

Code used for the Development of the Xgboost algorithm

“AUC_target” = the name of the column of the explained variable (Y)

“data” = the name of the dataset

“C_X” = the concentration measured at time X in mg/L

“MODN” = the categorical covariate for simulated population (from 1 to 6)

“SCR” = serum creatinine in μM

“C_diff” = the measured difference between the peak and trough in mg/L,

“TBW” = the body weight in Kg

“AGE” = age in years

R code

```
### Data splitting
```

```
set.seed(123)
```

```
data_split = initial_split(data, strata = AUC_target)
```

```
data_train = training(data_split)
```

```
data_test = testing(data_split)
```

```
### Preprocessing
```

```
data_recipe <- recipe(AUC_target ~ C_X + MODN + TBW + SEX + AGE + SCR + C_diff, data =  
data_train) %>%
```

```
  update_role(MODN, new_role = "simulated population")
```

```
data_prep <- prep(data_recipe)
```

```
data_train1 <- juice(data_prep)
```

```
data_test1 <- bake(data_prep, new_data = data_test)
```

```
### Definition of used model and hyperparameters to tune
```

```
xgb_spec <- boost_tree(mode = "regression",
```

```
  mtry = tune(),
```

```
  trees = 1000
```

```
  min_n = tune(),
```

```
  tree_depth = tune(),
```

```
  learn_rate = tune()) %>% set_engine("xgboost")
```

```
## Creation of workflow, add of recipe and model
```

```
xgb_wf <- workflow() %>%
```

```
  add_recipe(data_recipe) %>%
```

```
  add_model(xgb_spec)
```

```

### Cross validation hyperparameters
set.seed(2345)
data_folds <- vfold_cv(data_train)

### Tuning of hyperparameters
set.seed(345)
tune_xgb <- tune_grid(
  xgb_wf,
  resamples = data_folds,
  finalize(mtry(), data_train1),
  grid = 30 )

### Visualisation of results plot as function of rmse
autoplot (tune_xgb, metric = "rmse", scientific = FALSE) +
  ggtitle("tuning hyperparameter")

### Choice of best model
best_rmse_xgb <- select_best(tune_xgb, "rmse")

### Finalization of model with the best hyperparameters
final_xgb <- finalize_model(xgb_spec,
  best_rmse_xgb)

### Creation of Variables Importance Plot
final_xgb %>%
  set_engine("xgboost") %>%
  fit(AUC_target ~ .,
    data = juice(data_train)
  ) %>%
  vip::vip(geom = "col")

### Finalization of workflow
final_wf_xgb <- workflow() %>%
  add_recipe(data_recipe) %>%
  add_model(final_xgb)
final_wf_xgb

### Resamples
set.seed( 456 )
folds <- vfold_cv(data_train) #par défaut 10 fois

```

```

#### Fit with resampled training dataset
xgb_rs <- fit_resamples(object = final_wf_xgb,
                        resamples = folds,
                        control = control_resamples(verbose=T, save_pred = T))

#### Obtain the predicted outcomes
pred_obs_xgb <- xgb_rs %>% collect_predictions() %>%
mutate (bias_rel = (.pred - AUC_target)/AUC_target,
       bias_rel_square = bias_rel * bias_rel)
pred_obs_xgb_gen <- pred_obs_xgb %>% summarise(biais_rel = mean(bias_rel),
       relative_rmse = sqrt(mean(bias_rel_square)))

#### Fit workflow
fit_workflow <- fit(final_wf_xgb, data_train)

#### Save fitworkflow
saveRDS(fit_workflow, file = "fit_workflow_07.12.rds")

#### Validation in test set
final_fit <- fit_workflow %>%
last_fit(data_split)
final_fit %>% collect_metrics()
final_fit_gen <- final_fit %>% collect_predictions() %>%
mutate (bias_rel = (.pred - AUC_target)/AUC_target,
       bias_rel_square = bias_rel * bias_rel)
final_fit_gen %>% summarise(biais_rel = mean(bias_rel), relative_rmse =
sqrt(mean(bias_rel_square)))

```