

# Variable Selection Using Random Forests

## The VSURF R package

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## Random Forests

- introduced by Breiman (2001)
- ensemble methods family Dietterich (1999, 2000)
- very efficient algorithm of statistical learning, for both classification and regression problems.

$\mathcal{L}_n = \{(X_1, Y_1), \dots, (X_n, Y_n)\}$  i.i.d. r.v. with the same distribution as  $(X, Y)$ .

$X = (X^1, \dots, X^p) \in \mathbb{R}^p$  (input variables)

$Y \in \mathcal{Y}$  (response variable)

- $\mathcal{Y} = \mathbb{R}$  : regression
- $\mathcal{Y} = \{1, \dots, L\}$  : classification

**Goal** : build a predictor  $\hat{h} : \mathbb{R}^p \rightarrow \mathcal{Y}$ .

## Definition : Random Forests (Breiman 2001)

$\{\hat{h}(\cdot, \Theta_\ell), 1 \leq \ell \leq q\}$  tree-predictor collection,  $(\Theta_\ell)_{1 \leq \ell \leq q}$  i.i.d. r.v. independent with  $\mathcal{L}_n$ .

Random forests predictor  $\hat{h}$  obtained by aggregating the collection of trees.

Agreggation :

$$\blacksquare \hat{h}(x) = \frac{1}{q} \sum_{\ell=1}^q \hat{h}(x, \Theta_\ell) \quad \text{regression}$$

$$\blacksquare \hat{h}(x) = \operatorname{argmax}_{1 \leq c \leq L} \sum_{\ell=1}^q \mathbb{1}_{\hat{h}(x, \Theta_\ell)=c} \quad \text{classification}$$

Tree : piece-wise constant predictor, obtained by a recursive dyadic partitioning of  $\mathbb{R}^p$ .

Restriction : splits parallel to axes.

Typically, at each step of the partitioning, we seek the "best" split of the data  $\mathcal{L}_n$ .

Example : **CART**, Breiman et.al. (1984).

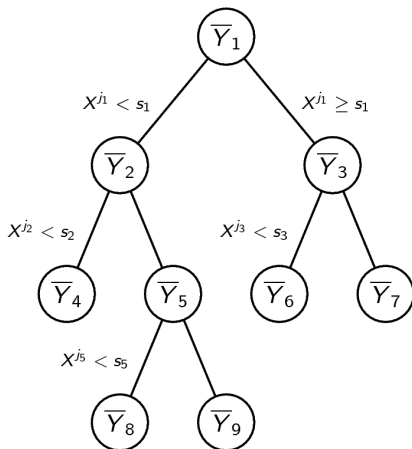
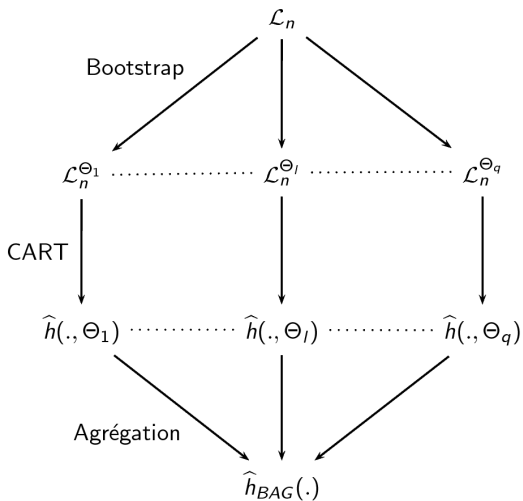


Figure : Regression tree

# Bagging (Breiman 1996)



CART instability  $\Rightarrow$  increase of efficiency

# Random Forests-Random Inputs (Breiman 2001)

## Definition : RI-tree

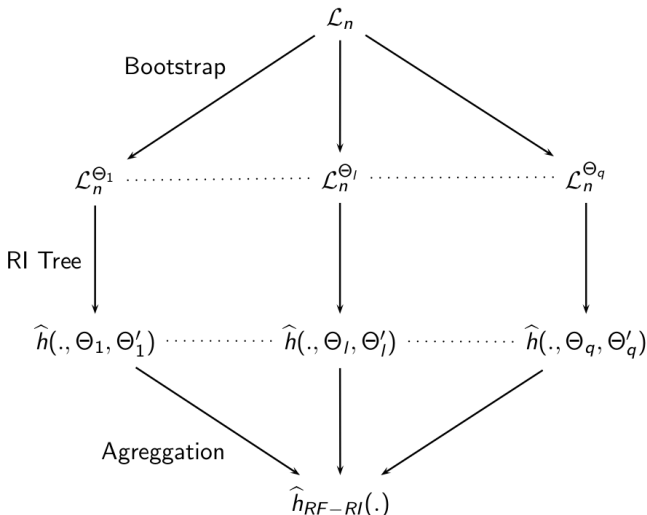
We define a RI-tree as the variant of CART consisting to select at random, at each node, **mtry** variables, and split using only the selected variables.

**mtry** is the same for all nodes of all trees in the forest.

## Definition : Random Forests-RI

A Random Forests-RI is obtained by doing Bagging with RI-trees.

## Random Forests-RI



Additional randomness  $\Rightarrow$  increase of efficiency

# Random Forests-RI

R package `randomForest`:

- based on the initial code of Breiman, Cutler (2000)
- well described in Liaw, Wiener (2002)

Main parameters of the `randomForest` procedure :

- `ntree` : number of trees in the forest (default = 500)
- `mtry` : number of variables randomly selected at each node (default =  $\sqrt{p}$ )



# Prediction estimator error

OOB = Out Of Bag ( $\approx$  "Out Of Bootstrap")

## OOB error

To predict  $X_i$ , we only aggregate predictors  $\hat{h}(\cdot, \Theta_\ell)$  built on bootstrap samples **which does not contain**  $(X_i, Y_i)$ .

$\Rightarrow$  OOB error :

- $\frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2$  regression
- $\frac{1}{n} \sum_{i=1}^n \mathbb{1}_{Y_i \neq \hat{Y}_i}$  classification

# Variable importance

Breiman (2001), Strobl *et al.* (2007, 2008), Ishwaran (2007), Archer *et al.* (2008), Louppe *et al.* (2013)

## Definition: Variable importance (VI)

Let  $j \in \{1, \dots, p\}$ . For each OOB sample we permute at random the  $j$ -th variable values of the data.

**Variable importance of the  $j$ -th variable** = mean increase of the error of a tree after permutation.

*The more the error increases, the more important is the variable.*

## 1 Introduction

- Definition
- Examples

## 2 Variable selection

- Procedure
- Application

# Variable Selection

Genuer, Poggi, Tuleau (2010)

We distinguish **two different objectives**:

- 1 to select all important variables, even with high redundancy, for **interpretation** purpose
- 2 to find a sufficient parsimonious set of important variables for **prediction**

*Our aim is to build an automatic procedure,  
which fulfills these two objectives*

One earlier work must be cited: **Díaz-Uriarte, Alvarez de Andrés (2006)**.

# SRBCT

A **high dimensional classification** dataset, available in `mixOmics` package

$$n = 63 \quad p = 2308$$

- **Input variables** : gene expressions
- **Output variable** : class tumour of each sample (4 classes)

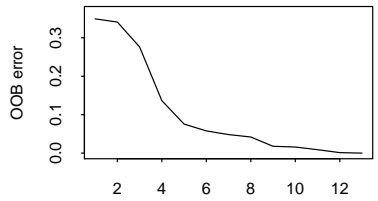
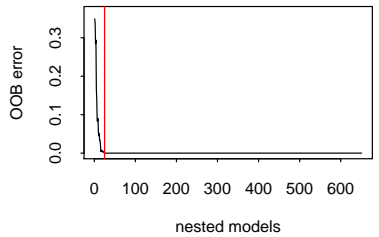
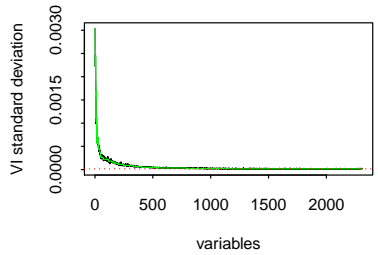
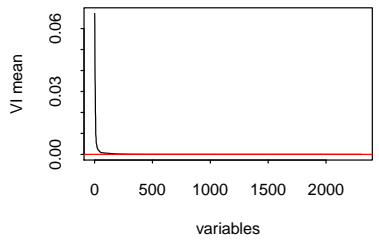
```
library(VSURF)
library(mixOmics)
data(srbct)
```

```
vSRBCT <- VSURF(x = srbct$gene, y = srbct$class)
```

```
summary(vSRBCT)
```

```
##  
## VSURF computation time: 2.7 hours  
##  
## VSURF selected:  
## 651 variables at thresholding step (in 7.2 mins)  
## 25 variables at interpretation step (in 2.6 hours)  
## 13 variables at prediction step (in 14.6 secs)
```

# plot(vSRBCT)



# Computational remarks

The first step keeps obviously too many variables for this example. Increasing the `nmin` parameter significantly reduces the overall computation time:

```
vSRBCT.nmin10 <- VSURF(x = srbct$gene, y = srbct$class,  
  nmin = 10)
```

```
summary(vSRBCT.nmin10)
```

```
##  
## VSURF computation time: 25.3 mins  
##  
## VSURF selected:  
## 233 variables at thresholding step (in 6.3 mins)  
## 25 variables at interpretation step (in 18.7 mins)  
## 14 variables at prediction step (in 13.6 secs)
```



# Computational remarks

To reduce computational time, we can also use the parallel version of VSURF on one computer (my laptop):

```
vSRBCT.laptop <- VSURF.parallel(x = srbct$gene, y = srbct$class,  
  nmin = 10)
```

```
summary(vSRBCT.laptop)
```

```
##  
## VSURF computation time: 11.3 mins  
##  
## VSURF selected:  
## 233 variables at thresholding step (in 3 mins)  
## 25 variables at interpretation step (in 8.1 mins)  
## 14 variables at prediction step (in 14 secs)  
##  
## VSURF ran in parallel on a PSOCK cluster and used 3 cores
```

# Computational remarks

Or on a cluster of several computers:

```
vSRBCT.cluster <- VSURF.parallel(x = srbct$gene, y = srbct$class,  
  nmin = 10, clusterType = "MPI", ncores = 50)
```

```
summary(vSRBCT.cluster)
```

```
##  
## VSURF computation time: 1.4 mins  
##  
## VSURF selected:  
## 228 variables at thresholding step (in 32.2 secs)  
## 25 variables at interpretation step (in 38.3 secs)  
## 16 variables at prediction step (in 16 secs)  
##  
## VSURF ran in parallel on a MPI cluster and used 50 cores
```

# Ozone

Ozone : A **standard regression** dataset, from mlbench package.

$$n = 366 \quad p = 12$$

## Input variables

V1	Month	V8	Temperature (Sandburg)
V2	Day of month	V9	Temperature (El Monte)
V3	Day of week	V10	Inversion base height
V5	Pressure height	V11	Pressure gradient
V6	Wind speed	V12	Inversion base temperature
V7	Humidity	V13	Visibility

## Output variable

V4 Daily maximum one-hour-average ozone

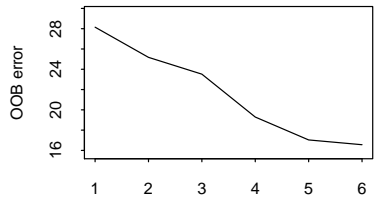
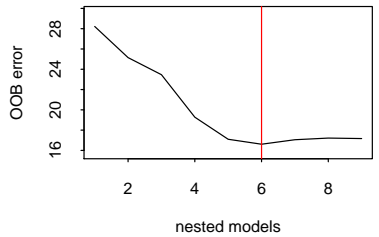
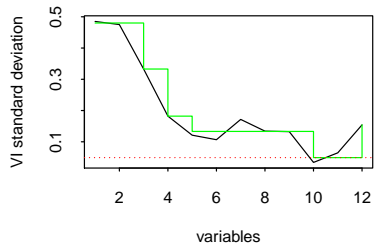
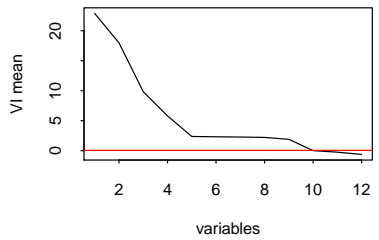
```
library(VSURF)
library(mlbench)
data(Ozone)
```

```
vozone <- VSURF(formula = V4~., data = Ozone,
                na.action = na.omit)
```

```
summary(vozone)
```

```
##
## VSURF computation time: 1.7 mins
##
## VSURF selected:
## 9 variables at thresholding step (in 57.3 secs)
## 6 variables at interpretation step (in 28 secs)
## 6 variables at prediction step (in 17.4 secs)
```

# plot(vozone)









## Concluding Remarks

- Variable selection procedure **fully data-driven**
- Can be applied for **both classification and regression** problems involving **both standard and high-dimensional** datasets
- Handles **mixed data** (categorical and continuous input variables) and **missing data**
- R package available on CRAN (still in development). We invite you to test it:

```
install.packages("VSURF")
```

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# Short bibliography

-  Breiman, L., Friedman J., Olshen R., Stone C. *Classification And Regression Trees*. Chapman & Hall (1984)
-  Breiman, L. *Bagging*. Machine Learning (1996)
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-  Díaz-Uriarte R., Alvarez de Andrés S. *Gene Selection and classification of microarray data using random forest*. BMC Bioinformatics (2006)
-  Genuer R., Poggi J.-M. and Tuleau-Malot C. *Variable selection using random forests*. Pattern Recognition Letters (2010)
-  Genuer R., Poggi J.-M. and Tuleau-Malot C. *VSURF: An R Package for Variable Selection Using Random Forests* (submitted)