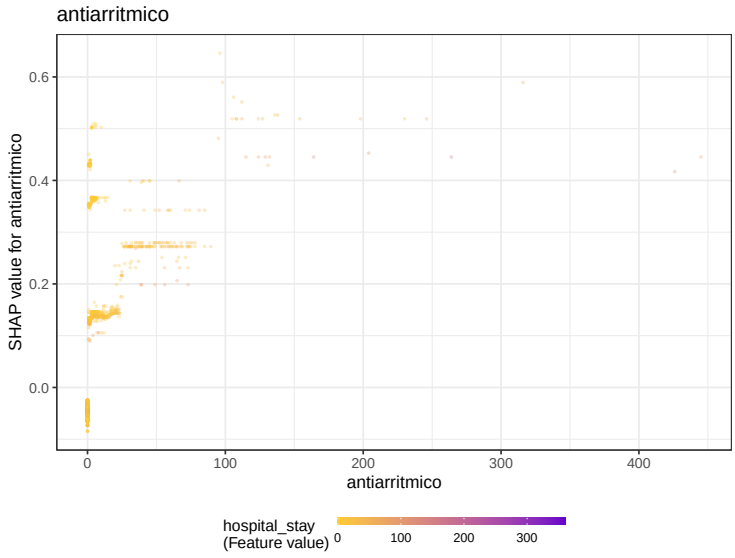
```r
  if (plotted < n_plots) {
    print(p)
    plotted <- plotted + 1
  }

  ggsave(sprintf("./auxiliar/final_model/shap_plots/%s.png", x),
         plot = p,
         dpi = 300)
}
```

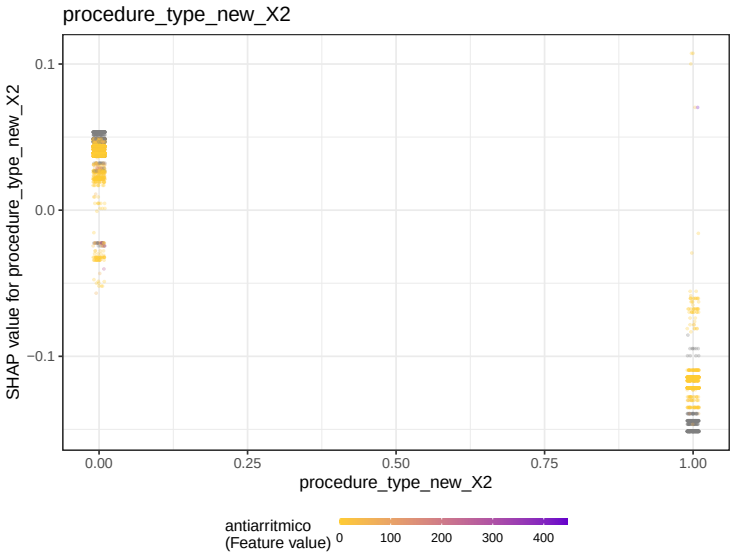
```
## Saving 6.5 x 5 in image
## Saving 6.5 x 5 in image
## Warning: Removed 1050 rows containing missing values (geom_point).
## Saving 6.5 x 5 in image
## Warning: Removed 1050 rows containing missing values (geom_point).
## Saving 6.5 x 5 in image
## Saving 6.5 x 5 in image
## Warning: Removed 1050 rows containing missing values (geom_point).
## Saving 6.5 x 5 in image
## Warning: Removed 1050 rows containing missing values (geom_point).
## Saving 6.5 x 5 in image
## Warning: Removed 1077 rows containing missing values (geom_point).
## Saving 6.5 x 5 in image
## Saving 6.5 x 5 in image
```

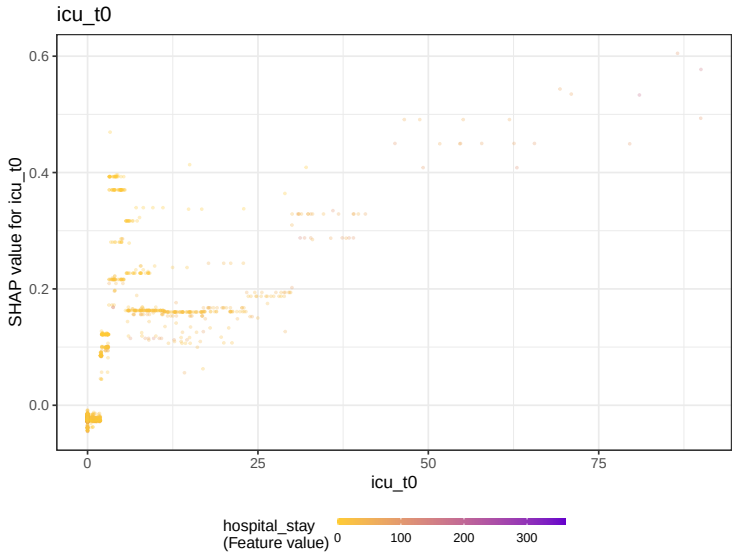


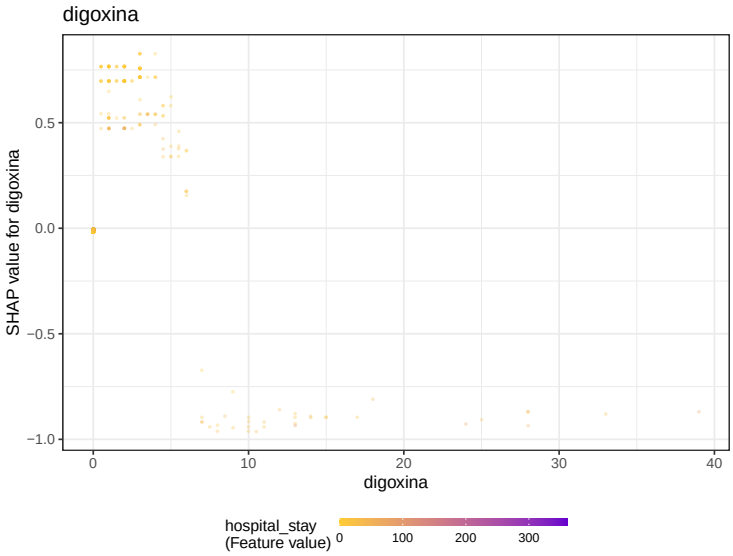












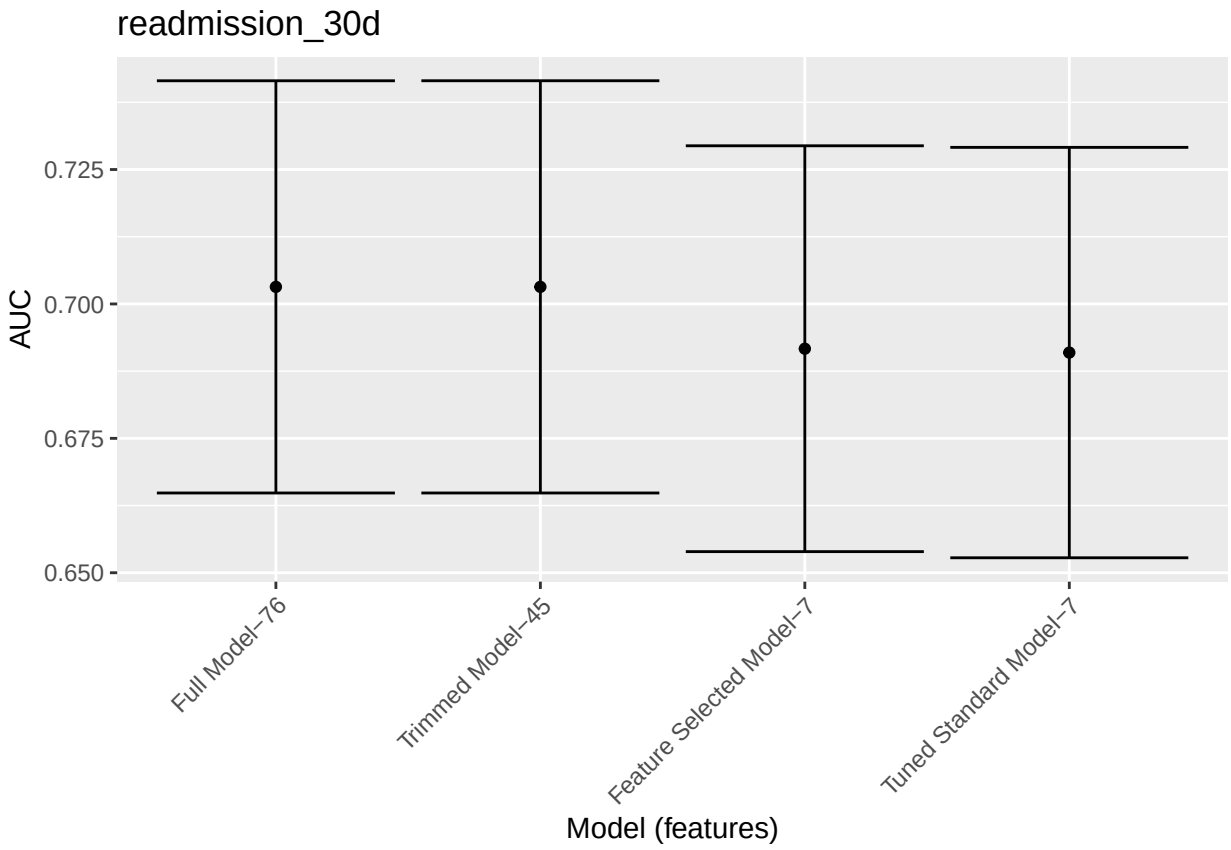

```
## $num_iterations
## [1] 96
##
## $learning_rate
## [1] 0.05568281
##
## $max_depth
```

```
## [1] 2
##
## $feature_fraction
## [1] 1
##
## $min_data_in_leaf
## [1] 56
##
## $min_gain_to_split
## [1] 0
##
## $bagging_fraction
## [1] 1
##
## $num_class
## [1] 1
##
## $objective
## [1] "binary"
##
## $num_threads
## $num_threads$num_threads
## [1] 0
##
##
## $nthread
## [1] 8
##
## $seed
## [1] 60956
##
## $deterministic
## [1] TRUE
##
## $verbose
## [1] -1
##
## $metric
## list()
##
## $interaction_constraints
## list()
##
## $feature_pre_filter
## [1] FALSE
```

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
) %>%
  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))
```