Final Model - death_2year

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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_2year
## .  k = double 1= 10
## .  grid_size = double 1= 50
## .  repeats = double 1= 2
```

Minutes to run: 0

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
```

Minutes to run: 0.001

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))
```

Minutes to run: 0.007

```
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)
```

Minutes to run: 0

Eligible features

```
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)
```

Minutes to run: 0

```
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)
```

Minutes to run: 0

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. comorbidities_count
19. procedure_type_1
20. reop_type_1
21. procedure_type_new
22. cied_final_1
23. cied_final_group_1
24. admission_pre_t0_count
25. admission_pre_t0_180d
26. year_adm_t0
27. icu_t0
28. dialysis_t0
29. admission_t0_emergency
30. aco
31. antiarritmico
32. ieca_bra
33. dva
34. digoxina
35. estatina
36. diuretico
37. vasodilatador
38. insuf_cardiaca
39. espironolactona
40. antiplaquetario_ev
41. insulina
42. psicofarmacos
43. antifungico
44. antiviral
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. angioplastia
54. cateterismo
55. cateter_venoso_central
56. proced_invasivos_qtde
57. transfusao
58. interconsulta
59. equipe_multiprof
60. holter
61. teste_esforco
62. tilt_teste
63. metodos_graficos_qtde
64. laboratorio
65. cultura
66. analises_clinicas_qtde
67. citologia
68. histopatologia_qtde
69. angio_tc
70. cintilografia
71. ecocardiograma
72. endoscopia
73. flebografia
74. pet_ct
75. ultrassom
76. tomografia
77. ressonancia
78. exames_imagem_qtde
79. bic
80. hospital_stay Minutes to run: 0

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)
```

Minutes to run: 0.001

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]
    )
  )
}
```

Minutes to run: 0

```
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: 0.798"
```

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

```
## [1] "Full Model Test AUC: 0.802"
```

Minutes to run: 0.397

Features with zero importance on the initial model:

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

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

1. hemodialysis
2. vni
3. transplante_cardiaco
4. angioplastia
5. cateter_venoso_central
6. transfusao
7. teste_esforco
8. histopatologia_qtde
9. ressonancia Minutes to run: 0

```
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: 0.802"
```

Minutes to run: 0.368

```
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] "70"                 "-8e-04"             "-0.0013"            "procedure_type_new"
## [1] "69"          "-1e-04"      "7e-04"       "flebografia"
## [1] "68"         "-5e-04"     "-4e-04"     "tilt_teste"
## [1] "67"        "1e-04"     "6e-04"     "antiviral"
## [1] "66"               "1e-04"            "0"                "procedure_type_1"
## [1] "65"       "-5e-04"   "-5e-04"   "angio_tc"
## [1] "64"         "-5e-04"      "-1e-04"      "antifungico"
## [1] "63"        "-6e-04"    "-1e-04"    "citologia"
## [1] "62"      "-0.0012" "-6e-04"  "holter"
## [1] "61"     "-7e-04" "5e-04"  "pet_ct"
## [1] "60"         "-4e-04"      "3e-04"       "cateterismo"
## [1] "59"     "-6e-04" "-1e-04" "stroke"
## [1] "58"             "-4e-04"         "1e-04"          "cardiac_arrest"
## [1] "57"      "-0.0016" "-0.0011" "copd"
## [1] "56"     "-0.001" "5e-04"  "sex"
## [1] "55"          "6e-04"       "0.0017"      "dialysis_t0"
## [1] "54"           "-0.0019"       "-0.0025"       "heart_failure"
## [1] "53"                "-0.0013"            "6e-04"              "antiplaquetario_ev"
## [1] "52"             "-0.0036"        "-0.0023"        "ecocardiograma"
## [1] "51"         "-0.0039"    "-4e-04"     "endoscopia"
## [1] "50"        "-0.0022"   "0.0018"    "ultrassom"
## [1] "49"         "-0.0021"    "0"          "tomografia"
## [1] "49"       "-0.0021"  "0.0022"   "prior_mi"
## [1] "48"       "-0.0033"  "-0.0011"  "insulina"
## [1] "47"         "-0.0025"    "8e-04"      "valvopathy"
## [1] "47"                    "-0.0025"               "0.0038"                "analises_clinicas_qtde"
## [1] "46"           "-0.0027"       "-2e-04"        "heart_disease"
## [1] "45"                   "-0.0028"               "-1e-04"               "admission_pre_t0_180d"
## [1] "44"       "-0.0018"  "0.001"    "digoxina"
## [1] "43"      "-0.0027" "-9e-04"  "icp"
## [1] "43"           "-0.0027"       "0.0021"        "renal_failure"
## [1] "42"           "-0.0037"       "-0.001"        "cintilografia"
## [1] "41"          "-0.0026"      "0.0011"       "hypertension"
## [1] "40"       "-0.0019"  "7e-04"    "diabetes"
## [1] "39"                  "-0.0015"             "4e-04"               "ventilacao_mecanica"
## [1] "38"                       "-0.0027"                  "-0.0012"                  "outros_proced_cirurgico
## [1] "37"                     "-0.0029"                "-2e-04"               "admission_t0_emergency"
## [1] "36"                    "-0.0043"               "-0.0015"              "proced_invasivos_qtde"
## [1] "36"          "-0.0043"     "0.0028"      "reop_type_1"
## [1] "36"           "-0.0043"       "0.0026"        "interconsulta"
## [1] "36"      "-0.0043" "0.0021"  "af"
## [1] "36"           "-0.0043"      "0.0029"       "cied_final_1"
## [1] "36"      "-0.0043" "0.0031"  "cultura"
## [1] "36"                "-0.0043"           "0.0027"             "cied_final_group_1"
## [1] "35"      "-0.0054" "-0.0011" "bic"
## [1] "35"      "-0.0054" "0.0035"  "dva"
## [1] "35"      "-0.0054" "0.0044"  "aco"
## [1] "35"                      "-0.0054"                  "0.0049"                   "underlying_heart_diseas
## [1] "35"               "-0.0054"          "0.0027"           "equipe_multiprof"
## [1] "35"             "-0.0054"        "0.0021"         "insuf_cardiaca"
## [1] "35"            "-0.0054"       "0.0063"        "antiarritmico"
## [1] "35"                "-0.0054"            "0.0023"             "exames_imagem_qtde"
## [1] "35"               "-0.0054"          "0.0021"           "classe_meds_qtde"
## [1] "35"       "-0.0054"  "0.0034"   "estatina"
```

```
## [1] "35"                    "-0.0054"              "0.0036"               "meds_cardiovasc_qtde"
## [1] "35"            "-0.0054"       "0.0034"        "psicofarmacos"
## [1] "35"                    "-0.0054"              "0.0035"               "meds_antimicrobianos"
## [1] "35"        "-0.0054"   "0.0042"    "diuretico"
## [1] "35"      "-0.0054" "0.0042"  "icu_t0"
## [1] "35"         "-0.0054"    "0.0035"     "nyha_basal"
## [1] "35"                    "-0.0054"              "0.0036"                "metodos_graficos_qtde"
## [1] "35"            "-0.0054"       "0.0028"        "vasodilatador"
## [1] "35"       "-0.0054"  "0.007"    "ieca_bra"
## [1] "35"                   "-0.0054"             "0.0073"              "comorbidities_count"
## [1] "35"          "-0.0054"     "0.0029"      "laboratorio"
## [1] "35"              "-0.0054"         "0.0089"          "education_level"
## [1] "35"              "-0.0054"         "0.0132"          "espironolactona"
## [1] "35"                      "-0.0054"               "0.0181"                  "admission_pre_t0_count"
## [1] "35"          "-0.0054"     "0.0213"      "year_adm_t0"
## [1] "35"      "-0.0054" "0.01"    "age"
## [1] "35"            "-0.0054"       "0.0076"        "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	80	0.7975	0.0061	0.0000	0.0000
All unimportant	TRUE	71	0.7970	0.0060	0.0005	0.0005
procedure_type_new	TRUE	70	0.7983	0.0063	-0.0008	-0.0013
flebografia	TRUE	69	0.7976	0.0063	-0.0001	0.0007
tilt_teste	TRUE	68	0.7980	0.0063	-0.0005	-0.0004
antiviral	TRUE	67	0.7975	0.0063	0.0001	0.0006
procedure_type_1	TRUE	66	0.7975	0.0063	0.0001	0.0000
angio_tc	TRUE	65	0.7980	0.0063	-0.0005	-0.0005
antifungico	TRUE	64	0.7981	0.0063	-0.0005	-0.0001
citologia	TRUE	63	0.7981	0.0064	-0.0006	-0.0001
holter	TRUE	62	0.7987	0.0063	-0.0012	-0.0006
pet_ct	TRUE	61	0.7982	0.0059	-0.0007	0.0005
cateterismo	TRUE	60	0.7980	0.0060	-0.0004	0.0003
stroke	TRUE	59	0.7981	0.0062	-0.0006	-0.0001
cardiac_arrest	TRUE	58	0.7980	0.0060	-0.0004	0.0001
copd	TRUE	57	0.7991	0.0059	-0.0016	-0.0011
sex	TRUE	56	0.7986	0.0061	-0.0010	0.0005
dialysis_t0	TRUE	55	0.7969	0.0064	0.0006	0.0017
heart_failure	TRUE	54	0.7994	0.0059	-0.0019	-0.0025
antiplaquetario_ev	TRUE	53	0.7989	0.0061	-0.0013	0.0006
ecocardiograma	TRUE	52	0.8011	0.0062	-0.0036	-0.0023
endoscopia	TRUE	51	0.8015	0.0061	-0.0039	-0.0004
ultrassom	TRUE	50	0.7997	0.0060	-0.0022	0.0018
tomografia	TRUE	49	0.7997	0.0061	-0.0021	0.0000
prior_mi	FALSE	48	0.7975	0.0061	-0.0021	0.0022
insulina	TRUE	48	0.8008	0.0060	-0.0033	-0.0011
valvopathy	TRUE	47	0.8000	0.0063	-0.0025	0.0008
analises_clinicas_qtde	FALSE	46	0.7962	0.0064	-0.0025	0.0038
heart_disease	TRUE	46	0.8002	0.0057	-0.0027	-0.0002
admission_pre_t0_180d	TRUE	45	0.8003	0.0057	-0.0028	-0.0001
digoxina	TRUE	44	0.7993	0.0058	-0.0018	0.0010
icp	TRUE	43	0.8002	0.0055	-0.0027	-0.0009

Table 1: *(continued)*

Tested Feature	Dropped	Features	CV AUC	CV AUC Std Error	Total AUC Loss	Instant AUC Loss
renal_failure	FALSE	42	0.7982	0.0061	-0.0027	0.0021
cintilografia	TRUE	42	0.8012	0.0056	-0.0037	-0.0010
hypertension	TRUE	41	0.8001	0.0058	-0.0026	0.0011
diabetes	TRUE	40	0.7994	0.0060	-0.0019	0.0007
ventilacao_mecanica	TRUE	39	0.7990	0.0063	-0.0015	0.0004
outros_proced_cirurgicos	TRUE	38	0.8002	0.0063	-0.0027	-0.0012
admission_t0_emergency	TRUE	37	0.8004	0.0060	-0.0029	-0.0002
proced_invasivos_qtde	TRUE	36	0.8019	0.0059	-0.0043	-0.0015
reop_type_1	FALSE	35	0.7991	0.0063	-0.0043	0.0028
interconsulta	FALSE	35	0.7992	0.0060	-0.0043	0.0026
af	FALSE	35	0.7997	0.0054	-0.0043	0.0021
cied_final_1	FALSE	35	0.7990	0.0059	-0.0043	0.0029
cultura	FALSE	35	0.7988	0.0066	-0.0043	0.0031
cied_final_group_1	FALSE	35	0.7992	0.0060	-0.0043	0.0027
bic	TRUE	35	0.8030	0.0058	-0.0054	-0.0011
dva	FALSE	34	0.7995	0.0060	-0.0054	0.0035
aco	FALSE	34	0.7985	0.0060	-0.0054	0.0044
underlying_heart_disease	FALSE	34	0.7980	0.0059	-0.0054	0.0049
equipe_multiprof	FALSE	34	0.8003	0.0063	-0.0054	0.0027
insuf_cardiaca	FALSE	34	0.8009	0.0064	-0.0054	0.0021
antiarritmico	FALSE	34	0.7967	0.0063	-0.0054	0.0063
exames_imagem_qtde	FALSE	34	0.8007	0.0061	-0.0054	0.0023
classe_meds_qtde	FALSE	34	0.8008	0.0063	-0.0054	0.0021
estatina	FALSE	34	0.7995	0.0061	-0.0054	0.0034
meds_cardiovasc_qtde	FALSE	34	0.7994	0.0057	-0.0054	0.0036
psicofarmacos	FALSE	34	0.7996	0.0060	-0.0054	0.0034
meds_antimicrobianos	FALSE	34	0.7995	0.0061	-0.0054	0.0035
diuretico	FALSE	34	0.7987	0.0058	-0.0054	0.0042
icu_t0	FALSE	34	0.7988	0.0057	-0.0054	0.0042
nyha_basal	FALSE	34	0.7994	0.0054	-0.0054	0.0035
metodos_graficos_qtde	FALSE	34	0.7994	0.0061	-0.0054	0.0036
vasodilatador	FALSE	34	0.8002	0.0063	-0.0054	0.0028
ieca_bra	FALSE	34	0.7960	0.0063	-0.0054	0.0070
comorbidities_count	FALSE	34	0.7957	0.0066	-0.0054	0.0073
laboratorio	FALSE	34	0.8001	0.0060	-0.0054	0.0029
education_level	FALSE	34	0.7941	0.0065	-0.0054	0.0089
espironolactona	FALSE	34	0.7898	0.0058	-0.0054	0.0132
admission_pre_t0_count	FALSE	34	0.7849	0.0062	-0.0054	0.0181
year_adm_t0	FALSE	34	0.7817	0.0067	-0.0054	0.0213
age	FALSE	34	0.7929	0.0078	-0.0054	0.0100
hospital_stay	FALSE	34	0.7953	0.0070	-0.0054	0.0076

Minutes to run: 22.381

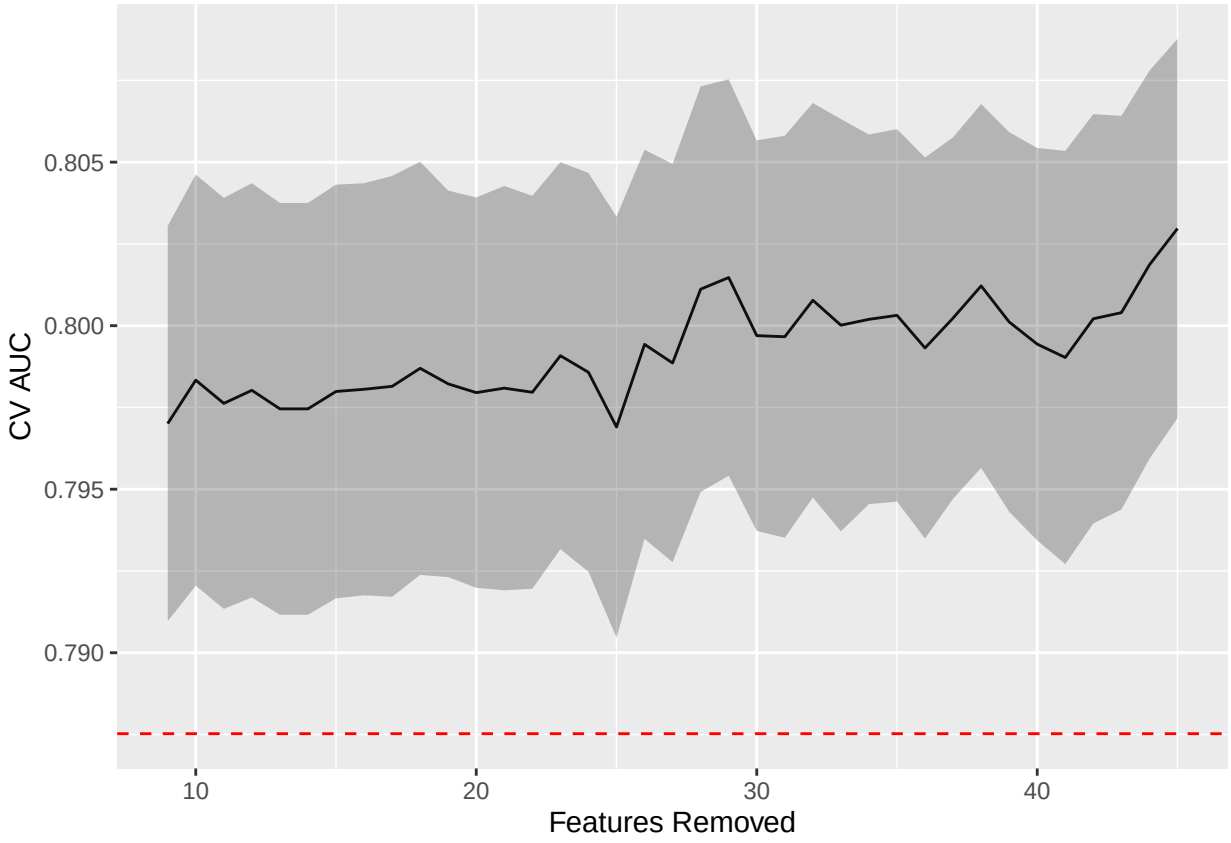
```
selected_features <- current_features

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: 0.803"
```

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

```
## [1] "Selected Model Test AUC: 0.797"
```

```
 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")
```



Minutes to run: 0.3

Hyperparameter tuning

Selected features:

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

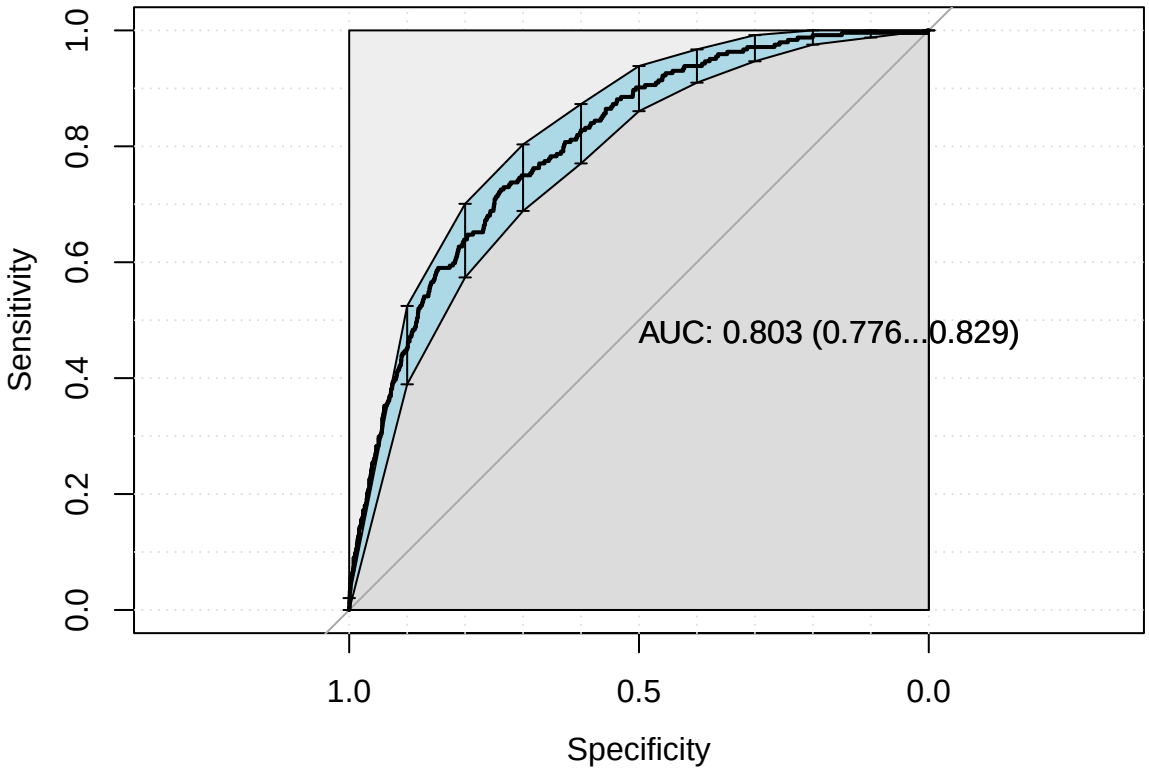
1. hospital_stay
2. age
3. year_adm_t0

4. admission_pre_t0_count
5. espironolactona
6. education_level
7. laboratorio
8. comorbidities_count
9. ieca_bra
10. nyha_basal
11. vasodilatador
12. diuretico
13. metodos_graficos_qtde
14. psicofarmacos
15. icu_t0
16. meds_antimicrobianos
17. estatina
18. insuf_cardiaca
19. meds_cardiovasc_qtde
20. exames_imagem_qtde
21. antiarritmico
22. classe_meds_qtde
23. underlying_heart_disease
24. aco
25. equipe_multiprof
26. dva
27. af
28. cied_final_group_1
29. cultura
30. interconsulta
31. cied_final_1
32. analises_clinicas_qtde
33. prior_mi
34. reop_type_1
35. renal_failure Minutes to run: 0

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(5L, 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)
```




```
##   |
```

```
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))
```

Minutes to run: 9.527

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.png", x),
         plot = p,
         dpi = 300)
}
```

```
## Saving 6.5 x 5 in image
## Saving 6.5 x 5 in image

## Warning: Removed 5 rows containing missing values (geom_point).

## Saving 6.5 x 5 in image

## Warning: Removed 5 rows containing missing values (geom_point).

## Saving 6.5 x 5 in image

## Warning: Removed 1044 rows containing missing values (geom_point).

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## Warning: Removed 1044 rows containing missing values (geom_point).

## Saving 6.5 x 5 in image
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## Saving 6.5 x 5 in image

## Warning: Removed 810 rows containing missing values (geom_point).

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## Warning: Removed 1044 rows containing missing values (geom_point).

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## Warning: Removed 1044 rows containing missing values (geom_point).

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```

```
## Warning: Removed 810 rows containing missing values (geom_point).

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## Warning: Removed 1044 rows containing missing values (geom_point).

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## Warning: Removed 810 rows containing missing values (geom_point).

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## Warning: Removed 1044 rows containing missing values (geom_point).

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## Warning: Removed 810 rows containing missing values (geom_point).

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## Saving 6.5 x 5 in image
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## Warning: Removed 810 rows containing missing values (geom_point).

## Saving 6.5 x 5 in image
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## Warning: Removed 1044 rows containing missing values (geom_point).

## Saving 6.5 x 5 in image
## Saving 6.5 x 5 in image

## Warning: Removed 1044 rows containing missing values (geom_point).

## Saving 6.5 x 5 in image

## Warning: Removed 810 rows containing missing values (geom_point).
```

```
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```
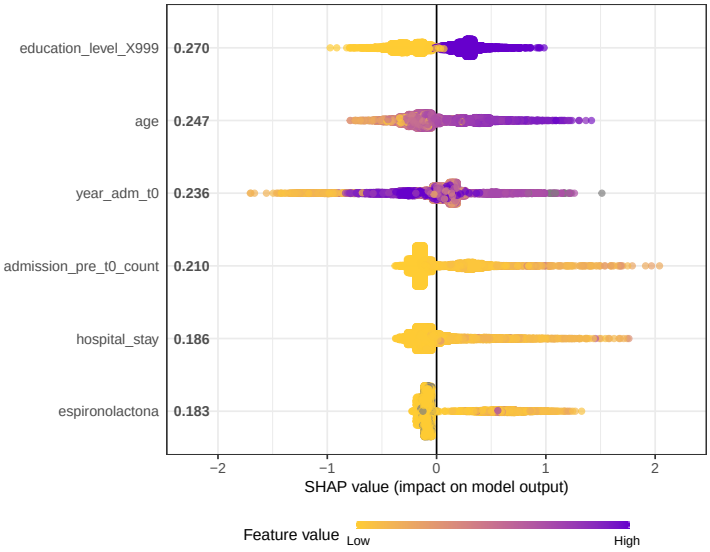
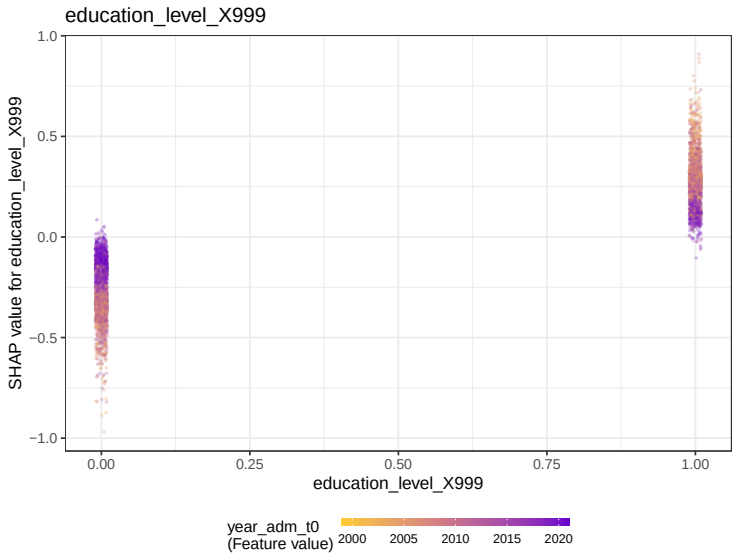
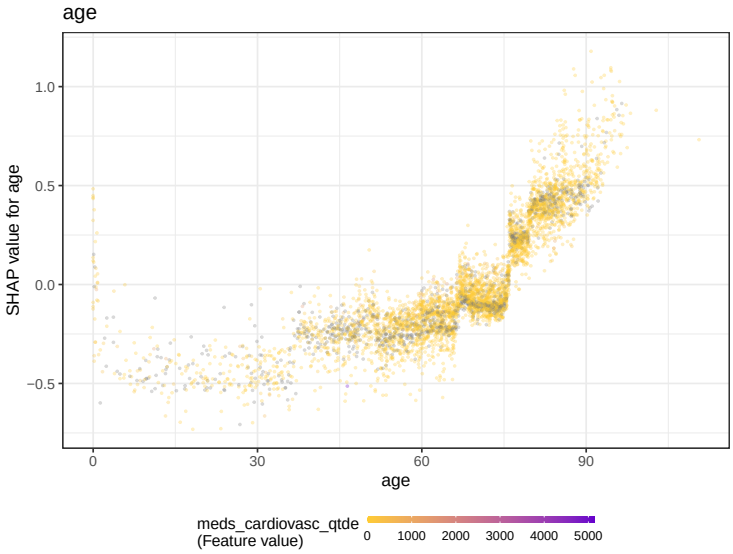
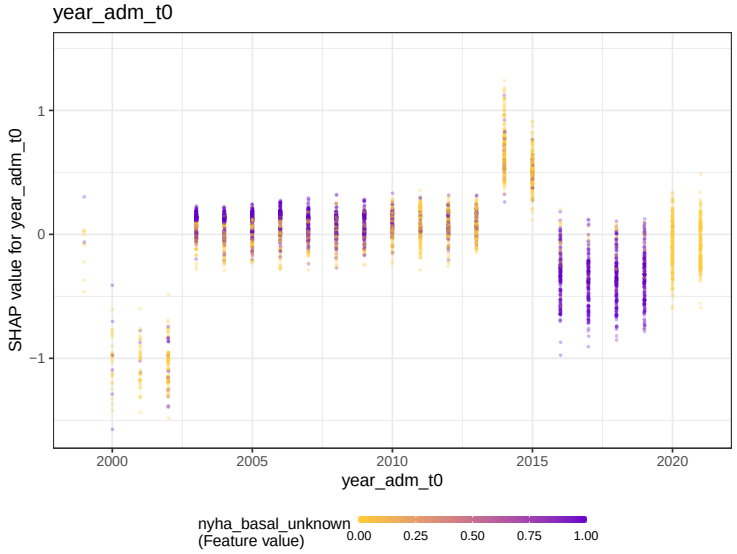
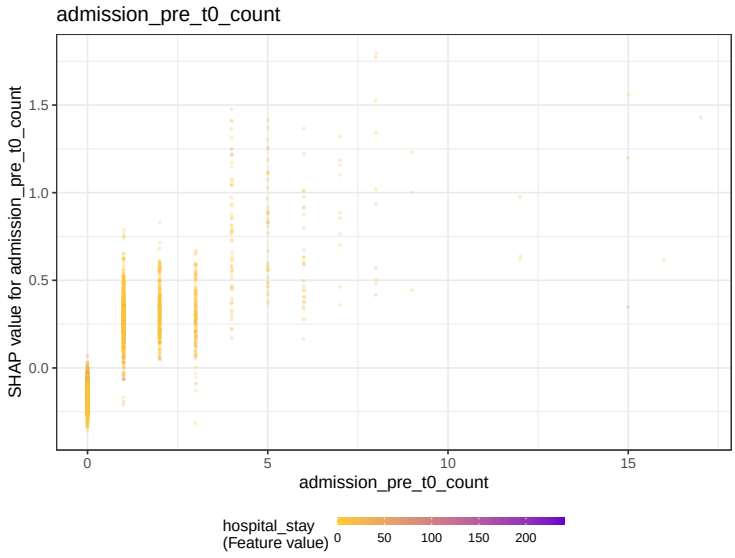
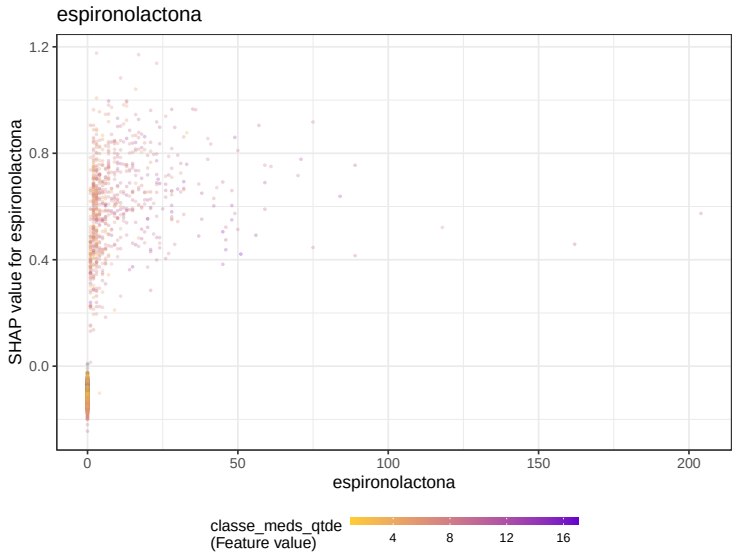



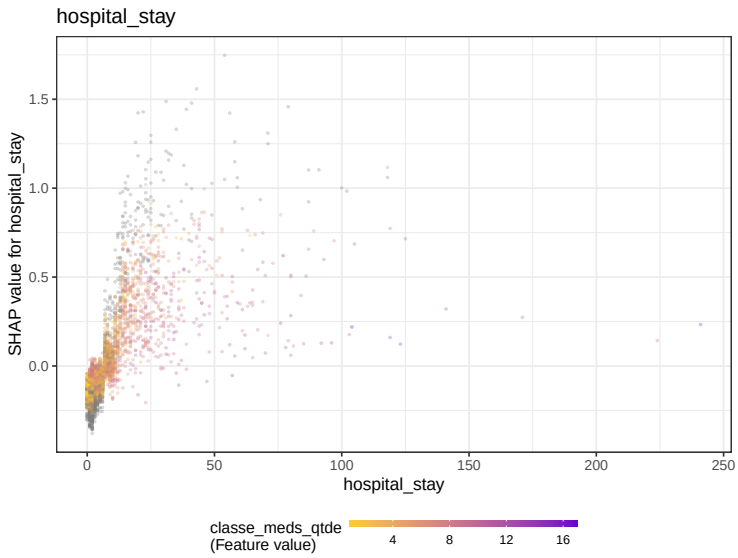












Minutes to run: 0.601

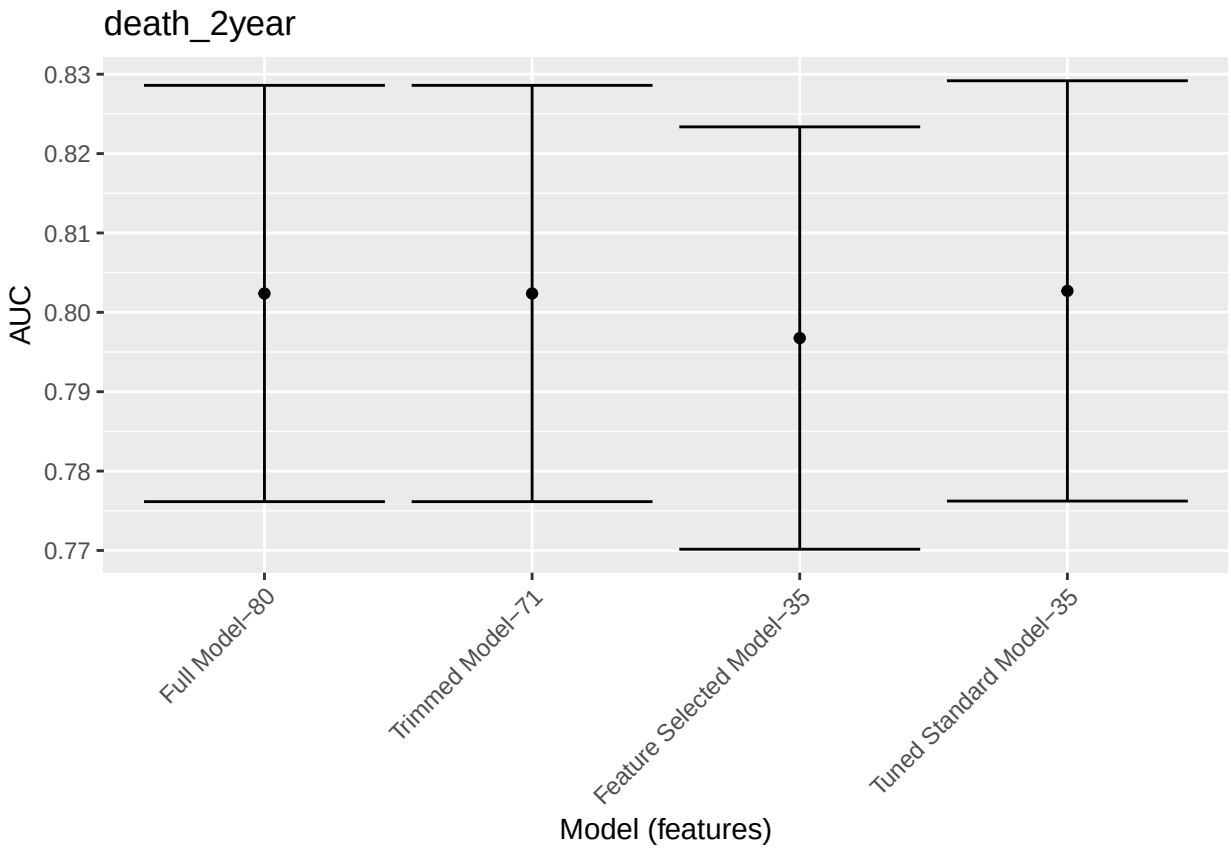
```
## $num_iterations
## [1] 97
##
## $learning_rate
## [1] 0.03897956
##
## $max_depth
## [1] 14
##
## $feature_fraction_bynode
## [1] 1
##
## $min_data_in_leaf
## [1] 27
##
## $min_gain_to_split
## [1] 0
##
## $bagging_fraction
## [1] 1
##
## $num_class
## [1] 1
##
```

```
## $objective
## [1] "binary"
##
## $num_threads
## $num_threads$num_threads
## [1] 0
##
##
## $nthread
## [1] 8
##
## $seed
## [1] 86075
##
## $deterministic
## [1] TRUE
##
## $verbose
## [1] -1
##
## $metric
## list()
##
## $interaction_constraints
## list()
##
## $feature_pre_filter
## [1] FALSE
```

Minutes to run: 0

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))
```

Minutes to run: 0.002