Random Splitting Random Forest for Categorical Response

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Setting Up

We download and install the **RSRF** in the Rstudio:

```
#library(devtools)
#install_github("mohammad-fayaz/RSRF")
library(RSRF)
library(data.table)
```

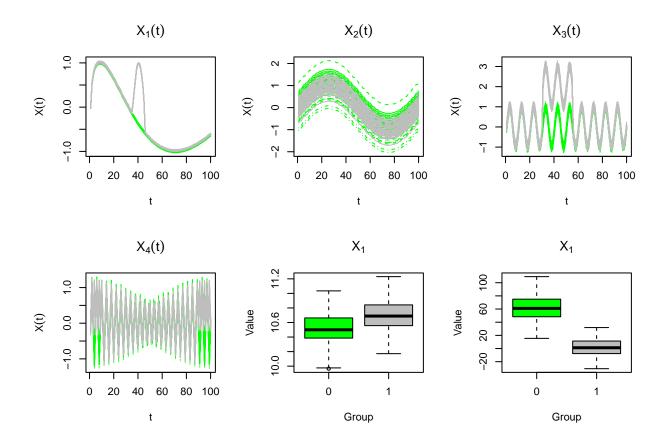
Simulating Data

We simulate the dataset with **makeSIMData** function. It has four arguments including: **nss_1** is the number of sample size of group 1,**nss_2** is the number of sample size of group 2, *responseType* is the type of response and **Seed** is the seed number in the memory.

```
nSample_1 = 100
nSample_2 = 100
Sim_Data <- makeSIMData(nSS_1 = 100 , nSS_2 = 100 , responseType = "Categorical", Seed=2022)</pre>
```

We plot the simulated data.

```
par(mfrow=c(2,3))
matplot(t(Sim_Data[[1]]),type="l",col=c(rep("Green",nSample_1),rep("Grey",nSample_2)),xlab = expression
matplot(t(Sim_Data[[2]]),type="l",col=c(rep("Green",nSample_1),rep("Grey",nSample_2)),xlab = expression
matplot(t(Sim_Data[[3]]),type="l",col=c(rep("Green",nSample_1),rep("Grey",nSample_2)),xlab = expression
matplot(t(Sim_Data[[4]]),type="l",col=c(rep("Green",nSample_1),rep("Grey",nSample_2)),xlab = expression
boxplot(Sim_Data[[5]][1][-(1:4),] ~ Sim_Data[[6]][-(1:4)] ,col=c("Green","Grey"),main=expression(X[1]),
boxplot(Sim_Data[[5]][2][-(1:4),] ~ Sim_Data[[6]][-(1:4)] ,col=c("Green","Grey"),main=expression(X[1]),
```



Models

Model Specification

First we define the model arguments:

```
Response <- as.factor(c(Sim_Data[[6]]))</pre>
## Functional Covariate Specifications
FDList <- list()</pre>
FDList[[1]] <- Sim_Data[[1]]</pre>
FDList[[2]] <- Sim_Data[[2]]</pre>
FDList[[3]] <- Sim_Data[[3]]</pre>
FDList[[4]] <- Sim_Data[[4]]</pre>
 ## Parameter Specification for each Functioanl Covariate
Min <- list()</pre>
Max <- list()</pre>
PARAMS_1 <- list()</pre>
DIST_1 <- list()</pre>
TYPE <- list()</pre>
PARAMS_2 <- list()</pre>
STATS <- list()
DIST_2 <- list()</pre>
```

```
### Functional Covariate 1 Specificaion
Min[[1]] <- 1
                               ## minimum time domain
Max[[1]] \leftarrow 100
                               ## maximum time domain
DIST 1[[1]] <- c("Exponential") ## The Random splitting distribution
PARAMS_1[[1]] <- c(0.1,0,0) ## The parameter for the distribution TYPE[[1]] <- c("Disjoint") ## Type of splitting
DIST_2[[1]] <- c("")
                              ## if type is overlap , the distribution of the overlap
                             ## if type is overlap , the parameter of the distribution
PARAMS_2[[1]] \leftarrow c(0,0,0)
STATS[[1]]<- c("mean")
                             ## the statistics for each interval
### Functional Covariate 2 Specificaion
Min[[2]] <- 1
                                ## minimum time domain
Max[[2]] \leftarrow 100
                                ## maximum time domain
DIST_1[[2]] <- c("Exponential") ## The Random splitting distribution
PARAMS_1[[2]] <- c(0.1,0,0) ## The parameter for the distribution
TYPE[[2]] <- c("Disjoint")</pre>
                              ## Type of splitting
DIST_2[[2]] <- c("")
                              ## if type is overlap , the distribution of the overlap
                              ## if type is overlap , the parameter of the distribution
### Functional Covariate 3 Specificaion
Min[[3]] <- 1
                                ## minimum time domain
Max[[3]] \leftarrow 100
                                ## maximum time domain
DIST_1[[3]] <- c("Exponential") ## The Random splitting distribution
PARAMS_1[[3]] <- c(0.1,0,0) ## The parameter for the distribution
TYPE[[3]] <- c("Disjoint")</pre>
                              ## Type of splitting
DIST_2[[3]] <- c("")
                              ## if type is overlap , the distribution of the overlap
PARAMS_2[[3]] \leftarrow c(0,0,0)
                             ## if type is overlap , the parameter of the distribution
                      ## the statistics for each interval
STATS[[3]]<- c("mean")
### Functional Covariate 4 Specificaion
Min[[4]] <- 1
                                ## minimum time domain
Max[[4]] \leftarrow 100
                                ## maximum time domain
DIST_1[[4]] <- c("Exponential") ## The Random splitting distribution
DIST_2[[4]] <- c("")
                               ## if type is overlap , the distribution of the overlap
                             ## if type is overlap , the parameter of the distribution
PARAMS_2[[4]] \leftarrow c(0,0,0)
STATS[[4]]<- c("mean")
                             ## the statistics for each interval
## Non-Functional Covariate Specifications
Covariates_all <- data.frame(c_01= Sim_Data[[5]][,1],c_02= Sim_Data[[5]][,2])
## General Settings
mtree0 <- 100
k0 <- 500
```

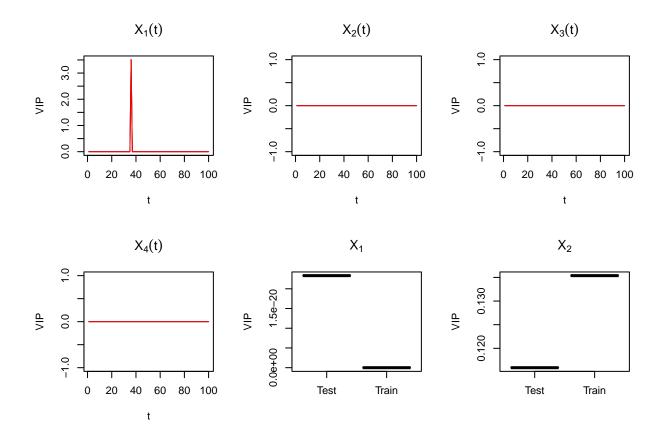
Bagging We run the bagging model. In this reagrd RFMethod = c("Bagging") and $VIP_Algorithm = c("Normal")$:

```
####### Running the model
BG_NO_Result <- RS_RF_SRC_H(
    ResponseVar=Response,
    Covariates=Covariates_all,</pre>
```

```
RawData=FDList,
Stat=STATS ,
min=Min,
max=Max,
Params=PARAMS 1,
Distribution=DIST 1,
Params2=PARAMS_2,
Distribution2=DIST_2,
type=TYPE,
m=mtree0,
k=k0,
ResponseType="Categorical",
RFMethod = c("Bagging"),
NUM_Covariates=1,
Block.Size = 10,
SplitRule = c("gini"),
Importance= TRUE,
Ensemble = c("all"),
Proximity = TRUE,
VIP Algorithm = c("Normal"))
```

We plot the Variable Importance Plot for each covariate:

```
BG_NO_Result_IMP <- data.table(BG_NO_Result$IMP_VALUE)</pre>
par(mfrow=c(2,3))
## X1(t)
plot(x=1:100,y=BG_NO_Result_IMP[,mean(VIMP_Train),by=VARS][3:102]$V1, xlab = expression(t),ylab = "VIP"
lines(x=1:100,y=BG_NO_Result_IMP[,mean(VIMP_Test),by=VARS][3:102]$V1, xlab = expression(t),ylab = "VIP"
## X2(t)
plot(x=1:100,y=BG NO Result IMP[,mean(VIMP Train),by=VARS][103:202]$V1, xlab = expression(t),ylab = "VI
lines(x=1:100,y=BG NO Result IMP[,mean(VIMP Test),by=VARS][103:202]$V1, xlab = expression(t),ylab = "VI
plot(x=1:100,y=BG_NO_Result_IMP[,mean(VIMP_Train),by=VARS][203:302]$V1, xlab = expression(t),ylab = "VI
lines(x=1:100,y=BG_NO_Result_IMP[,mean(VIMP_Test),by=VARS][203:302]$V1, xlab = expression(t),ylab = "VI
## X4(t)
plot(x=1:100,y=BG_NO_Result_IMP[,mean(VIMP_Train),by=VARS][303:402]$V1, xlab = expression(t),ylab = "VI
lines(x=1:100,y=BG_NO_Result_IMP[,mean(VIMP_Test),by=VARS][303:402]$V1, xlab = expression(t),ylab = "VI
boxplot(c(BG_NO_Result_IMP[,mean(VIMP_Train),by=VARS][1]$V1, BG_NO_Result_IMP[,mean(VIMP_Test),by=VARS]
## X2
boxplot(c(BG_NO_Result_IMP[,mean(VIMP_Train),by=VARS][2]$V1, BG_NO_Result_IMP[,mean(VIMP_Test),by=VARS]
```



We see only the first functional covariate between 35 and 40 has high VIP and the second non-functional covariate in both train (Black) and test(Red). We have following summary statistics **Accuracy**, **Sensitivity** and **Specificity** with **RS_Summary**() function:

```
RS_Summary(Dataset =BG_NO_Result$Result , Outcome_Type = c("Categorical"))
##
       Train_ACC_Mean Train_ACC_sd Train_ACC_Q1 Train_ACC_Q3 Test_ACC_Mean
## 25%
       Test_ACC_sd Test_ACC_Q1 Test_ACC_Q3 Train_SEN_Mean Train_SEN_sd
##
##
  25%
       0.01428722
       Train_SEN_Q1 Train_SEN_Q3 Test_SEN_Mean Test_SEN_sd Test_SEN_Q1 Test_SEN_Q3
##
                                      0.9974375 0.01846575
##
  25%
                  1
                                1
##
       Train_SPE_Mean Train_SPE_sd Train_SPE_Q1 Train_SPE_Q3 Test_SPE_Mean
                                  0
                                               1
                                                            1
                                                                  0.9911775
## 25%
##
       Test_SPE_sd Test_SPE_Q1 Test_SPE_Q3
## 25%
         0.0171091
                              1
```

Random Forest We run the random forest model. In this reagrd RFMethod = c("RandomForest") and $VIP_Algorithm = c("Normal")$. In this regard, we use only 2 covariate among 6 covariates in each tree by setting $NUM_Covariates=2$:

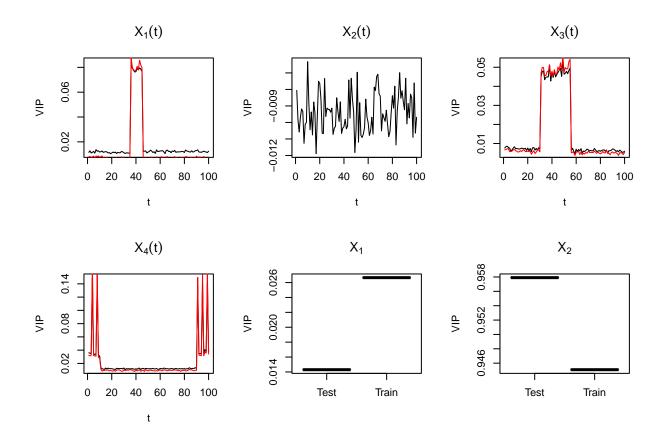
```
####### Running the model
RF_NO_Result <- RS_RF_SRC_H(
    ResponseVar=Response,
    Covariates=Covariates_all,</pre>
```

```
RawData=FDList,
Stat=STATS ,
min=Min,
max=Max,
Params=PARAMS 1,
Distribution=DIST 1,
Params2=PARAMS 2,
Distribution2=DIST_2,
type=TYPE,
m=mtree0,
k=k0,
ResponseType="Categorical",
RFMethod = c("RandomForest"),
NUM_Covariates=2,
Block.Size = 10,
SplitRule = c("gini"),
Importance= TRUE,
Ensemble = c("all"),
Proximity = TRUE,
VIP_Algorithm = c("Normal"))
```

We plot the Variable Importance Plot for each covariate:

```
RF_NO_Result_IMP <- data.table(RF_NO_Result$IMP_VALUE)</pre>
RF_NO_Result_IMP <- RF_NO_Result_IMP[is.na(COV_NUM) == FALSE]</pre>
RF_NO_Result_IMP_Train <- RF_NO_Result_IMP[,mean(VIMP_Train),by=VARS]</pre>
RF_NO_Result_IMP_Test <- RF_NO_Result_IMP[,mean(VIMP_Test),by=VARS]</pre>
## Train VIP
VIP C1 Train <- RF NO Result IMP Train[which(substr(RF NO Result IMP Train$VARS,1,4) == "c 01"),]
VIP C2 Train <- RF NO Result IMP Train[which(substr(RF NO Result IMP Train$VARS,1,4) == "c 02"),]
VIP_X1_Train <- RF_NO_Result_IMP_Train[which(substr(RF_NO_Result_IMP_Train$VARS,1,4) == "x_01"),]</pre>
VIP_X2_Train <- RF_NO_Result_IMP_Train[which(substr(RF_NO_Result_IMP_Train$VARS,1,4) == "x_02"),]</pre>
VIP_X3_Train <- RF_NO_Result_IMP_Train[which(substr(RF_NO_Result_IMP_Train$VARS,1,4) == "x_03"),]</pre>
VIP_X4_Train <- RF_NO_Result_IMP_Train[which(substr(RF_NO_Result_IMP_Train$VARS,1,4) == "x_04"),]</pre>
VIP_X1_Train$Time <- as.numeric(substr(VIP_X1_Train$VARS,6,9))</pre>
VIP_X2_Train$Time <- as.numeric(substr(VIP_X2_Train$VARS,6,9))</pre>
VIP_X3_Train$Time <- as.numeric(substr(VIP_X3_Train$VARS,6,9))</pre>
VIP_X4_Train$Time <- as.numeric(substr(VIP_X4_Train$VARS,6,9))</pre>
VIP_X1_Train <- VIP_X1_Train[order(VIP_X1_Train$Time,decreasing = FALSE)]</pre>
VIP_X2_Train <- VIP_X2_Train[order(VIP_X2_Train$Time,decreasing = FALSE)]</pre>
VIP_X3_Train <- VIP_X3_Train[order(VIP_X3_Train$Time, decreasing = FALSE)]</pre>
VIP_X4_Train <- VIP_X4_Train[order(VIP_X4_Train$Time,decreasing = FALSE)]</pre>
## Test VIP
VIP_C1_Test <- RF_NO_Result_IMP_Test[which(substr(RF_NO_Result_IMP_Test$VARS,1,4) == "c_01"),]</pre>
VIP_C2_Test <- RF_NO_Result_IMP_Test[which(substr(RF_NO_Result_IMP_Test$VARS,1,4) == "c_02"),]</pre>
VIP_X1_Test <- RF_NO_Result_IMP_Test[which(substr(RF_NO_Result_IMP_Test$VARS,1,4) == "x_01"),]</pre>
```

```
VIP_X2_Test <- RF_NO_Result_IMP_Test[which(substr(RF_NO_Result_IMP_Test$VARS,1,4) == "x_02"),]</pre>
VIP_X3_Test <- RF_NO_Result_IMP_Test[which(substr(RF_NO_Result_IMP_Test$VARS,1,4) == "x_03"),]</pre>
VIP_X4_Test <- RF_NO_Result_IMP_Test[which(substr(RF_NO_Result_IMP_Test$VARS,1,4) == "x_04"),]</pre>
VIP_X1_Test$Time <- as.numeric(substr(VIP_X1_Test$VARS,6,9))</pre>
VIP_X2_Test$Time <- as.numeric(substr(VIP_X2_Test$VARS,6,9))</pre>
VIP_X3_Test$Time <- as.numeric(substr(VIP_X3_Test$VARS,6,9))</pre>
VIP X4 Test$Time <- as.numeric(substr(VIP X4 Test$VARS,6,9))</pre>
VIP_X1_Test <- VIP_X1_Test[order(VIP_X1_Test$Time, decreasing = FALSE)]</pre>
VIP_X2_Test <- VIP_X2_Test[order(VIP_X2_Test$Time, decreasing = FALSE)]</pre>
VIP_X3_Test <- VIP_X3_Test[order(VIP_X3_Test$Time, decreasing = FALSE)]</pre>
VIP_X4_Test <- VIP_X4_Test[order(VIP_X4_Test$Time, decreasing = FALSE)]</pre>
par(mfrow=c(2,3))
## X1(t)
\texttt{plot}(\texttt{x=1:100,y=VIP\_X1\_Train\$V1}, \ \texttt{xlab} = \texttt{expression}(\texttt{t}), \\ \texttt{ylab} = \texttt{"VIP"}, \\ \texttt{main=expression}(\texttt{X[1](t))}, \\ \texttt{type="l"})
lines(x=1:100,y=VIP_X1_Test$V1, xlab = expression(t),ylab = "VIP", main= expression(X[1](t)),type="l",c
plot(x=1:100,y=VIP_X2_Train$V1, xlab = expression(t),ylab = "VIP" ,main= expression(X[2](t)),type="l")
\label{eq:continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_continuous_simple_
plot(x=1:100,y=VIP_X3_Train$V1, xlab = expression(t),ylab = "VIP" ,main= expression(X[3](t)),type="1")
lines(x=1:100,y=VIP_X3_Test$V1, xlab = expression(t),ylab = "VIP" ,main= expression(X[3](t)),type="l",c
plot(x=1:100,y=VIP_X4_Train$V1, xlab = expression(t),ylab = "VIP" ,main= expression(X[4](t)),type="l")
lines(x=1:100,y=VIP X4 Test$V1, xlab = expression(t),ylab = "VIP", main= expression(X[4](t)),type="1",c
boxplot(c(VIP_C1_Train$V1, VIP_C1_Test$V1) ~ c("Train", "Test"), xlab = c(""),ylab = "VIP", main= expres
## X2
boxplot(c(VIP_C2_Train$V1, VIP_C2_Test$V1) ~ c("Train", "Test"), xlab = c(""), ylab = "VIP", main= expres
```



As we expected the VIP plot for all covariates are made. The summary statistics of this model is:

```
RS_Summary(Dataset =RF_NO_Result$Result , Outcome_Type = c("Categorical"))
       Train_ACC_Mean Train_ACC_sd Train_ACC_Q1 Train_ACC_Q3 Test_ACC_Mean
##
## 25%
##
       Test_ACC_sd Test_ACC_Q1 Test_ACC_Q3 Train_SEN_Mean Train_SEN_sd
## 25%
       0.03215903
                     0.9666667
##
       Train_SEN_Q1 Train_SEN_Q3 Test_SEN_Mean Test_SEN_sd Test_SEN_Q1 Test_SEN_Q3
##
  25%
                                     0.9872641 0.02947529
                               1
##
       Train_SPE_Mean Train_SPE_sd Train_SPE_Q1 Train_SPE_Q3 Test_SPE_Mean
## 25%
                                                            1
                                                                  0.9689505
##
       Test_SPE_sd Test_SPE_Q1 Test_SPE_Q3
       0.04671908
                     0.9480249
## 25%
```

Random Splitting Random Forest We run the random splitting random forest model. In this reagrd RFMethod = c("RandomForest") and VIP_Algorithm = c("RS"). In this regard, we use only 2 covariate among 6 covariates in each tree by setting NUM_Covariates=2:

```
####### Running the model
RF_RS_Result <- RS_RF_SRC_H(
    ResponseVar=Response,
    Covariates=Covariates_all,
    RawData=FDList,
    Stat=STATS ,</pre>
```

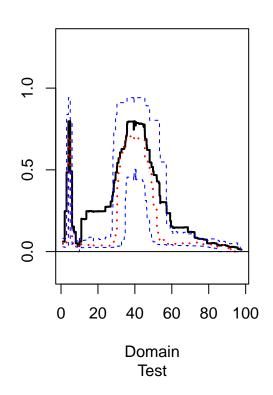
```
min=Min,
max=Max,
Params=PARAMS_1,
Distribution=DIST_1,
Params2=PARAMS_2,
Distribution2=DIST_2,
type=TYPE,
m=mtree0,
k=k0,
ResponseType="Categorical",
RFMethod = c("RandomForest"),
NUM_Covariates=2,
Block.Size = 10,
SplitRule = c("gini"),
Importance= TRUE,
Ensemble = c("all"),
Proximity = TRUE,
VIP_Algorithm = c("RS"))
```

We plot the Variable Importance Plot for each covariate:

```
## X1(t)
par(mfrow=c(1,2))
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function")
```

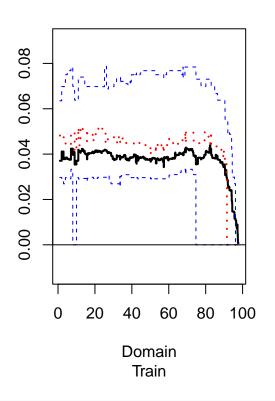
The VI Plot: Curve 1

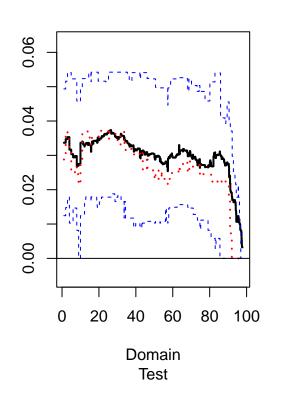
0 20 40 60 80 100 Domain Train



```
## X2(t)
par(mfrow=c(1,2))
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function")
```

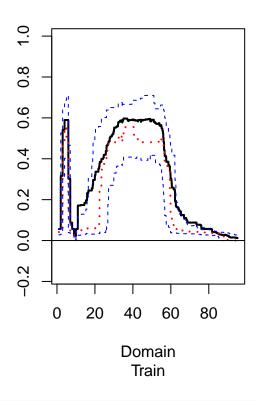
The VI Plot: Curve 2

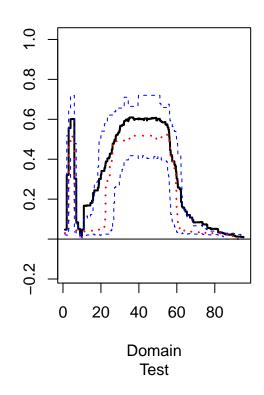




```
## X3(t)
par(mfrow=c(1,2))
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function")
```

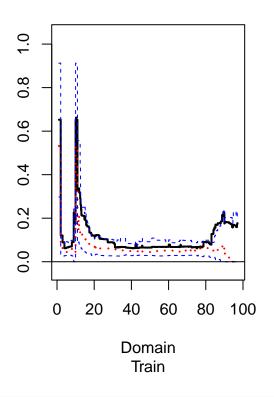
The VI Plot: Curve 3

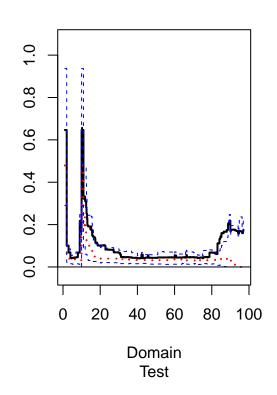




```
## X4(t)
par(mfrow=c(1,2))
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Function")
```

The VI Plot: Curve 4

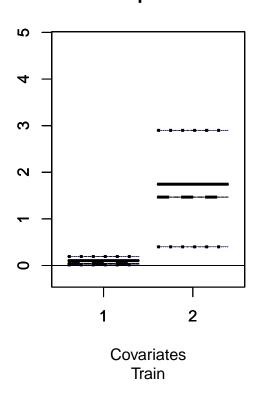


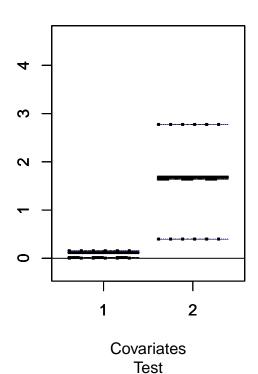


```
## X1 and X2
par(mfrow=c(1,2))
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Non-Func"
RS_VARIMP_SRC_PLOT(Dataset = RF_RS_Result$IMP_VALUE, VIP_Algorithm = c("RS"), COVAR_TYPE = c("Non-Func")
```

Varibale Importance Plot

Varibale Importance Plot





As we expected the VIP plot for all co variates are made. The summary statistics of this model is:

```
RS_Summary(Dataset =RF_RS_Result$Result , Outcome_Type = c("Categorical"))
```

```
Train_ACC_Mean Train_ACC_sd Train_ACC_Q1 Train_ACC_Q3 Test_ACC_Mean
##
## 25%
##
       Test_ACC_sd Test_ACC_Q1 Test_ACC_Q3 Train_SEN_Mean Train_SEN_sd
## 25%
       0.03408249
                     0.9833333
##
       Train_SEN_Q1 Train_SEN_Q3 Test_SEN_Mean Test_SEN_sd Test_SEN_Q1 Test_SEN_Q3
##
  25%
                                       0.98538 0.03465776
##
       Train_SPE_Mean Train_SPE_sd Train_SPE_Q1 Train_SPE_Q3 Test_SPE_Mean
## 25%
##
       Test_SPE_sd Test_SPE_Q1 Test_SPE_Q3
## 25% 0.05332915
                     0.9655172
```

Conclusion

The VIP for random splitting random forest is more informative than the VIP for random forest and bagging.