

# Support Vector Machine (SVM) Linear kernel

Feature space partition ensemble model for replication (FESPAE)

EGG data-based experiments

**Article:** Lizbeth Naranjo, Carlos J. Perez, Daniel F. Merino (2025). A data ensemble-based approach for detecting vocal disorders using replicated acoustic biomarkers from electroglottography. *Sensing and Bio-Sensing Research Journal*, vol, num, pages.

```
library(tidyverse)
library(e1071)
## change the address where the file will be saved
address = "~/Documents/GitHub/"
setwd("~/Documents/GitHub/")
```

## EGG data-based experiments

```
## Comment or uncomment the options: EGG-a, EGG-i, EGG-u
```

```
## EGG-a
datos2 <- read.csv(paste0(address,"a_egg_saarbrucken.csv"),
                  sep = ";",header=TRUE, dec=",")

## name of the files to save results
archivo = "FESPAE_crossval_strata_allvar_SVM_linear_Saarbrucken_egg_a"
```

```
## EGG-i
## datos2 <- read.csv(paste0(address,"i_egg_saarbrucken.csv"),
##                  sep = ";",header=TRUE, dec=",")

## name of the files to save results
## archivo = "FESPAE_crossval_strata_allvar_SVM_linear_Saarbrucken_egg_i"
```

```
## EGG-u
## datos2 <- read.csv(paste0(address,"u_egg_saarbrucken.csv"),
##                  sep = ";",header=TRUE, dec=",")

## name of the files to save results
## archivo = "FESPAE_crossval_strata_allvar_SVM_linear_Saarbrucken_egg_u"
```

```
dim(datos2)
```

```
[1] 675 36
```

```
summary(datos2)
```

ID_fact	status_fact	SEX	JITTER
Min. : 1.0	Min. :0	Min. :0.0000	Min. : 0.11
1st Qu.:169.5	1st Qu.:0	1st Qu.:0.0000	1st Qu.: 0.49
Median :338.0	Median :1	Median :0.0000	Median : 5.52
Mean :338.0	Mean :1	Mean :0.4133	Mean : 18.90
3rd Qu.:506.5	3rd Qu.:2	3rd Qu.:1.0000	3rd Qu.: 25.89
Max. :675.0	Max. :2	Max. :1.0000	Max. :281.41
SHIMMER	CPP	D2	FZCF
Min. :0.01000	Min. :12.26	Min. : 2.480	Min. : 2.00
1st Qu.:0.03000	1st Qu.:21.08	1st Qu.: 4.130	1st Qu.: 5.00
Median :0.04000	Median :24.60	Median : 5.100	Median : 9.00
Mean :0.05887	Mean :24.26	Mean : 5.666	Mean : 45.86
3rd Qu.:0.08000	3rd Qu.:27.36	3rd Qu.: 6.795	3rd Qu.: 20.00
Max. :0.37000	Max. :35.94	Max. :27.380	Max. :5323.00
GENE	HNHR	HURST	LZ
Min. :0.3800	Min. : -4.40	Min. :0.0400	Min. : 19.00
1st Qu.:0.6300	1st Qu.:14.07	1st Qu.:0.4200	1st Qu.: 55.50
Median :0.7700	Median :18.40	Median :0.6300	Median : 83.00
Mean :0.9037	Mean :17.38	Mean :0.7015	Mean : 86.81
3rd Qu.:1.0000	3rd Qu.:21.66	3rd Qu.:0.9100	3rd Qu.:107.00
Max. :4.6300	Max. :32.35	Max. :1.7800	Max. :304.00
MFCC0	MFCC1	MFCC2	MFCC3
Min. : -2.6200	Min. : -23.850	Min. : -47.190	Min. : -49.37
1st Qu.: -0.5700	1st Qu.: 3.300	1st Qu.: -22.285	1st Qu.: -24.59
Median : 0.1700	Median : 9.150	Median : -9.750	Median : -15.21
Mean : 0.1388	Mean : 8.767	Mean : -9.716	Mean : -14.79
3rd Qu.: 0.8600	3rd Qu.: 14.980	3rd Qu.: 2.915	3rd Qu.: -4.03
Max. : 3.0700	Max. : 30.920	Max. : 23.390	Max. : 19.56
MFCC4	MFCC5	MFCC6	MFCC7
Min. : -61.070	Min. : -67.210	Min. : -62.600	Min. : -39.460
1st Qu.: -21.130	1st Qu.: -12.535	1st Qu.: -16.040	1st Qu.: -11.790
Median : -8.770	Median : -2.020	Median : -3.600	Median : -2.960
Mean : -9.488	Mean : -3.153	Mean : -4.740	Mean : -3.146
3rd Qu.: 2.400	3rd Qu.: 7.065	3rd Qu.: 5.175	3rd Qu.: 4.690
Max. : 38.080	Max. : 36.640	Max. : 46.700	Max. : 40.120
MFCC8	MFCC9	MFCC10	MFCC11
Min. : -44.230	Min. : -35.240	Min. : -41.950	Min. : -41.300
1st Qu.: -14.685	1st Qu.: -12.990	1st Qu.: -12.415	1st Qu.: -11.705
Median : -5.340	Median : -4.580	Median : -4.830	Median : -4.040
Mean : -5.353	Mean : -3.993	Mean : -4.637	Mean : -4.130
3rd Qu.: 2.660	3rd Qu.: 3.420	3rd Qu.: 2.760	3rd Qu.: 2.755
Max. : 49.090	Max. : 49.370	Max. : 41.220	Max. : 36.180
MFCC12	PERMUTATION	PPE	SHANNON
Min. : -36.840	Min. :1.150	Min. :0.1900	Min. :11.79
1st Qu.: -10.890	1st Qu.:1.640	1st Qu.:0.5300	1st Qu.:12.12
Median : -3.390	Median :1.810	Median :0.5500	Median :12.16
Mean : -2.904	Mean :1.827	Mean :0.5312	Mean :12.15

3rd Qu.: 3.935	3rd Qu.:1.990	3rd Qu.:0.5700	3rd Qu.:12.19
Max. : 31.870	Max. :2.550	Max. :0.5700	Max. :12.26
ZCR	energyentropy	spectralcentroid	spectralspread
Min. :0.01000	Min. :2.540	Min. :0.0600	Min. :0.1100
1st Qu.:0.04000	1st Qu.:3.230	1st Qu.:0.1200	1st Qu.:0.1600
Median :0.07000	Median :3.300	Median :0.1500	Median :0.1800
Mean :0.07056	Mean :3.248	Mean :0.1545	Mean :0.1805
3rd Qu.:0.09000	3rd Qu.:3.310	3rd Qu.:0.1800	3rd Qu.:0.2000
Max. :0.23000	Max. :3.320	Max. :0.3200	Max. :0.2800
spectralentropy	spectralrolloff	RPDE	rep
Min. :0.0100	Min. :0.0100	Min. :0.1000	Min. :1
1st Qu.:0.1900	1st Qu.:0.0700	1st Qu.:0.2700	1st Qu.:1
Median :0.6600	Median :0.1100	Median :0.3500	Median :2
Mean :0.6867	Mean :0.1178	Mean :0.3948	Mean :2
3rd Qu.:1.0700	3rd Qu.:0.1600	3rd Qu.:0.4950	3rd Qu.:3
Max. :1.9100	Max. :0.4500	Max. :0.9100	Max. :3

```
head(datos2)
```

	ID_fact	status_fact	SEX	JITTER	SHIMMER	CPP	D2	FZCF	GNE	HNR	HURST	LZ
1	1		0	0	6.76	0.06	28.26	3.71	23	0.67	18.96	1.11 44
2	2		0	0	0.31	0.06	23.32	3.40	48	0.47	17.76	1.58 36
3	3		0	0	0.19	0.04	23.55	3.68	58	0.46	21.86	1.70 24
4	4		0	0	0.45	0.01	33.64	2.96	37	0.42	25.78	1.45 27
5	5		0	0	0.39	0.07	26.95	2.66	50	0.39	21.44	1.63 29
6	6		0	0	0.34	0.04	35.36	3.03	35	0.44	28.32	1.45 28
	MFCC0	MFCC1	MFCC2	MFCC3	MFCC4	MFCC5	MFCC6	MFCC7	MFCC8	MFCC9	MFCC10	MFCC11
1	-0.75	11.11	-0.88	-4.03	4.01	-0.10	-5.14	-4.07	-7.72	-9.94	-12.93	-13.10
2	-1.16	-0.60	12.22	4.06	5.84	3.35	6.71	1.68	2.86	3.01	1.88	1.35
3	-1.70	2.81	15.53	7.78	7.22	8.27	3.33	3.90	4.74	6.15	1.74	2.75
4	-1.00	11.34	5.69	1.20	1.84	8.61	-0.60	4.50	0.59	2.95	-0.09	1.14
5	-1.91	11.97	7.29	7.30	7.14	4.34	6.10	3.49	2.89	2.92	2.73	2.47
6	-1.43	6.93	3.04	11.37	1.89	1.65	3.27	5.75	-0.33	4.49	-1.93	2.00
	MFCC12	PERMUTATION	PPE	SHANNON	ZCR	energyentropy	spectralcentroid					
1	-10.64		1.94	0.40	12.18	0.02	3.30 0.12					
2	2.93		2.53	0.57	12.20	0.01	3.21 0.13					
3	2.26		2.41	0.53	12.16	0.01	3.26 0.12					
4	-0.36		1.34	0.55	12.18	0.01	3.28 0.10					
5	2.88		1.76	0.57	12.20	0.01	3.23 0.09					
6	-1.05		1.38	0.55	12.05	0.01	3.29 0.13					
	spectralspread	spectralentropy	spectralrolloff	RPDE	rep							
1	0.19		0.16	0.04	0.50 1							
2	0.23		0.07	0.02	0.57 2							
3	0.21		0.06	0.02	0.43 3							
4	0.18		0.07	0.03	0.41 1							
5	0.16		0.03	0.01	0.47 2							
6	0.20		0.09	0.03	0.28 3							

## Re-Scale explanatory variables

```
## Scale the variables
datos2 <- as.data.frame(datos2)
datos2$STATUS_fact = as.factor(as.numeric(factor(datos2$status_fact)))

table(datos2$STATUS_fact)
```

```
 1    2    3
225 225 225
```

```
datos <- transform(datos2,
sJITTER= scale(JITTER), sSHIMMER= scale(SHIMMER), sCPP= scale(CPP),
sD2= scale(D2), sFZCF= scale(FZCF), sGNE= scale(GNE),
sHNR= scale(HNR), sHURST= scale(HURST), sLZ= scale(LZ),
sMFCC0= scale(MFCC0),
sMFCC1= scale(MFCC1), sMFCC2= scale(MFCC2), sMFCC3= scale(MFCC3),
sMFCC4= scale(MFCC4), sMFCC5= scale(MFCC5), sMFCC6= scale(MFCC6),
sMFCC7= scale(MFCC7), sMFCC8= scale(MFCC8), sMFCC9= scale(MFCC9),
sMFCC10= scale(MFCC10), sMFCC11= scale(MFCC11), sMFCC12= scale(MFCC12),
sPERMUTATION= scale(PERMUTATION), sPPE= scale(PPE), sSHANNON= scale(SHANNON),
sZCR= scale(ZCR),
senenergyentropy= scale(energyentropy), sspectralcentroid= scale(spectralcentroid),
sspectralspread= scale(spectralspread), sspectralentropy= scale(spectralentropy),
sspectralrolloff= scale(spectralrolloff), sRPDE= scale(RPDE))

datos$ID_fact = rep(1:225,each=3)

dim(datos)
```

```
[1] 675 69
```

```
## data set
trainc <- datos %>% select(
sJITTER, sSHIMMER, sCPP, sD2, sFZCF,
sGNE, sHNR, sHURST, sLZ, sMFCC0,
sMFCC1, sMFCC2, sMFCC3, sMFCC4, sMFCC5,
sMFCC6, sMFCC7, sMFCC8, sMFCC9, sMFCC10,
sMFCC11, sMFCC12,
sPERMUTATION, sPPE, sSHANNON, sZCR,
senenergyentropy, sspectralcentroid, sspectralspread,
sspectralentropy, sspectralrolloff, sRPDE,
STATUS_fact,SEX, rep,ID_fact)
```

# Crossvalidation

## Subspaces

```
## Function to compute the Mode
Mode <- function(x, na.rm = FALSE) {
  if(na.rm){
    x = x[!is.na(x)]
  }
  ux <- unique(x)
  return(ux[which.max(tabulate(match(x, ux)))]])
}

## Partition of subspaces
## The feature space is randomly partitioned into K subspaces with roughly equal sizes
## k = number of predictors
## K = subspaces

K0 = 4 ## sub-spaces
k = 32 ## explanatory variables
k2 = round(k/K0)
space = 1:k
subspaces = rep(list(rep(NA,k2)),K0) ## Subspaces
set.seed(12345)
for(j in 1:(K0-1)){
  space1 = sample(space, size=k2, replace=FALSE)
  space = setdiff(space,space1)
  subspaces[[j]] = space1[order(space1)]
}
space1 = space
subspaces[[K0]] = space1[order(space1)]
## 32 features = 1x32, 2x16, 4x8,
subspaces

## [[1]]
## [1] 11 14 16 19 24 26 28 29
##
## [[2]]
## [1] 2 6 7 10 12 21 30 32
##
## [[3]]
## [1] 1 4 5 9 13 15 27 31
##
## [[4]]
## [1] 3 8 17 18 20 22 23 25
```

## Training and testing data subsets

```
## Select data: 75% training & 25% testing stratified per category
SIM = 100  ## repeat N times the cross-validation process
N = 225  ## sample size
Nfit = 168  ## sample size for training subset
Ntest = 57  ## sample size for testing subset
Ncat = 75  ## sample size per category
Ncatfit = 56  ## training per category
Ncattest = 19  ## testing per category
FIT <- matrix(0,SIM,Nfit)  ## training subsets
TEST <- matrix(0,SIM,Ntest)  ## testing subsets

categoria = trainc %>% filter(rep==1) %>% select(STATUS_fact)
categoria = as.numeric(categoria$STATUS_fact)
id = 1:N
set.seed(12345)
for(si in 1:SIM){
  for(j in 1:3){
    idcat = id[categoria==j]  ## stratified per category j
    ran0 = sample(idcat, size=Ncatfit, replace=FALSE)

    FIT[si,(j-1)*Ncatfit+1:Ncatfit] <- sort(ran0)
    TEST[si,(j-1)*Ncattest+1:Ncattest] <- setdiff(idcat,ran0)
  }
}
```

## Classification metrics for models predicting nominal outcomes

```
## Functions to compute classification metrics
## Ytrue = true response variable
## Ypred = predicted outcome
## cat = category
## TP = true positive
## TN = true negative
## FP = false positive
## FN = false negative

## Function to compute the precision per class=cat
fn_precision_class <- function(Ytrue,Ypred,cat){
  TP = sum(Ypred[Ytrue==cat]==cat)
  FP = sum(Ypred[Ytrue!=cat]==cat)
  precision = TP/(TP+FP)
  return(precision)
}

## Function to compute the recall per class=cat
fn_recall_class <- function(Ytrue,Ypred,cat){ ## cat==category
  TP = sum(Ypred[Ytrue==cat]==cat)
  FN = sum(Ypred[Ytrue==cat]!=cat)
  recall = TP/(TP+FN)
  return(recall)
}

## Function to compute the F1-score per class=cat
fn_f1score_class <- function(Ytrue,Ypred,cat){ ## cat==category
  TP = sum(Ypred[Ytrue==cat]==cat)
  FP = sum(Ypred[Ytrue!=cat]==cat)
  FN = sum(Ypred[Ytrue==cat]!=cat)
  precision = TP/(TP+FP)
  recall = TP/(TP+FN)
  f1score = 2*(precision*recall)/(precision+recall)
  return(f1score)
}

## To save classification metrics
## Fitxxx: metric for training subset. Testxxx: metric for testing subset
FitAccuracy = TestAccuracy <- array(NA,dim=c(SIM,1)) ## Accuracy Rate
FitPrecisionClass = TestPrecisionClass <- array(NA,dim=c(SIM,1,3)) ## Precision per class
FitRecallClass = TestRecallClass <- array(NA,dim=c(SIM,1,3)) ## Recall per class
FitF1ScoreClass = TestF1ScoreClass <- array(NA,dim=c(SIM,1,3)) ## F1-score per class
FitPrecisionMacroAve = TestPrecisionMacroAve <- array(NA,dim=c(SIM,1)) ## Precision Macro Average
FitRecallMacroAve = TestRecallMacroAve <- array(NA,dim=c(SIM,1)) ## Recall Macro Average
FitF1ScoreMacroAve = TestF1ScoreMacroAve <- array(NA,dim=c(SIM,1)) ## F1-score Macro Average
```

## Cross-validation

```
##-----
for(sim in 1:SIM){ ### BEGIN sim
##-----

my_fit = FIT[sim,]    ## training subset
my_test = TEST[sim,]  ## testing subset

## Training data subset
train1 <- trainc %>% filter(ID_fact%in%my_fit, rep==1) ## repetition=1
train2 <- trainc %>% filter(ID_fact%in%my_fit, rep==2) ## repetition=2
train3 <- trainc %>% filter(ID_fact%in%my_fit, rep==3) ## repetition=3

Yc = train1$STATUS_fact ## categorical response variable for training
n = length(Yc)
G = 3 # classes

## Testing data subset
test1 <- trainc %>% filter(ID_fact%in%my_test, rep==1) ## repetition=1
test2 <- trainc %>% filter(ID_fact%in%my_test, rep==2) ## repetition=2
test3 <- trainc %>% filter(ID_fact%in%my_test, rep==3) ## repetition=3

Yc.new = test1$STATUS_fact ## categorical response variable for testing
n.new = length(Yc.new)

## Delete variables which are not used
train1 <- train1 %>% select(-c(rep,ID_fact))
train2 <- train2 %>% select(-c(rep,ID_fact))
train3 <- train3 %>% select(-c(rep,ID_fact))
test1 <- test1 %>% select(-c(rep,ID_fact))
test2 <- test2 %>% select(-c(rep,ID_fact))
test3 <- test3 %>% select(-c(rep,ID_fact))

##-----
## Algorithm FESPAE
## Feature space partition ensemble model for replication
##-----

## Algo1: The feature space is randomly partitioned into M subspaces, {S1,S2,...,SM}

K0 = 4 ## sub-spaces
k = 32 ## explanatory variables
k2 = round(k/K0)
space = 1:k
subspaces = rep(list(rep(NA,k2)),K0) ## Subspaces
set.seed(12345)
for(j in 1:(K0-1)){
  space1 = sample(space, size=k2, replace=FALSE)
  space = setdiff(space,space1)
  subspaces[[j]] = space1[order(space1)]
}
space1 = space
```



```

subspaces[[K0]] = space1[order(space1)]
# 32 features = 1x32, 2x16, 4x8,

##-----
## Algo2: for feature subspace m = 1 to M do

pred.vgam = array(NA,dim=c(n,K0,3)) ## 3 repetitions
pred.new.vgam = array(NA,dim=c(n.new,K0,3)) ## 3 repetitions
##-----
## Algo3: for replication j = 1 to J do

## REPLICATION j=1:
for(parti1 in 1:K0){ ## partition of the subspaces
train1_par = train1[,c(subspaces[[parti1]],k+1)]
test1_par = test1[,c(subspaces[[parti1]],k+1)]

## Algo4: Fit a classifier  $T(x_j, z)$ ,  $x_j \in S_m$ , to the training data
mod1 <- tune( "svm", STATUS_fact ~ . ,
              data = train1_par,
              kernel = "linear",
              ranges = list(cost=c(0.01,0.1,0.5,1,5,10,20,50)) )
## summary(mod1)
mejor_mod1 <- mod1$best.model

## Algo5: Compute the C response probabilities  $\{\pi^{(m,j)}_{ic}\}$ , for  $i=1, \dots, n$ .
## Predictions
predict1 <- predict(mejor_mod1, newdata = train1_par)
predict1.new <- predict(mejor_mod1, newdata = test1_par)

pred.vgam[,parti1,1] = predict1
pred.new.vgam[,parti1,1] = predict1.new
}

## REPLICATION j=2:
for(parti2 in 1:K0){ ## partition of the subspaces
train2_par = train2[,c(subspaces[[parti2]],k+1)]
test2_par = test2[,c(subspaces[[parti2]],k+1)]

## Algo4: Fit a classifier  $T(x_j, z)$ ,  $x_j \in S_m$ , to the training data
mod2 <- tune( "svm", STATUS_fact ~ . ,
              data = train2_par,
              kernel = "linear",
              ranges = list(cost=c(0.01,0.1,0.5,1,5,10,20,50)) )
## summary(mod2)
mejor_mod2 <- mod2$best.model

## Algo5: Compute the C response probabilities  $\{\pi^{(m,j)}_{ic}\}$ , for  $i=1, \dots, n$ .
## Predictions
predict2 <- predict(mejor_mod2, newdata = train2_par)
predict2.new <- predict(mejor_mod2, newdata = test2_par)

pred.vgam[,parti2,2] = predict2
pred.new.vgam[,parti2,2] = predict2.new

```

```

}

## REPLICATION j=3:
for(parti3 in 1:K0){ ## partition of the subspaces
train3_par = train3[,c(subspaces[[parti3]],k+1)]
test3_par = test3[,c(subspaces[[parti3]],k+1)]

## Algo4: Fit a classifier  $T(x_j, z)$ ,  $x_j \in S_m$ , to the training data
mod3 <- tune( "svm", STATUS_fact ~ . ,
             data = train3_par,
             kernel = "linear",
             ranges = list(cost=c(0.01,0.1,0.5,1,5,10,20,50)) )
## summary(mod3)
mejor_mod3 <- mod3$best.model

## Algo5: Compute the C response probabilities  $\{\pi^{(m,j)}_{ic}\}$ , for  $i=1, \dots, n$ .
## Predictions
predict3 <- predict(mejor_mod3, newdata = train3_par)
predict3.new <- predict(mejor_mod3, newdata = test3_par)

pred.vgam[,parti3,3] = predict3
pred.new.vgam[,parti3,3] = predict3.new
}

##-----
## Algo6: End for replication  $j = 1$  to  $J$ 
## Algo7: End for feature subspace  $m = 1$  to  $M$ 
##-----
## Algo8: Output: compute the response probabilities  $\pi_{ic} = \text{mean}(\{\pi^{(m,j)}_{ic}\})$ 
##-----
## Algo8: Output: compute the response category  $T^*(x, z) = \arg \max \{\pi_{ic}\}$ 

pred.vgam_max = array(NA, dim=n)
for(i in 1:n){
  pred.vgam_max[i] = Mode(pred.vgam[i,,])
}
### Predict new subjects
pred.new.vgam_max = array(NA, dim=n.new)
for(i in 1:n.new){
  pred.new.vgam_max[i] = Mode(pred.new.vgam[i,,])
}

##-----
## End FESPAE
##-----
## Classification Metrics for models predicting nominal outcomes

## Accuracy Rate
FitAccuracy[sim,] = c(sum(Yc==pred.vgam_max)/n)

TestAccuracy[sim,] = c(sum(Yc.new==pred.new.vgam_max)/n.new)

## Precision

```

```

for(cate in 1:3){
  FitPrecisionClass[sim,1, cate] = fn_precision_class(Yc, pred.vgam_max, cate)
  TestPrecisionClass[sim,1, cate] = fn_precision_class(Yc.new, pred.new.vgam_max, cate)
}
FitPrecisionMacroAve[sim, 1] = mean(FitPrecisionClass[sim, 1,])
TestPrecisionMacroAve[sim,1] = mean(TestPrecisionClass[sim,1,])

## Recall
for(cate in 1:3){
  FitRecallClass[sim,1, cate] = fn_recall_class(Yc, pred.vgam_max, cate)
  TestRecallClass[sim,1, cate] = fn_recall_class(Yc.new, pred.new.vgam_max, cate)
}
FitRecallMacroAve[sim, 1] = mean(FitRecallClass[sim, 1,])
TestRecallMacroAve[sim,1] = mean(TestRecallClass[sim,1,])

## F1-Score
for(cate in 1:3){
  FitF1ScoreClass[sim,1, cate]= fn_f1score_class(Yc, pred.vgam_max, cate)
  TestF1ScoreClass[sim,1, cate] = fn_f1score_class(Yc.new, pred.new.vgam_max, cate)
}
FitF1ScoreMacroAve[sim, 1] = mean(FitF1ScoreClass[sim, 1,])
TestF1ScoreMacroAve[sim,1] = mean(TestF1ScoreClass[sim,1,])

##-----
} ## END sim
##-----

```

# Results

## Accuracy Rate

```
columna = c("ensemble")
renglon = c("fit_mean", "fit_sd", "test_mean", "test_sd")

summary(FitAccuracy)
```

```
##           V1
##  Min.      :0.6488
## 1st Qu.:0.6905
##  Median :0.7083
##   Mean   :0.7044
## 3rd Qu.:0.7202
##   Max.   :0.7500
```

```
apply(FitAccuracy, 2, "sd")
```

```
## [1] 0.02257851
```

```
summary(TestAccuracy)
```

```
##           V1
##  Min.      :0.4737
## 1st Qu.:0.5921
##  Median :0.6316
##   Mean   :0.6251
## 3rd Qu.:0.6491
##   Max.   :0.7719
```

```
apply(TestAccuracy, 2, "sd")
```

```
## [1] 0.05930596
```

```
RESaccuracy <- rbind(apply(FitAccuracy, 2, "mean"), apply(FitAccuracy, 2, "sd"),
                     apply(TestAccuracy, 2, "mean"), apply(TestAccuracy, 2, "sd"))
colnames(RESaccuracy) = columna
rownames(RESaccuracy) = renglon
write.csv(RESaccuracy, file=paste0(archivo, "_accuracy", ".csv"))
```

## Precision Macro Average

```
summary(FitPrecisionMacroAve)
```

```
##          V1
##  Min.    :0.6819
## 1st Qu.:0.7182
##  Median :0.7401
##   Mean   :0.7361
## 3rd Qu.:0.7511
##   Max.   :0.7994
```

```
apply(FitPrecisionMacroAve,2,"sd")
```

```
## [1] 0.02336404
```

```
summary(TestPrecisionMacroAve)
```

```
##          V1
##  Min.    :0.5231
## 1st Qu.:0.6238
##  Median :0.6635
##   Mean   :0.6632
## 3rd Qu.:0.7088
##   Max.   :0.7769
```

```
apply(TestPrecisionMacroAve,2,"sd")
```

```
## [1] 0.05851073
```

```
RESprecision <- rbind(apply(FitPrecisionMacroAve,2,"mean"), apply(FitPrecisionMacroAve,2,"sd"),
                      apply(TestPrecisionMacroAve,2,"mean"), apply(TestPrecisionMacroAve,2,"sd"))
colnames(RESprecision) = columna
rownames(RESprecision) = renglon
write.csv(RESprecision, file=paste0(archivo,"_precision",".csv"))
```

## Recall Macro Average

```
summary(FitRecallMacroAve)
```

```
##          V1
##  Min.    :0.6488
## 1st Qu.:0.6905
##  Median :0.7083
##   Mean  :0.7044
## 3rd Qu.:0.7202
##   Max.  :0.7500
```

```
apply(FitRecallMacroAve,2,"sd")
```

```
## [1] 0.02257851
```

```
summary(TestRecallMacroAve)
```

```
##          V1
##  Min.    :0.4737
## 1st Qu.:0.5921
##  Median :0.6316
##   Mean  :0.6251
## 3rd Qu.:0.6491
##   Max.  :0.7719
```

```
apply(TestRecallMacroAve,2,"sd")
```

```
## [1] 0.05930596
```

```
RESrecall <- rbind(apply(FitRecallMacroAve,2,"mean"), apply(FitRecallMacroAve,2,"sd"),
                    apply(TestRecallMacroAve,2,"mean"),apply(TestRecallMacroAve,2,"sd"))
colnames(RESrecall) = columna
rownames(RESrecall) = renglon
write.csv(RESrecall, file=paste0(archivo,"_recall",".csv"))
```

## F1-Score Macro Average

```
summary(FitF1ScoreMacroAve)
```

```
##          V1
##  Min.    :0.6510
## 1st Qu.:0.6911
##  Median :0.7097
##   Mean   :0.7073
## 3rd Qu.:0.7235
##   Max.   :0.7534
```

```
apply(FitF1ScoreMacroAve,2,"sd")
```

```
## [1] 0.02286065
```

```
summary(TestF1ScoreMacroAve)
```

```
##          V1
##  Min.    :0.4817
## 1st Qu.:0.5935
##  Median :0.6343
##   Mean   :0.6259
## 3rd Qu.:0.6556
##   Max.   :0.7721
```

```
apply(TestF1ScoreMacroAve,2,"sd")
```

```
## [1] 0.05910695
```

```
RESf1score <- rbind(apply(FitF1ScoreMacroAve,2,"mean"), apply(FitF1ScoreMacroAve,2,"sd"),
                    apply(TestF1ScoreMacroAve,2,"mean"), apply(TestF1ScoreMacroAve,2,"sd"))
colnames(RESf1score) = columna
rownames(RESf1score) = renglon
write.csv(RESf1score, file=paste0(archivo,"_f1score",".csv"))
```