

R Notebook

Parametros:

```
Measure = G-mean
Columns = learner
Performance = holdout_measure_residual
Filter keys = sampling, weight_space, ruspool
Filter values = FALSE, FALSE, FALSE
```

```
library("scmamp")
library(dplyr)
```

Tratamento dos dados

Carregando data set compilado

```
ds = read.csv("/home/rodrigo/Dropbox/UNICAMP/IC/estudo_cost_learning/SummaryResults/summary_compilation.
summary(ds)
```

```
##           learner      weight_space
##  classif.ksvm      :17100  Mode :logical
##  classif.randomForest:17100  FALSE:41040
##  classif.xgboost     :17100  TRUE :10260
##                               NA's :0
##
##
##
##           measure      sampling      ruspool
##  Accuracy              :10260  ADASYN:10260  Mode :logical
##  Area under the curve    :10260  FALSE :30780  FALSE:41040
##  F1 measure              :10260  SMOTE :10260  TRUE :10260
##  G-mean                 :10260                NA's :0
##  Matthews correlation coefficient:10260
##
##
##  tuning_measure  holdout_measure  holdout_measure_residual
##  Min.      :-0.1277  Min.      :-0.2120  Min.      :-0.4658
##  1st Qu.: 0.5924  1st Qu.: 0.3114  1st Qu.: 0.1648
##  Median : 0.9624  Median : 0.8193  Median : 0.5192
##  Mean   : 0.7570  Mean   : 0.6469  Mean   : 0.5099
##  3rd Qu.: 0.9965  3rd Qu.: 0.9879  3rd Qu.: 0.8636
##  Max.    : 1.0000  Max.    : 1.0000  Max.    : 1.0000
##  NA's    :1761    NA's    :1761    NA's    :1761
##  iteration_count      dataset      imba.rate
##  Min.      :1      abalone      : 900  Min.      :0.0010
##  1st Qu.:1      adult      : 900  1st Qu.:0.0100
##  Median :2      bank      : 900  Median :0.0300
##  Mean   :2      car      : 900  Mean   :0.0286
##  3rd Qu.:3      cardiotocography-10clases: 900  3rd Qu.:0.0500
##  Max.    :3      cardiotocography-3clases : 900  Max.    :0.0500
```

```
## NA's :1761 (Other) :45900
```

Filtrando pela metrica

```
ds = filter(ds, measure == params$measure)
```

Filtrando o data set

```
if(params$filter_keys != 'NULL' && !is.null(params$filter_keys)){  
  ds = filter_at(ds, .vars = params$filter_keys, .vars_predicate = any_vars(. == params$filter_values))  
}
```

```
summary(ds)
```

```
##           learner      weight_space  
## classif.ksvm      :3420  Mode :logical  
## classif.randomForest:3420 FALSE:8208  
## classif.xgboost    :3420  TRUE :2052  
##                   NA's :0  
##  
##  
##  
##           measure      sampling      ruspool  
## Accuracy           : 0 ADASYN:2052  Mode :logical  
## Area under the curve : 0 FALSE :6156  FALSE:8208  
## F1 measure           : 0 SMOTE :2052  TRUE :2052  
## G-mean              :10260           NA's :0  
## Matthews correlation coefficient: 0  
##  
##  
## tuning_measure  holdout_measure  holdout_measure_residual  
## Min. :0.0000  Min. :0.0000  Min. :0.0000  
## 1st Qu.:0.4958  1st Qu.:0.0000  1st Qu.:0.1064  
## Median :0.9108  Median :0.7004  Median :0.4331  
## Mean :0.7066  Mean :0.5513  Mean :0.4500  
## 3rd Qu.:0.9931  3rd Qu.:0.9414  3rd Qu.:0.7846  
## Max. :1.0000  Max. :1.0000  Max. :1.0000  
## NA's :318    NA's :318    NA's :318  
## iteration_count      dataset      imba.rate  
## Min. :1      abalone      : 180  Min. :0.0010  
## 1st Qu.:1      adult      : 180  1st Qu.:0.0100  
## Median :2      bank      : 180  Median :0.0300  
## Mean :2      car      : 180  Mean :0.0286  
## 3rd Qu.:3      cardiotocography-10clases: 180  3rd Qu.:0.0500  
## Max. :3      cardiotocography-3clases : 180  Max. :0.0500  
## NA's :318    (Other)      :9180
```

Computando as médias das iteracoes

```
ds = group_by(ds, learner , weight_space , measure , sampling , ruspool , dataset , imba.rate)  
ds = summarise(ds, tuning_measure = mean(tuning_measure), holdout_measure = mean(holdout_measure),  
               holdout_measure_residual = mean(holdout_measure_residual))
```

```
ds = as.data.frame(ds)
```

Criando dataframe

```

# Dividindo o ds em n, um para cada técnica
splited_df = ds %>% group_by_at(.vars = params$columns) %>% do(vals = as.data.frame(.)) %>% select(vals)

# Juntando cada uma das partes horizontalmente em um data set
df_tec_wide = do.call("cbind", splited_df)

# Renomeando duplicacao de nomes
colnames(df_tec_wide) = make.unique(colnames(df_tec_wide))

# Selecionando apenas as medidas da performance escolhida
df_tec_wide_residual = select(df_tec_wide, matches(paste("^", params$performance, "$|", params$performance)))

# Renomeando colunas
new_names = NULL
for(i in (1:length(splited_df))){
  id = toString(sapply(splited_df[[i]][1, params$columns], as.character))
  new_names = c(new_names, id)
}
colnames(df_tec_wide_residual) = new_names

# Verificando a dimensao do df
dim(df_tec_wide_residual)

## [1] 1140    3

# Removendo linhas com NA's
df_tec_wide_residual = na.omit(df_tec_wide_residual)

# Renomeando a variavel
df = df_tec_wide_residual

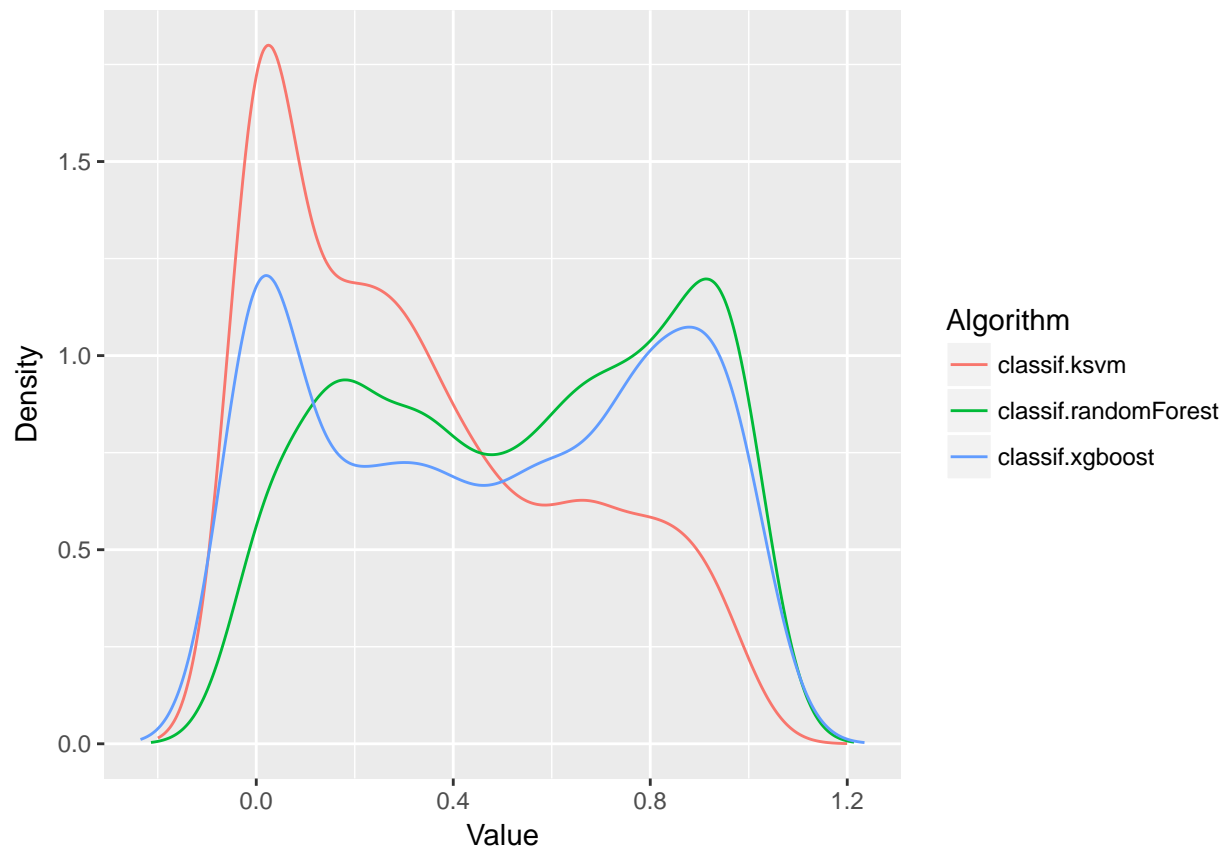
summary(df)

##   classif.ksvm   classif.randomForest classif.xgboost
## Min.   :0.00000   Min.   :0.0000    Min.   :0.0000
## 1st Qu.:0.04729   1st Qu.:0.2405    1st Qu.:0.1326
## Median :0.26945   Median :0.5670    Median :0.4941
## Mean   :0.33095   Mean   :0.5385    Mean   :0.4760
## 3rd Qu.:0.55656   3rd Qu.:0.8286    3rd Qu.:0.8027
## Max.   :0.99996   Max.   :1.0000    Max.   :1.0000

```

Fazendo teste de normalidade

```
plotDensities(data = df)
```



Testando as diferencas

```
friedmanTest(df)

##
## Friedman's rank sum test
##
## data: df
## Friedman's chi-squared = 435.82, df = 2, p-value < 2.2e-16
```

Testando as diferencas par a par

```
test <- nemenyiTest (df, alpha=0.05)
abs(test$diff.matrix) > test$statistic

##      classif.ksvm classif.randomForest classif.xgboost
## [1,]      FALSE              TRUE      TRUE
## [2,]       TRUE              FALSE      TRUE
## [3,]       TRUE              TRUE      FALSE
```

Plotando grafico de Critical Difference

```
result = tryCatch({  
  plotCD(df, alpha=0.05, cex = 0.35)  
}, error = function(e) {})
```

