Final Model - death_180days

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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= death_180days
## .  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
predict <- stats::predict
```

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

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

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

features_list = c(cat_features_list, num_features_list)
```

```
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:

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

1. sex
2. age
3. education_level
4. underlying_heart_disease
5. heart_disease
6. nyha_basal

7. hypertension
8. prior_mi
9. heart_failure
10. af
11. cardiac_arrest
12. valvopathy
13. diabetes
14. renal_failure
15. hemodialysis
16. stroke
17. copd
18. cancer
19. comorbidities_count
20. procedure_type_1
21. reop_type_1
22. procedure_type_new
23. cied_final_1
24. cied_final_group_1
25. admission_pre_t0_count
26. admission_pre_t0_180d
27. year_adm_t0
28. icu_t0
29. dialysis_t0
30. admission_t0_emergency
31. aco
32. antiarritmico
33. ieca_bra
34. dva
35. digoxina
36. estatina
37. diuretico
38. vasodilatador
39. insuf_cardiaca
40. espironolactona
41. antiplaquetario_ev
42. insulina
43. psicofarmacos
44. antifungico
45. classe_meds_qtde
46. meds_cardiovasc_qtde
47. meds_antimicrobianos
48. vni
49. ventilacao_mecanica
50. transplante_cardiaco
51. outros_proced_cirurgicos
52. icp
53. cateterismo
54. cateter_venoso_central
55. proced_invasivos_qtde
56. transfusao
57. interconsulta
58. equipe_multiprof
59. holter
60. teste_esforco
61. metodos_graficos_qtde
62. laboratorio
63. cultura
64. analises_clinicas_qtde
65. citologia
66. histopatologia_qtde
67. angiografia

68. aortografia
69. arteriografia
70. cintilografia
71. ecocardiograma
72. endoscopia
73. ultrassom
74. tomografia
75. ressonancia
76. exames_imagem_qtde
77. bic
78. 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 <- read_yaml(
  sprintf(
    "./auxiliar/model_selection/hyperparameters/%s.yaml",
    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: 0.798"
```

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

```
## [1] "Full Model Test AUC: 0.833"
```

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. valvopathy
4. hemodialysis
5. cancer
6. procedure_type_1
7. reop_type_1
8. procedure_type_new
9. dialysis_t0
10. digoxina

11. insulina
12. antifungico
13. vni
14. transplante_cardiaco
15. outros_proced_cirurgicos
16. icp
17. cateter_venoso_central
18. transfusao
19. teste_esforco
20. histopatologia_qtde
21. angiografia
22. aortografia
23. arteriografia
24. ressonancia
25. bic

```
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: 0.797"
```

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

```
## [1] "Trimmed Model Test AUC: 0.833"
```

```
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] "52"                    "8e-04"                 "2e-04"
## [4] "admission_t0_emergency"
## [1] "51"             "3e-04"          "-5e-04"         "cardiac_arrest"
## [1] "50"           "-8e-04"       "-0.0011"      "hypertension"
## [1] "49"     "-6e-04" "1e-04"  "aco"
## [1] "48"     "-4e-04" "3e-04"  "holter"
## [1] "47"                 "-2e-04"             "2e-04"               "ventilacao_mecanica"
## [1] "46"     "-2e-04" "0"      "copd"
## [1] "45"        "4e-04"     "7e-04"     "ultrassom"
## [1] "44"         "-0.0011"    "-0.0015"    "tomografia"
## [1] "43"                "-9e-04"             "2e-04"              "antiplaquetario_ev"
## [1] "42"           "-0.0023"       "-0.0014"       "heart_disease"
## [1] "41"         "-0.0028"    "-5e-04"     "endoscopia"
## [1] "40"           "-0.0011"      "0.0017"       "cied_final_1"
## [1] "39"     "-6e-04" "5e-04"  "sex"
## [1] "38"        "-0.0013"   "-7e-04"    "citologia"
## [1] "37"       "-0.0025"  "-0.0012"  "diabetes"
## [1] "36"          "-0.0014"     "0.0011"      "cateterismo"
## [1] "35"                "-0.0024"            "-0.0011"            "cied_final_group_1"
## [1] "34"      "-0.0023" "1e-04"   "stroke"
## [1] "33"            "-0.0037"       "-0.0013"       "renal_failure"
## [1] "32"      "-0.0025" "0.0011"  "af"
## [1] "31"      "-0.0025" "0"       "cultura"
```

```
## [1] "30"              "-0.0054"        "-0.0029"        "ecocardiograma"
## [1] "29"                    "-0.0037"               "0.0018"
## [4] "proced_invasivos_qtde"
## [1] "28"               "-0.0034"          "2e-04"            "classe_meds_qtde"
## [1] "27"                    "-0.0032"                "2e-04"
## [4] "analises_clinicas_qtde"
## [1] "26"       "-0.0042"  "-0.001"   "estatina"
## [1] "25"             "-0.0046"        "-4e-04"         "insuf_cardiaca"
## [1] "24"            "-0.0031"       "0.0015"        "interconsulta"
## [1] "23"            "-0.0045"       "-0.0014"       "antiarritmico"
## [1] "22"                        "-0.0038"                    "7e-04"
## [4] "underlying_heart_disease"
## [1] "21"                    "-0.0058"              "-0.0021"              "meds_antimicrobianos"
## [1] "20"            "-0.0067"       "-9e-04"        "cintilografia"
## [1] "19"                 "-0.0073"            "-6e-04"             "exames_imagem_qtde"
## [1] "18"      "-0.0061" "0.0012"  "dva"
## [1] "17"            "-0.0059"       "1e-04"         "psicofarmacos"
## [1] "16"                    "-0.0042"               "0.0017"
## [4] "admission_pre_t0_180d"
## [1] "15"        "-0.0053"   "-0.0011"   "diuretico"
## [1] "14"                    "-0.0061"               "-8e-04"
## [4] "metodos_graficos_qtde"
## [1] "13"         "-0.0064"    "-3e-04"     "nyha_basal"
## [1] "12"      "-0.0067" "-3e-04"  "icu_t0"
## [1] "11"               "-0.0062"          "5e-04"            "equipe_multiprof"
## [1] "10"                   "-0.0091"              "-0.0028"              "meds_cardiovasc_qtde"
## [1] "10"               "-0.0091"         "0.0172"          "education_level"
## [1] "10"            "-0.0091"       "0.0027"        "vasodilatador"
## [1] "10"                      "-0.0091"               "0.0154"
## [4] "admission_pre_t0_count"
## [1] "10"                    "-0.0091"             "0.0103"              "comorbidities_count"
## [1] "9"        "-0.0086"  "4e-04"    "ieca_bra"
## [1] "9"               "-0.0086"         "0.0137"          "espironolactona"
## [1] "9"           "-0.0086"     "0.0062"      "laboratorio"
## [1] "9"           "-0.0086"     "0.0134"      "year_adm_t0"
## [1] "9"       "-0.0086" "0.0108"  "age"
## [1] "9"             "-0.0086"       "0.0198"        "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	78	0.7976	0.0069	0.0000	0.0000
All unimportant	TRUE	53	0.7970	0.0072	0.0007	0.0007
admission_t0_emergency	TRUE	52	0.7968	0.0070	0.0008	0.0002
cardiac_arrest	TRUE	51	0.7973	0.0070	0.0003	-0.0005
hypertension	TRUE	50	0.7984	0.0070	-0.0008	-0.0011
aco	TRUE	49	0.7983	0.0071	-0.0006	0.0001
holter	TRUE	48	0.7980	0.0073	-0.0004	0.0003
ventilacao_mecanica	TRUE	47	0.7978	0.0071	-0.0002	0.0002
copd	TRUE	46	0.7978	0.0073	-0.0002	0.0000
ultrassom	TRUE	45	0.7972	0.0072	0.0004	0.0007
tomografia	TRUE	44	0.7987	0.0071	-0.0011	-0.0015
antiplaquetario_ev	TRUE	43	0.7985	0.0069	-0.0009	0.0002
heart_disease	TRUE	42	0.7999	0.0068	-0.0023	-0.0014
endoscopia	TRUE	41	0.8004	0.0069	-0.0028	-0.0005
cied_final_1	TRUE	40	0.7987	0.0070	-0.0011	0.0017

Table 1: *(continued)*

Tested Feature	Dropped	Features	CV AUC	CV AUC Std Error	Total AUC Loss	Instant AUC Loss
sex	TRUE	39	0.7982	0.0071	-0.0006	0.0005
citologia	TRUE	38	0.7990	0.0070	-0.0013	-0.0007
diabetes	TRUE	37	0.8001	0.0073	-0.0025	-0.0012
cateterismo	TRUE	36	0.7990	0.0071	-0.0014	0.0011
cied_final_group_1	TRUE	35	0.8001	0.0068	-0.0024	-0.0011
stroke	TRUE	34	0.8000	0.0067	-0.0023	0.0001
renal_failure	TRUE	33	0.8013	0.0068	-0.0037	-0.0013
af	TRUE	32	0.8001	0.0069	-0.0025	0.0011
cultura	TRUE	31	0.8001	0.0069	-0.0025	0.0000
ecocardiograma	TRUE	30	0.8031	0.0064	-0.0054	-0.0029
proced_invasivos_qtde	TRUE	29	0.8013	0.0065	-0.0037	0.0018
classe_meds_qtde	TRUE	28	0.8011	0.0067	-0.0034	0.0002
analises_clinicas_qtde	TRUE	27	0.8009	0.0066	-0.0032	0.0002
estatina	TRUE	26	0.8018	0.0069	-0.0042	-0.0010
insuf_cardiaca	TRUE	25	0.8022	0.0068	-0.0046	-0.0004
interconsulta	TRUE	24	0.8007	0.0073	-0.0031	0.0015
antiarritmico	TRUE	23	0.8021	0.0075	-0.0045	-0.0014
underlying_heart_disease	TRUE	22	0.8014	0.0072	-0.0038	0.0007
meds_antimicrobianos	TRUE	21	0.8035	0.0073	-0.0058	-0.0021
cintilografia	TRUE	20	0.8043	0.0076	-0.0067	-0.0009
exames_imagem_qtde	TRUE	19	0.8049	0.0078	-0.0073	-0.0006
dva	TRUE	18	0.8037	0.0074	-0.0061	0.0012
psicofarmacos	TRUE	17	0.8036	0.0077	-0.0059	0.0001
admission_pre_t0_180d	TRUE	16	0.8018	0.0075	-0.0042	0.0017
diuretico	TRUE	15	0.8030	0.0076	-0.0053	-0.0011
metodos_graficos_qtde	TRUE	14	0.8037	0.0075	-0.0061	-0.0008
nyha_basal	TRUE	13	0.8040	0.0078	-0.0064	-0.0003
icu_t0	TRUE	12	0.8044	0.0076	-0.0067	-0.0003
equipe_multiprof	TRUE	11	0.8038	0.0074	-0.0062	0.0005
meds_cardiovasc_qtde	TRUE	10	0.8067	0.0073	-0.0091	-0.0028
education_level	FALSE	9	0.7894	0.0075	-0.0091	0.0172
vasodilatador	FALSE	9	0.8040	0.0068	-0.0091	0.0027
admission_pre_t0_count	FALSE	9	0.7913	0.0064	-0.0091	0.0154
comorbidities_count	FALSE	9	0.7964	0.0069	-0.0091	0.0103
ieca_bra	TRUE	9	0.8063	0.0079	-0.0086	0.0004
espironolactona	FALSE	8	0.7926	0.0083	-0.0086	0.0137
laboratorio	FALSE	8	0.8001	0.0081	-0.0086	0.0062
year_adm_t0	FALSE	8	0.7928	0.0072	-0.0086	0.0134
age	FALSE	8	0.7954	0.0074	-0.0086	0.0108
hospital_stay	FALSE	8	0.7864	0.0105	-0.0086	0.0198

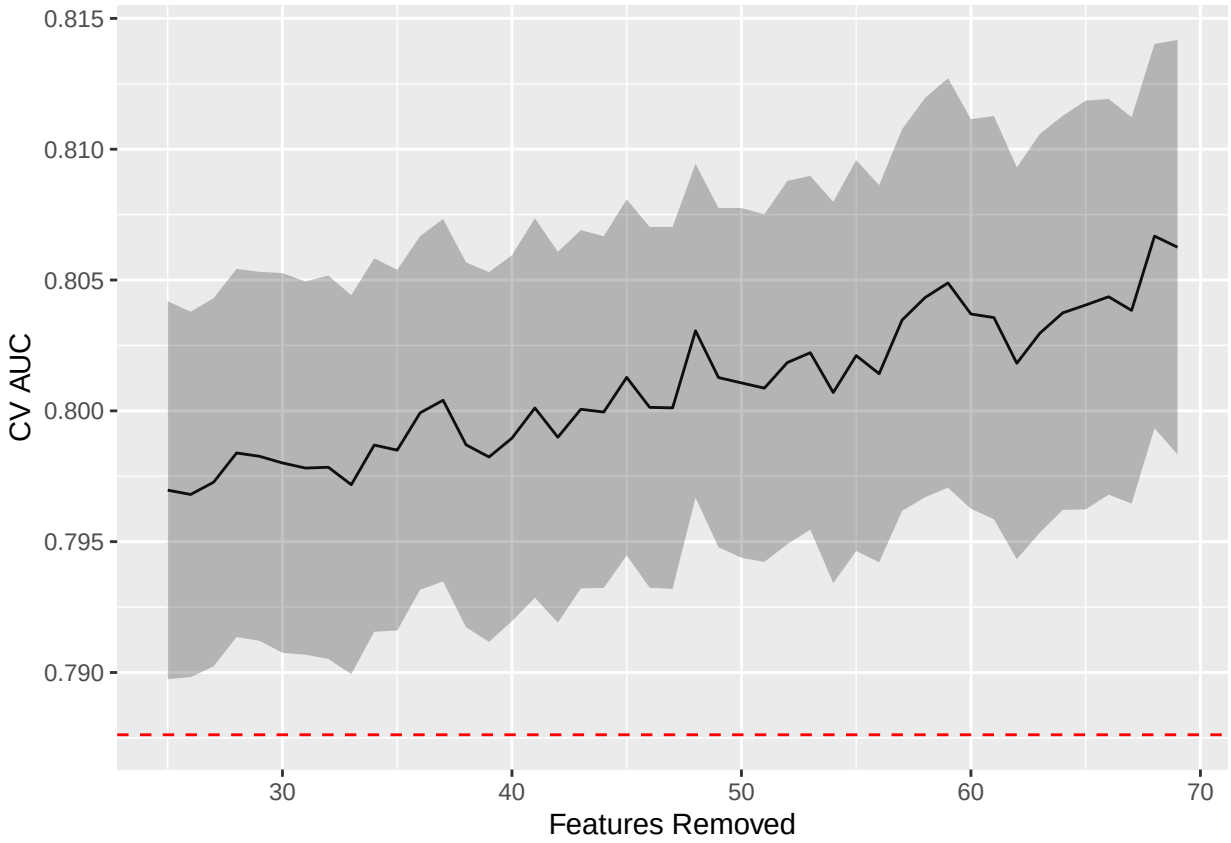
```
selected_features <- current_features

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: 0.806"
```

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

```
## [1] "Selected Model Test AUC: 0.827"
```

```
 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:

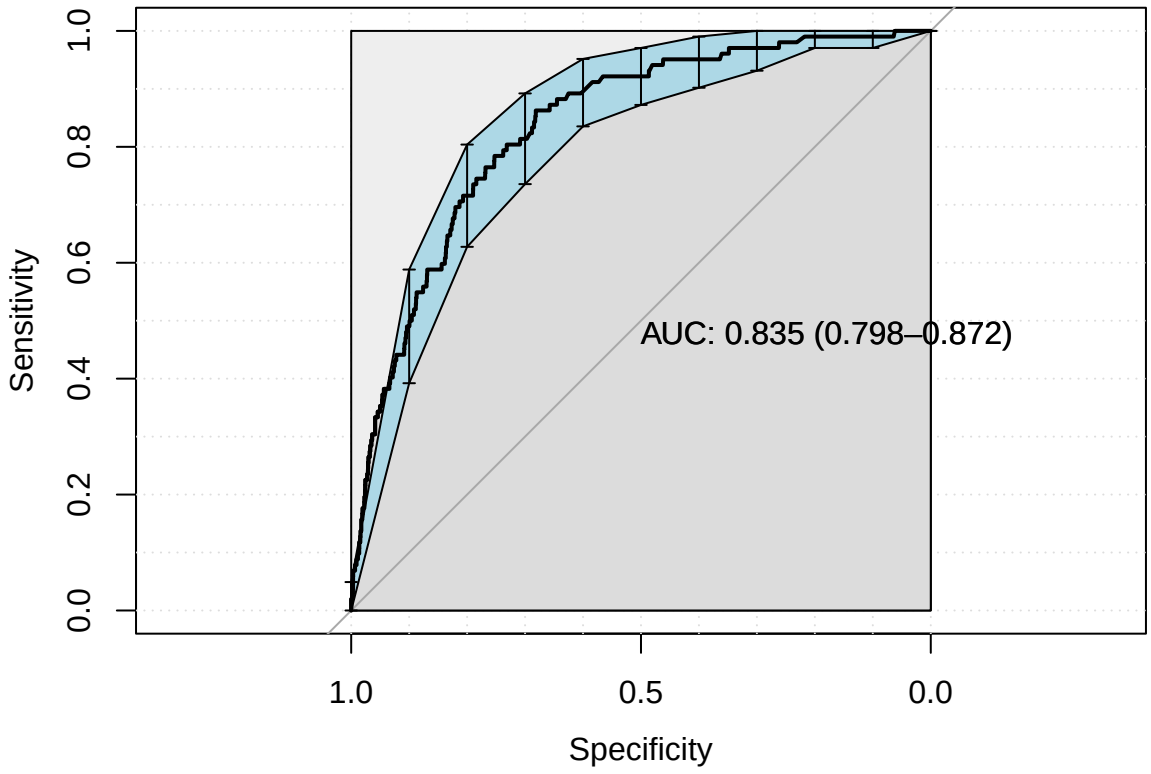
```
gluedown::md_order(selected_features, seq = TRUE, pad = TRUE)
```

1. hospital_stay
2. age
3. year_adm_t0
4. espironolactona
5. education_level
6. laboratorio
7. comorbidities_count
8. admission_pre_t0_count
9. vasodilatador

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: 0.02"
## Confusion Matrix and Statistics
##
##     reference
## data    0    1
##    0 3154   14
##    1 1474   88
##
##                Accuracy : 0.6854
##                  95% CI : (0.672, 0.6986)
##     No Information Rate : 0.9784
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.068
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.68150
##             Specificity : 0.86275
```

```
##          Pos Pred Value : 0.99558
##          Neg Pred Value : 0.05634
##              Prevalence : 0.97844
##          Detection Rate : 0.66681
##    Detection Prevalence : 0.66977
##       Balanced Accuracy : 0.77212
##
##        'Positive' Class : 0
##
```

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

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

# 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))
```

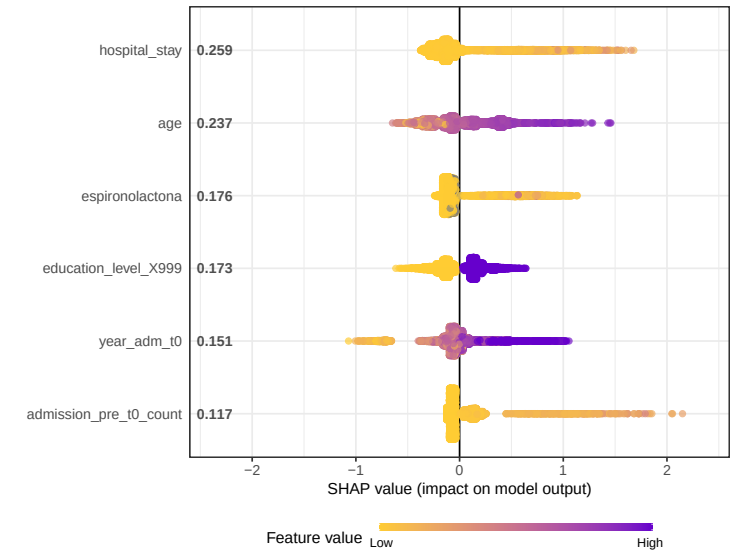
SHAP values

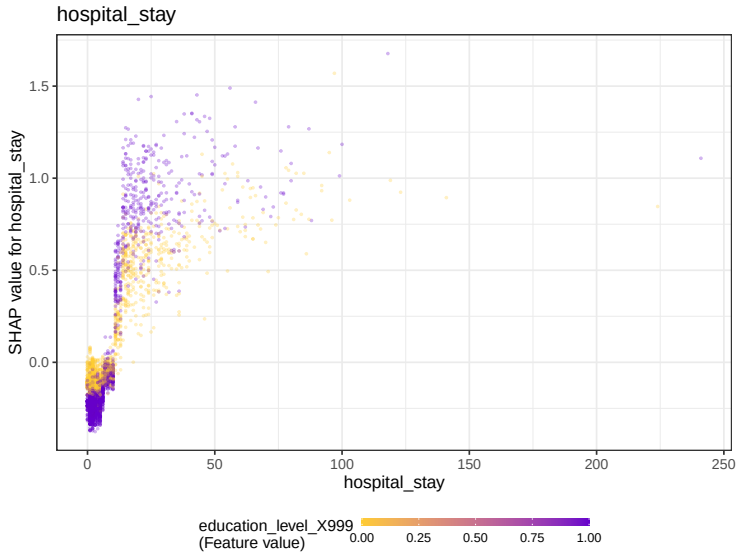
```
lightgbm_model <- parsnip::extract_fit_engine(final_lightgbm_fit)

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)

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

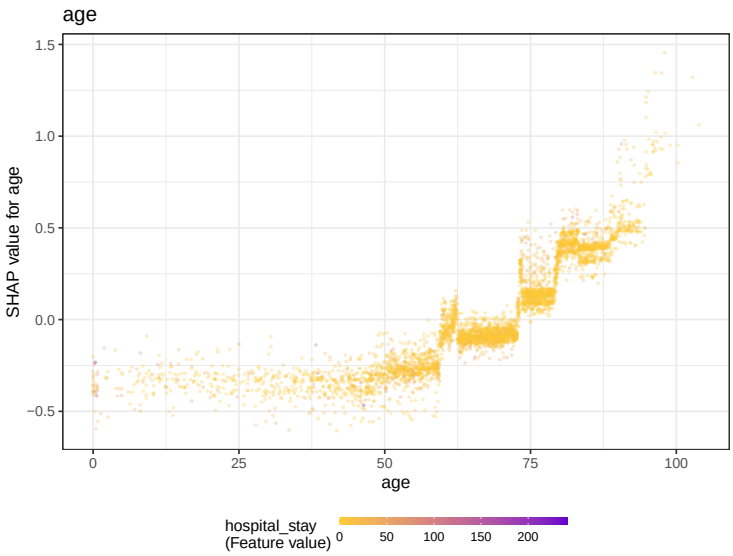
```
  # ggsave(sprintf("./auxiliar/final_model/shap_plots/%s/%s.png", outcome_column, x),
  #        plot = p,
  #        dpi = 300)
}
```

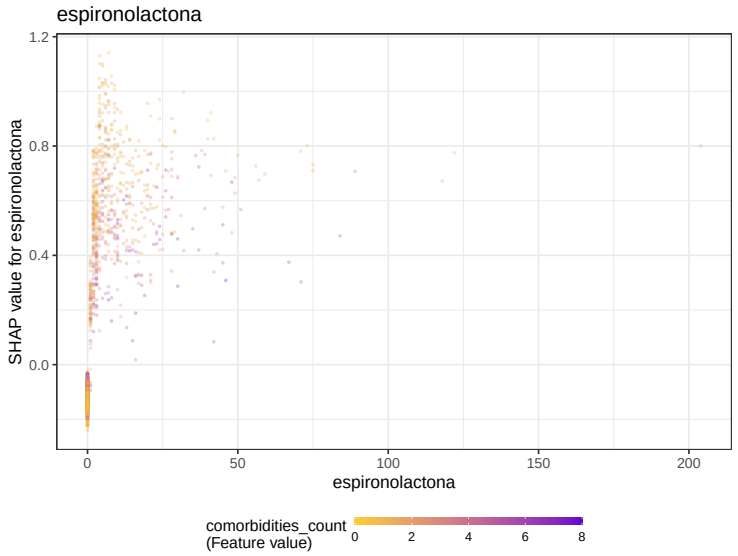
```
## Warning: Removed 1041 rows containing missing values (geom_point).
```

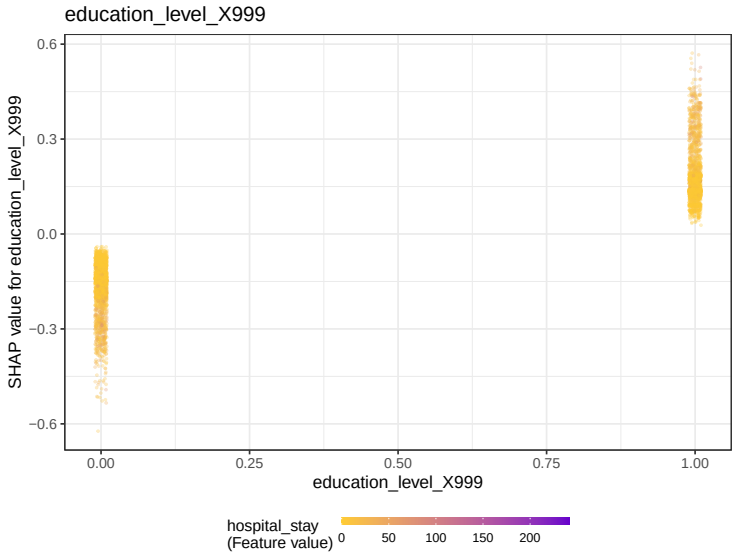
```
## Warning: Removed 7 rows containing missing values (geom_point).
```

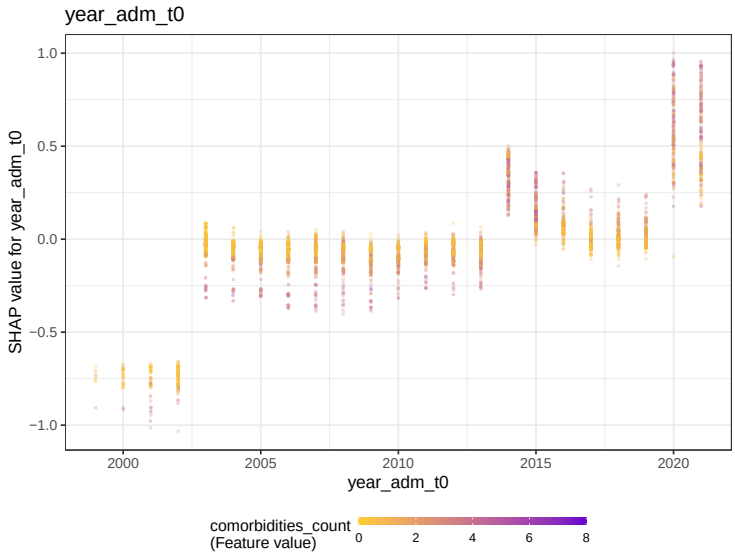


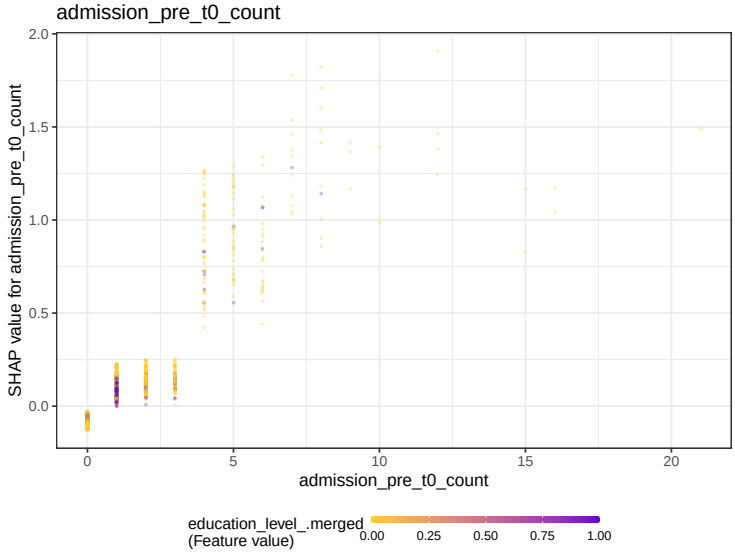










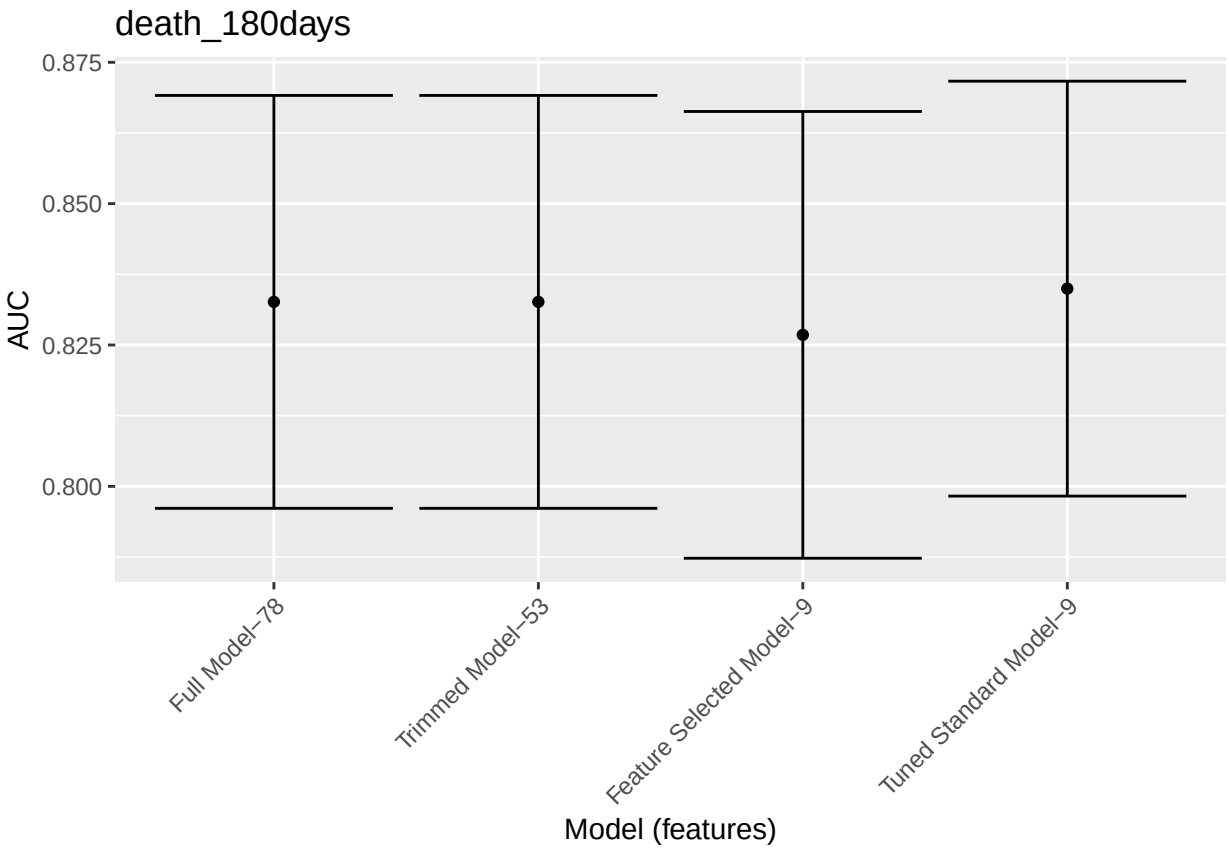



```
## $num_iterations
## [1] 55
##
## $learning_rate
## [1] 0.0477388
##
## $max_depth
## [1] 4
##
## $feature_fraction
## [1] 1
##
## $min_data_in_leaf
## [1] 87
##
## $min_gain_to_split
## [1] 0
##
## $bagging_fraction
## [1] 1
##
## $num_class
## [1] 1
##
## $objective
```

```
## [1] "binary"
##
## $num_threads
## $num_threads$num_threads
## [1] 0
##
##
## $nthread
## [1] 8
##
## $seed
## [1] 45791
##
## $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))
```




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