

BE3 - partie 1

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06 December, 2022

On reprend le jeu de données concernant la valeur des logements des villes aux alentours de Boston. On cherche à identifier un bon modèle par régression pénalisée, CART, Boosting et Random Forest.

Les variables utilisées sont les suivantes:

CRIM taux de criminalité par habitant

ZN proportion de terrains résidentiels

INDUS proportion de terrains industriels

CHAS 1 si ville en bordure de la rivière Charles 0 sinon

NOX concentration en oxydes d'azote

RM nombre moyen de pièces par logement

AGE proportion de logements construits avant 1940

DIS distance du centre de Boston

RAD accessibilité aux autoroutes de contournement

TAX taux de l'impôt foncier

PTRATIO rapport élèves-enseignant par ville

LSTAT % de la population à faibles revenus

class valeur du logement en 1000\$

L'objectif de ce BE est de comparer différents modèles de machines learning : le modèle linéaire, le modèle linéaire pénalisé (Ridge et Lasso), les modèles linéaires de réduction de dimension (PCR et PLS), les modèles à base d'arbres (CART, Boosting, Bagging et Random Forest).

Lasso = L1

Ridge = L2

Modèles linéaires

On commence par ajuster un modèle linéaire **sans et avec interactions** à partir de l'ensemble d'apprentissage constitué de 300 observations. Évaluer la qualité prédictive de ces deux modèles sur l'ensemble test constitué de 206 observations. On pourra utiliser la commande RMSE du package DiceEval.

```
library(DiceEval)
```

```
## Loading required package: DiceKriging
```

```
library(car)
```

```
## Loading required package: carData
```

```
library(MASS)
```

```
housing = read.table("housing_new.txt", header = T)
p = ncol(housing)
summary(housing)
```

```
##      CRIM      ZN      INDUS      CHAS
##  Min.   : 0.0060  Min.   : 0.00  Min.   : 0.46  Min.   :0.00000
## 1st Qu.: 0.0820  1st Qu.: 0.00  1st Qu.: 5.19  1st Qu.:0.00000
## Median : 0.2565  Median : 0.00  Median : 9.69  Median :0.00000
## Mean   : 3.6135  Mean   : 11.36  Mean   :11.14  Mean   :0.06917
## 3rd Qu.: 3.6770  3rd Qu.: 12.50  3rd Qu.:18.10  3rd Qu.:0.00000
## Max.   :88.9760  Max.   :100.00  Max.   :27.74  Max.   :1.00000
##      NOX      RM      AGE      DIS
##  Min.   :0.3850  Min.   :3.561  Min.   : 2.90  Min.   : 1.130
## 1st Qu.:0.4490  1st Qu.:5.886  1st Qu.: 45.02  1st Qu.: 2.100
## Median :0.5380  Median :6.208  Median : 77.50  Median : 3.208
## Mean   :0.5547  Mean   :6.285  Mean   : 68.57  Mean   : 3.795
## 3rd Qu.:0.6240  3rd Qu.:6.623  3rd Qu.: 94.08  3rd Qu.: 5.189
## Max.   :0.8710  Max.   :8.780  Max.   :100.00  Max.   :12.126
##      RAD      TAX      PTRATIO      LSTAT
##  Min.   : 1.000  Min.   :187.0  Min.   :12.60  Min.   : 1.73
## 1st Qu.: 4.000  1st Qu.:279.0  1st Qu.:17.40  1st Qu.: 6.95
## Median : 5.000  Median :330.0  Median :19.05  Median :11.36
## Mean   : 9.549  Mean   :408.2  Mean   :18.46  Mean   :12.65
## 3rd Qu.:24.000  3rd Qu.:666.0  3rd Qu.:20.20  3rd Qu.:16.95
## Max.   :24.000  Max.   :711.0  Max.   :22.00  Max.   :37.97
##      class
##  Min.   : 5.00
## 1st Qu.:17.02
## Median :21.20
## Mean   :22.53
## 3rd Qu.:25.00
## Max.   :50.00
```

```
dim(housing)
```

```
## [1] 506 13
```

```
set.seed(23)
u = sample(1:nrow(housing), 300)
housing.train = housing[u,]
housing.test = housing[-u,]
```

```
library(caret)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: lattice

##
## Attaching package: 'caret'

## The following objects are masked from 'package:DiceEval':
##
##      MAE, R2, RMSE

# Ajuster un modèle linéaire simple sans interactions
mod_lm <- lm(class ~., data = housing.train)
Y_pred_lm = predict(mod_lm, housing.test[, -p]) -p = excluir a coluna de previsão
RMSE_lm = RMSE(housing.test[, p], Y_pred_lm) # root mean square error
RMSE_lm # 5.9 p = pegar os dados de previsão
```

```
## [1] 5.900007
```

```
# Ajuster un modèle linéaire avec interactions
#a completer : todos os parametros e suas iterações duplas
mod_lm_inter <- lm(class ~., data = housing.train)
length(na.omit(mod_lm_inter$coefficients))
```

```
## [1] 79
```

```
#a completer :
Y_pred_lm_inter = predict(mod_lm_inter, housing.test[, -p])
#a completer :
RMSE_lm_inter = RMSE(housing.test[, p], Y_pred_lm_inter)
RMSE_lm_inter # 4.41
```

```
## [1] 4.416989
```

On remarque qu'en ajoutant les termes d'interaction l'erreur a diminué. Cependant le modèle avec interaction est très complexe (79 termes) donc certainement trop variable. L'idée est de chercher un modèle plus prédictif, i.e. avec une RMSE plus faible que 4.836.

Modèles linéaires pénalisés

Ajuster une régression lasso (commande lars du package lars). Pour ce faire, il est nécessaire de créer une matrice contenant tous les termes (variables principales et les interactions).

```
#-----
# lasso
#-----

library(lars)
```

```
## Loaded lars 1.3
```

```

y = as.matrix(housing.train[, p])
x = as.matrix(housing.train[, -p])
x_extend = x

# makes the binary combinations of all columns
for (i in 1:(p-2)) {
  for (j in 2:(p-1)) {
    x_extend = cbind(x_extend, x[, i] * x[, j])
  }
}

mod_lasso = lars(x_extend, y, type = "lasso")

```

lambda ~ 1/(soma dos coefficients)
t >= soma do modulo dos coeficientes = penalidade

— Etudier la matrice des coefficients (commande coef.lars) et tracer le modèle (commande plot).

```

dim(coef.lars(mod_lasso)) # 186 valeurs de lambda différentes et 133 coefficients
coeff = beta

```

```
## [1] 186 133
```

soma dos coefs é maior
t é maior

```

# Faire un choix de ligne entre 1 (très forte pénalité) et 186 (faible pénalité)
l = 10
sum(coef.lars(mod_lasso)[l, ] == 0) # n de coefs = 0

```

soma dos coefs é menor
t é menor

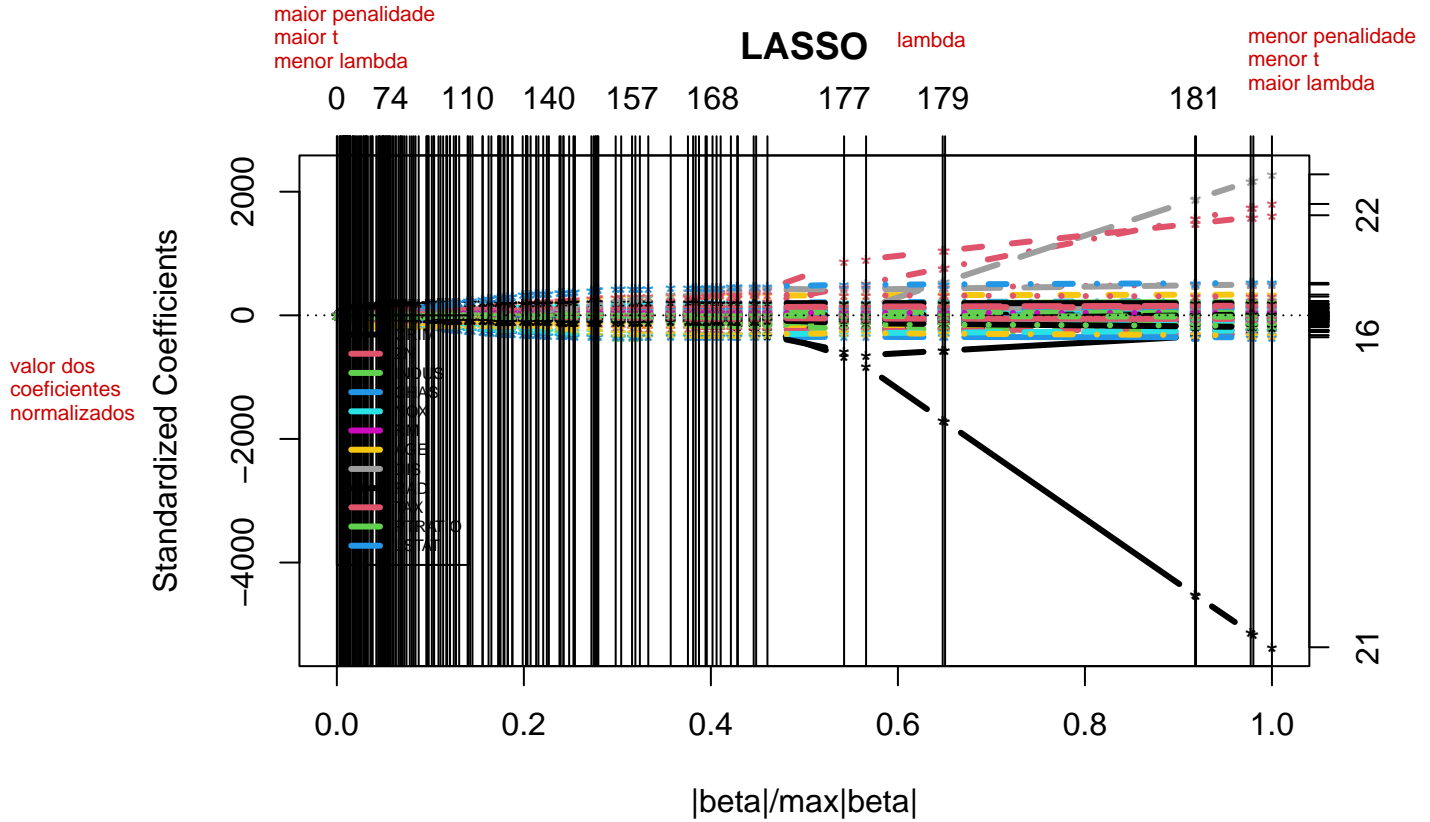
```
## [1] 127
```

With $l = 10$, sum equals 127, whereas with $l = 100$, sum equals 82. This shows that with a lesser l , more coefficients are getting 0 as a value.

```

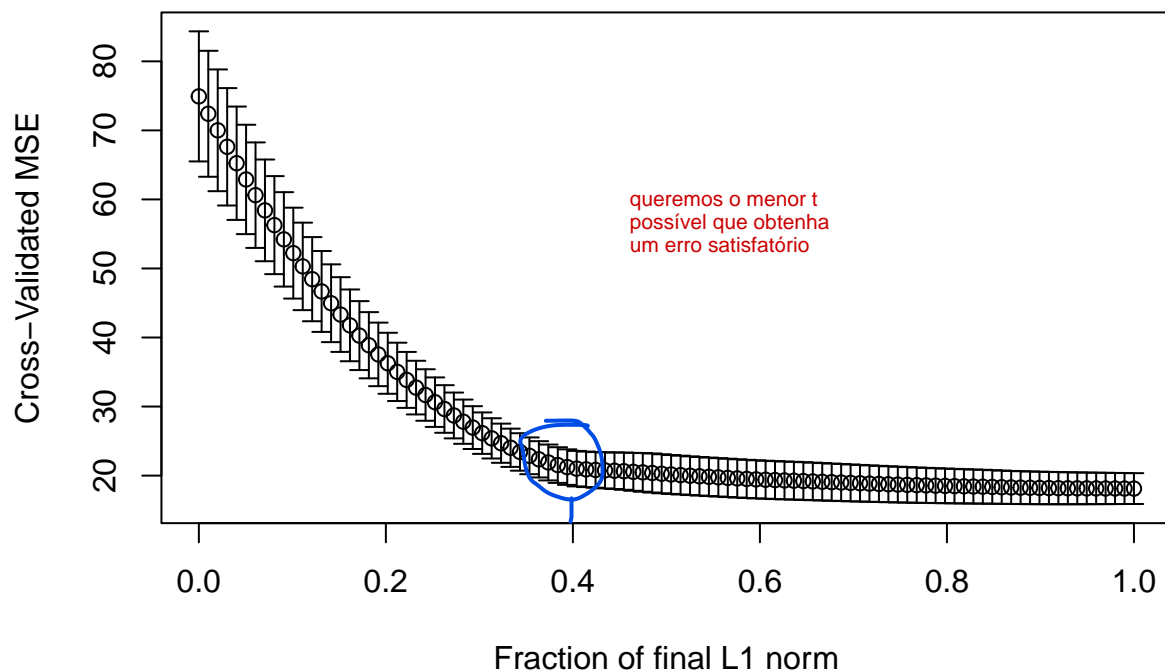
par(mfrow = c(1, 1))
plot(mod_lasso, cex = 1, lwd = 3, col = 1:(p-1))
legend(
  0,
  0,
  names(housing.train[, -p]),
  col = 1:(p-1),
  lty = rep(1, p-1),
  lwd = rep(3, p-1),
  cex = 0.5
)

```



— Faire un choix du meilleur modèle en étudiant la décroissance de l'erreur par validation croisée (commande `cv.lars`). Faire un choix de la meilleure fraction (directement liée à la valeur du λ). Fraction = 1 (resp. Fraction = 0) correspond à $\lambda = 0$ (resp. $\lambda = +\infty$).

```
CV = cv.lars(x, y, K = 10, index=seq(from = 0, to = 1, length = 100),
            trace = FALSE, plot.it = TRUE, se = TRUE, type = "lasso", mode = "fraction")
```



```
#a completer :
value = 0.4
```

- Donner le nombre de coefficients non nuls du modèle final retenu. La pénalité a-t-elle jouer son rôle ?

```
#a completer :
coef_lasso_beter <- predict.lars(mod_lasso, s = value, mode = "frac", type = "coef")
#a completer :
nb_coef_nul = sum(coef_lasso_beter$coefficients == 0)
nb_coef_nul
```

```
## [1] 51
```

Obtemos 51 coeficientes nulos. Um valor menor que os valores que obtivemos antes. L portanto seria maior que 100.

— Evaluer la qualité prédictive du modèle sur l'ensemble test (commande `predict.lars`).

```
newx = as.matrix(housing.test[, -p])
for (i in 1:(p-2))
{
  for (j in 2:(p-1))
  {
    newx = cbind(newx, newx[, i] * newx[, j])
  }
}
```

```

}
#a completer :
fits <- predict.lars(mod_lasso, newx, s = value, mode = "frac")
#a completer :
RMSE_lasso = RMSE(housing.test[, p], fits$fit)
c(RMSE_lm_inter, RMSE_lasso)

```

```
## [1] 4.416989 4.581404
```

Ajuster maintenant une régression Ridge. La pénalité Ridge ne s'applique pas sur **l'intercept**. Il est donc nécessaire d'enlever le terme constant avant d'appliquer la procédure `lm.ridge` de la library MASS.

```

#-----
#ajustement ridge
#-----
library(MASS)
#on part d'une matrice centrée réduite
housing.train2 = as.data.frame(scale(cbind(x_extend, y))) # scale does the normalization of columns
#on garde en mémoire moyenne et écart type des données initiales
mean.train = apply(cbind(x_extend, y), 2, mean) # 2 = mean is by column
sd.train = apply(cbind(x_extend, y), 2, sd) # 2 = sd is by column

#On se donne un vecteur de poids lambda
lambda = c(seq(0.01, 10, 0.01), seq(10, 100, 10), 1000, 2000)

p2 = ncol(housing.train2)
mod_ridge = lm.ridge(V134 ~.-1, data = housing.train2, lambda = lambda)
# V134 is the class column with centre réduit

```

- Tracer les différents beta en fonction du λ . Que remarquez-vous ?

```

#tracer des différentes valeurs des beta en fonction de lambda
beta_mat = mod_ridge$coef
par(mfrow = c(1, 1))
plot(lambda, beta_mat[1, ], ylim = c(min(beta_mat),
    max(beta_mat)), pch = 19, cex = 0.4, ylab = "coefficients", res = 600
)

```

```
## Warning in plot.window(...): "res" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "res" is not a graphical parameter
```

```
## Warning in axis(side = side, at = at, labels = labels, ...): "res" is not a
## graphical parameter
```

```
## Warning in axis(side = side, at = at, labels = labels, ...): "res" is not a
## graphical parameter
```

```
## Warning in box(...): "res" is not a graphical parameter
```

```
## Warning in title(...): "res" is not a graphical parameter
```

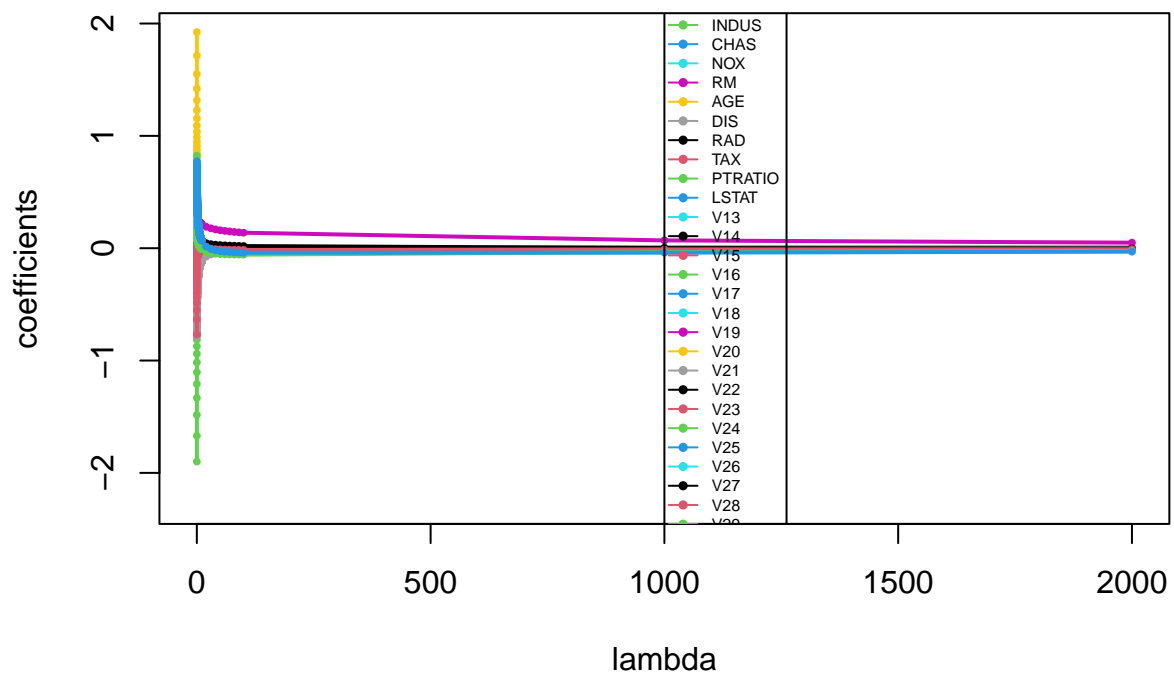
```

lines(lambda, beta_mat[1, ], lwd = 2)

for (i in 2:(p-1))
{
  points(lambda, beta_mat[i, ], col = i, pch = 19, cex=0.4)
  lines(lambda, beta_mat[i, ], col = i, lwd = 2)
}

legend(1000, 2.5, row.names(beta_mat),
      col = 1:p, lty = rep(1, p), cex = 0.5, pch = rep(19, 8)
)

```



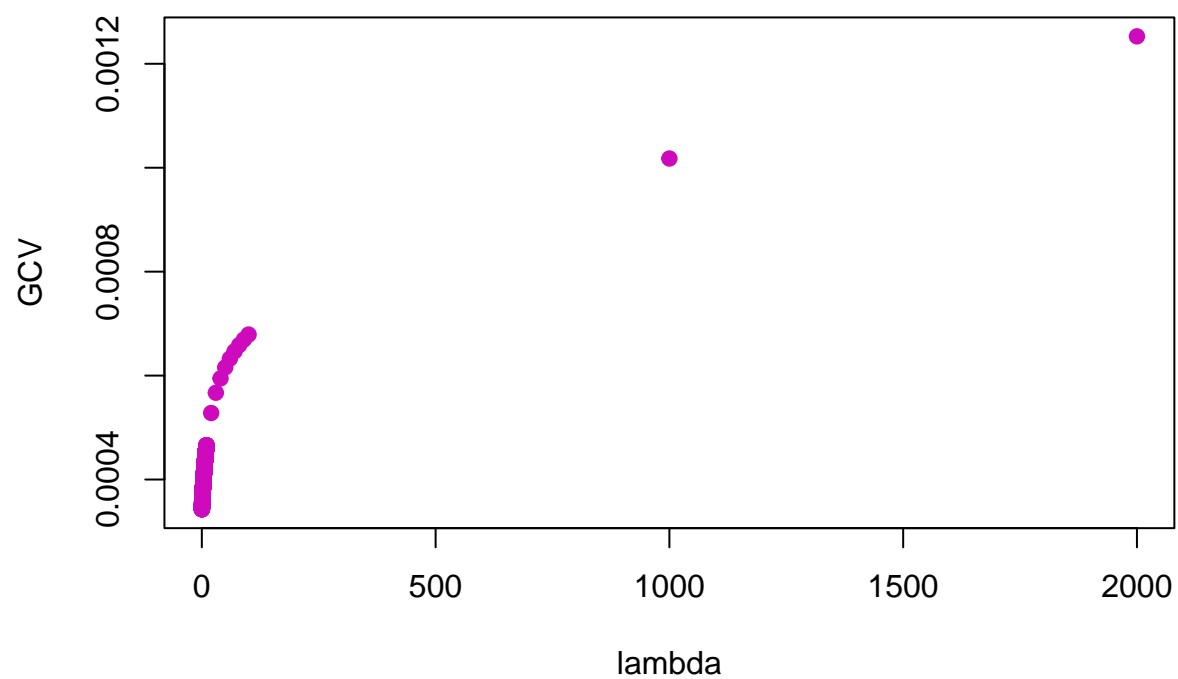
Nesse caso os termos não vão diretamente à zero, por mais que se aproximem dele.

Le choix du meilleur λ se fait par validation croisée.

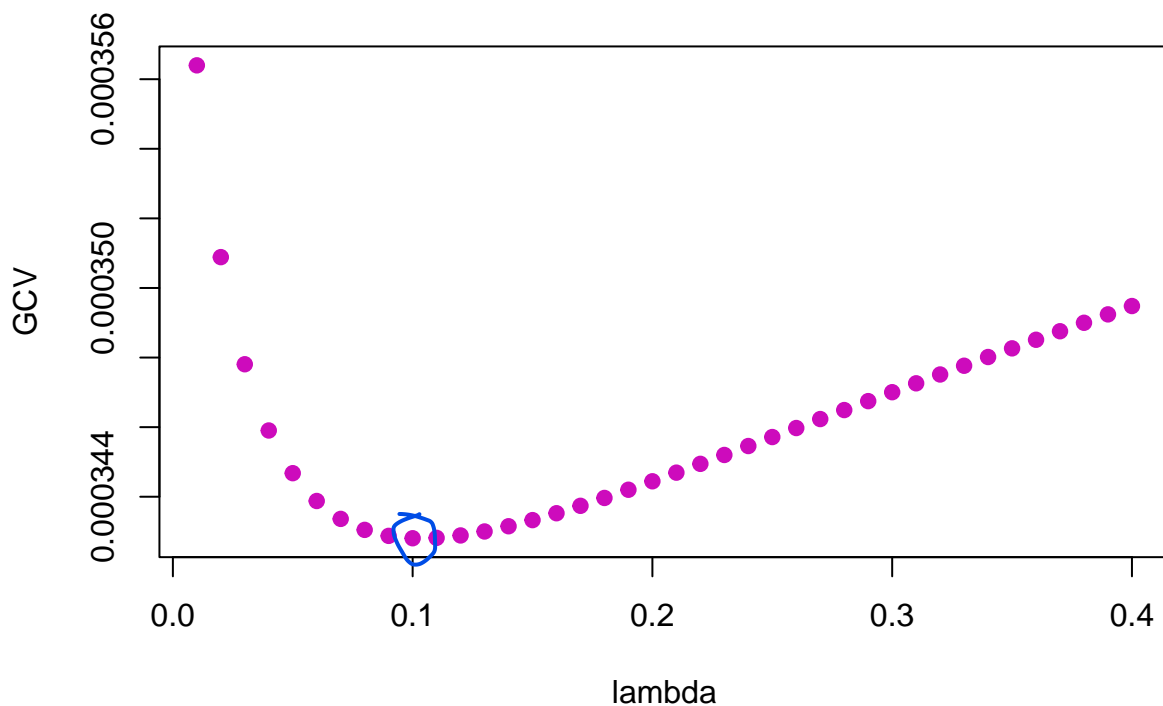
```

# tracer du GCV en fonction du lambda
plot(lambda, mod_ridge$GCV, pch = 19, col = 6, xlab = "lambda", ylab = "GCV")

```

```
plot(lambda[1:40], mod_ridge$GCV[1:40], pch = 19, col = 6, xlab = 'lambda', ylab = "GCV")
```



```
# choix du meilleur beta. On récupère la position (indice) où le GCV est minimum
indice = 10 # 0.1 : command which.min()      match(min(mod_ride$GCV),mod_ride$GCV)
beta = beta_mat[, indice]
```

La remise à l'échelle est nécessaire pour la prédiction.

```
#prédiction du modèle et remise à l'échelle pour comparer à diab.test
ypred = as.matrix((x_extend-t(matrix(rep(mean.train[-p2],300),p2-1,300)))/t(matrix(rep(sd.train[-p2],300),p2-1,300)))

X_test = as.matrix(newx - t(matrix(rep(mean.train[-p2], 206), p2-1, 206)))
X_test = X_test / t(matrix(rep(sd.train[-p2], 206), p2-1, 206))
Y_pred_ride = (as.matrix(X_test)%*%matrix(beta,p2-1,1))*sd.train[p2]+mean.train[p2]

RMSE_ride = RMSE(housing.test[, p], Y_pred_ride)
c(RMSE_lm_inter, RMSE_lasso, RMSE_ride)
```

```
## [1] 4.416989 4.581404 4.653380
```

Modèles à base d'arbres

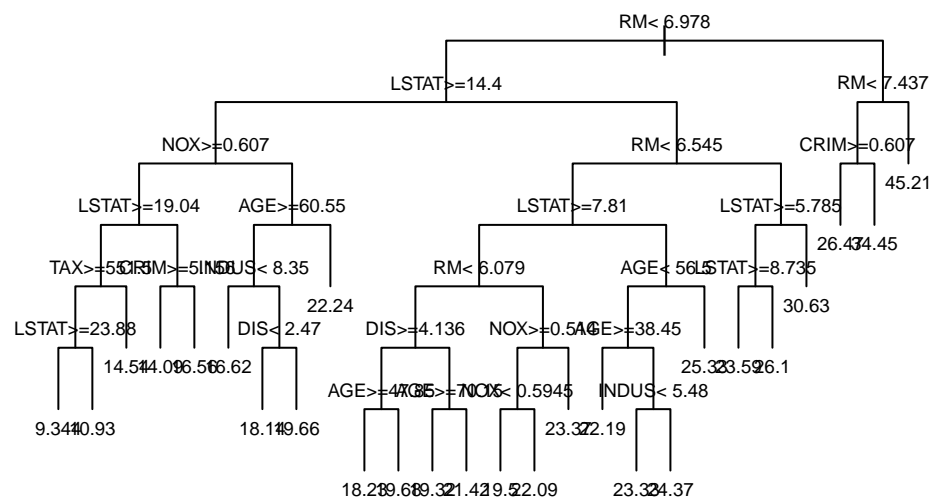
On commence par ajuster un modèle CART de la librairie Rpart.

Classification and regression tree

```

#-----
#ajustement cart + random forest
#-----
library(rpart)
cont = rpart.control(cp = 0.0001) # define minimum cp complexity parameter
mod_tree <- rpart(class ~., data = housing.train, control = cont)
par(mfrow = c(1, 1))
plot(mod_tree, uniform = TRUE, margin = 0.05)
text(mod_tree, cex = 0.6)

```



- A quoi correspond le paramètre *cp* ? Il contrôle la complexité de l'arbre (complexity parameter).
- Le choix de la valeur 0.0001 conduit-il à un arbre grossier ou détaillé ? Un *cp* petit entraîne un arbre profond avec beaucoup de noeuds.
- Quelles sont les variables les plus influentes ? RM et LSTAT (look both the height and frequency)
- Pourquoi n'est-il pas nécessaire ici de mettre en place un modèle avec interaction ? Trees already consider the interactions effects
- Faire un choix du meilleur *cp* par validation croisée (quatrième colonne de l'attribut *cptable* d'un objet de type *rpart*).

```

#Apparent : apprentissage, X relative : par validation croisée
mod_tree$cptable # ele testa cps maiores (árvores mais simples), antes de chegar em cp=0.0001

```

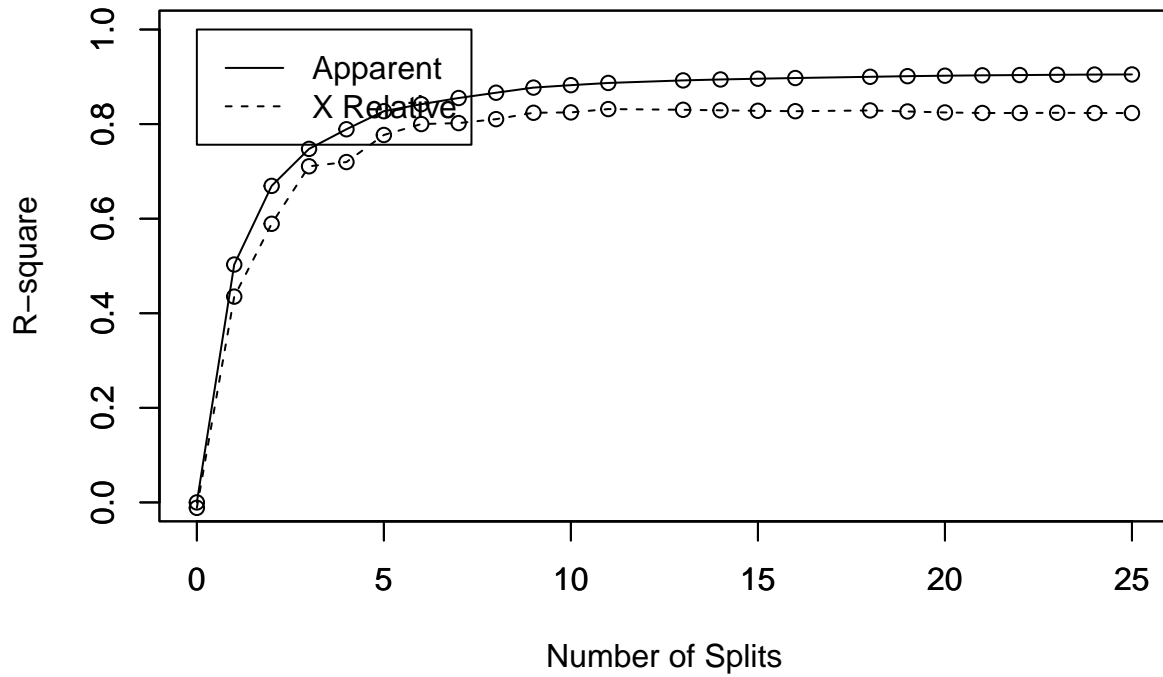
##	CP	nsplit	rel error	xerror	xstd
## 1	0.5030656136	0	1.00000000	1.0114478	0.11451713
## 2	0.1662686916	1	0.49693439	0.5647737	0.05827073
## 3	0.0782727816	2	0.33066569	0.4107676	0.05333136
## 4	0.0414868184	3	0.25239291	0.2892056	0.03197709
## 5	0.0382249961	4	0.21090609	0.2802356	0.03224474
## 6	0.0148019951	5	0.17268110	0.2229881	0.03005734
## 7	0.0130550489	6	0.15787910	0.1998693	0.02349025
## 8	0.0111708195	7	0.14482405	0.1978706	0.02406715
## 9	0.0108478201	8	0.13365324	0.1894953	0.02378675
## 10	0.0051137140	9	0.12280542	0.1760483	0.02352917
## 11	0.0047095058	10	0.11769170	0.1752187	0.02347684
## 12	0.0027083741	11	0.11298220	0.1681780	0.02349925
## 13	0.0019607608	13	0.10756545	0.1697190	0.02364828
## 14	0.0015930841	14	0.10560469	0.1708474	0.02350104
## 15	0.0014471054	15	0.10401160	0.1718676	0.02353299
## 16	0.0013119307	16	0.10256450	0.1727270	0.02363719
## 17	0.0012952061	18	0.09994064	0.1710708	0.02362531
## 18	0.0009682042	19	0.09864543	0.1732953	0.02440385
## 19	0.0008134445	20	0.09767723	0.1753319	0.02442750
## 20	0.0005885364	21	0.09686378	0.1764818	0.02444670
## 21	0.0005644762	22	0.09627524	0.1764812	0.02444766
## 22	0.0004751045	23	0.09571077	0.1761164	0.02445440
## 23	0.0002569774	24	0.09523566	0.1766070	0.02447482
## 24	0.0001000000	25	0.09497869	0.1766223	0.02447450

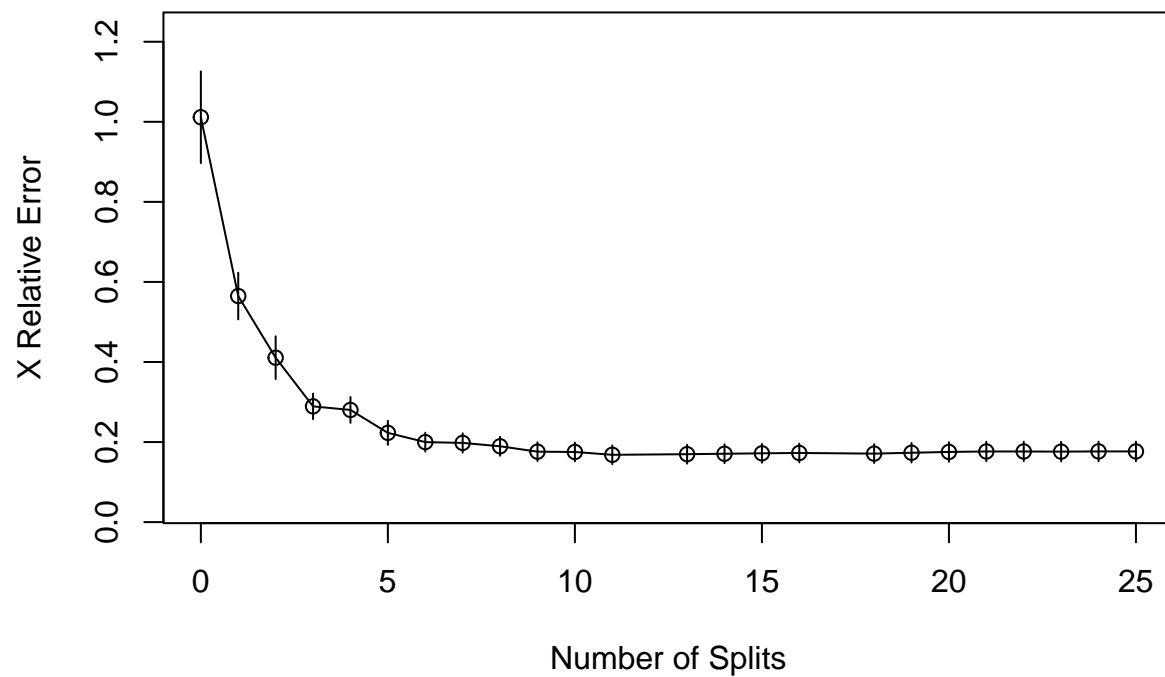
```
#affichage uniquement cp>0.01
#summary(mod_tree, cp=0.01)
```

```
par(mfrow = c(1, 1)) # one plot on one page
rsq.rpart(mod_tree) # visualize cross-validation results
```

```
##
## Regression tree:
## rpart(formula = class ~ ., data = housing.train, control = cont)
##
## Variables actually used in tree construction:
## [1] AGE    CRIM  DIS   INDUS LSTAT NOX   RM    TAX
##
## Root node error: 22208/300 = 74.025
##
## n= 300
##
##          CP nsplit rel error  xerror    xstd
## 1  0.50306561      0  1.000000  1.01145  0.114517
## 2  0.16626869      1  0.496934  0.56477  0.058271
## 3  0.07827278      2  0.330666  0.41077  0.053331
## 4  0.04148682      3  0.252393  0.28921  0.031977
## 5  0.03822500      4  0.210906  0.28024  0.032245
## 6  0.01480200      5  0.172681  0.22299  0.030057
## 7  0.01305505      6  0.157879  0.19987  0.023490
## 8  0.01117082      7  0.144824  0.19787  0.024067
## 9  0.01084782      8  0.133653  0.18950  0.023787
## 10 0.00511371      9  0.122805  0.17605  0.023529
```

## 11	0.00470951	10	0.117692	0.17522	0.023477
## 12	0.00270837	11	0.112982	0.16818	0.023499
## 13	0.00196076	13	0.107565	0.16972	0.023648
## 14	0.00159308	14	0.105605	0.17085	0.023501
## 15	0.00144711	15	0.104012	0.17187	0.023533
## 16	0.00131193	16	0.102564	0.17273	0.023637
## 17	0.00129521	18	0.099941	0.17107	0.023625
## 18	0.00096820	19	0.098645	0.17330	0.024404
## 19	0.00081344	20	0.097677	0.17533	0.024427
## 20	0.00058854	21	0.096864	0.17648	0.024447
## 21	0.00056448	22	0.096275	0.17648	0.024448
## 22	0.00047510	23	0.095711	0.17612	0.024454
## 23	0.00025698	24	0.095236	0.17661	0.024475
## 24	0.00010000	25	0.094979	0.17662	0.024474



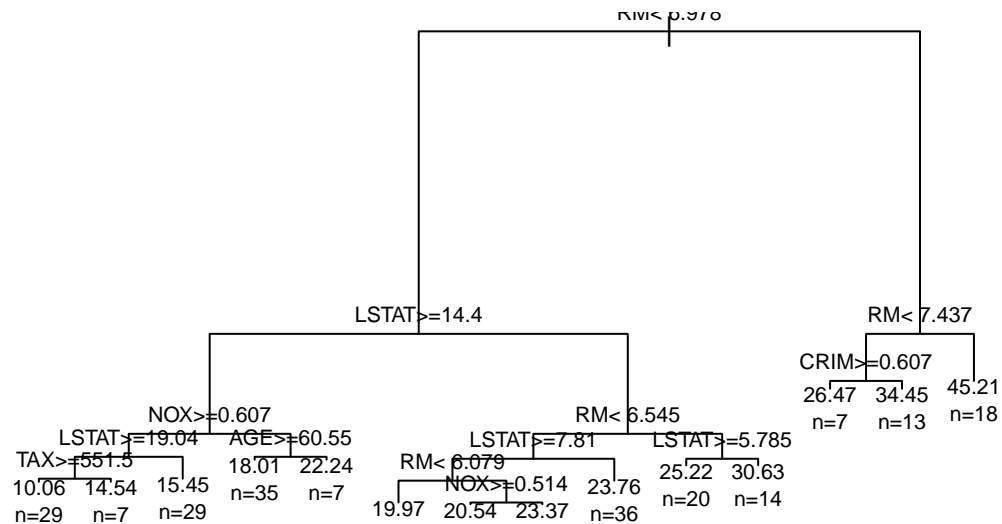


```
# the best result is given by nsplit = 11
mod_tree$cptable[12, 1]
```

```
## [1] 0.002708374
```

- Elaguer l'arbre avec ce choix de *cp* (fonction *prune*)

```
#a completer :
mod_tree_pruned = prune(mod_tree, cp = 0.002708374)
par(mfrow = c(1, 1))
plot(mod_tree_pruned)
text(mod_tree_pruned, use.n = TRUE, cex = 0.7)
```



```

#a completer :
y_pred_tree <- predict(mod_tree_pruned, housing.test[, -p])
#a completer :
RMSE_cart = RMSE(housing.test[, p], y_pred_tree)
RMSE_cart

```

```
## [1] 5.479321
```

- Mettre en place un modèle de boosting en utilisant la routine *gbm* de la librairie *gbm*.
- Combien d'arbres doit-on considérer ? 726
- Quelles sont les variables les plus influentes avec ce modèle ? RM et LSTAT

```

#modèle boosted trees
library(gbm)

```

```
## Loaded gbm 2.1.8.1
```

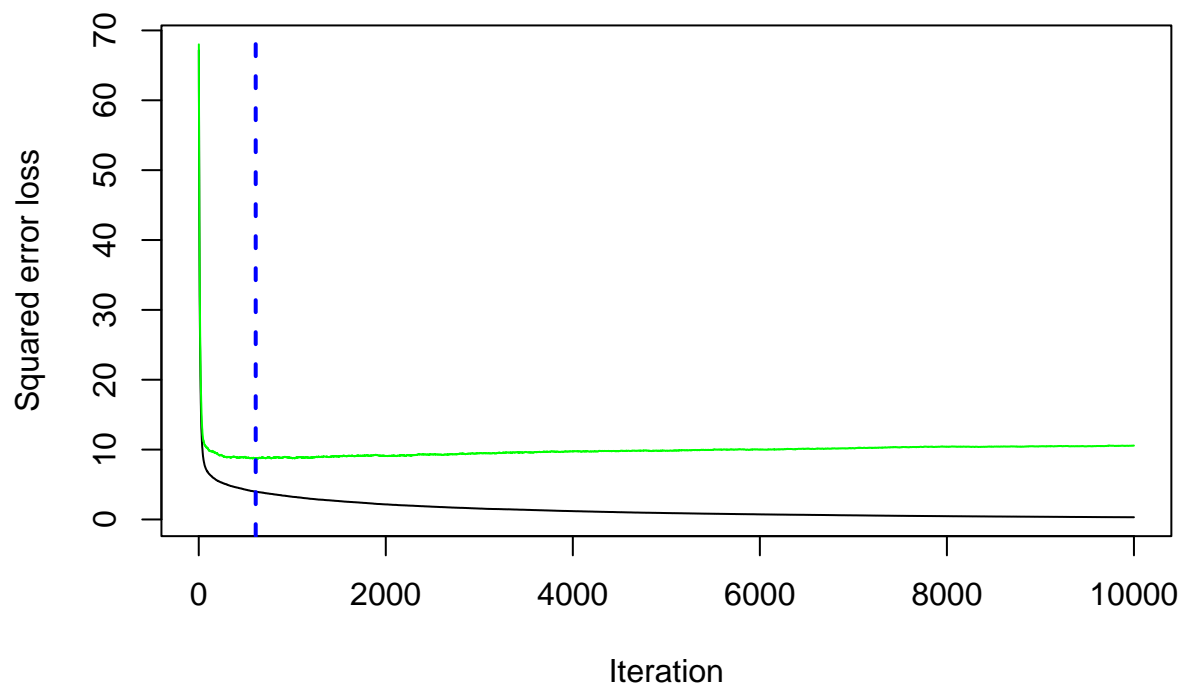
```
mod_boosted <- gbm(class ~., data = housing.train, n.trees = 10000, cv.folds = 10)
```

```
## Distribution not specified, assuming gaussian ...
```

```

par(mfrow = c(1, 1))
best.iter <- gbm.perf(mod_boosted, method = "cv")

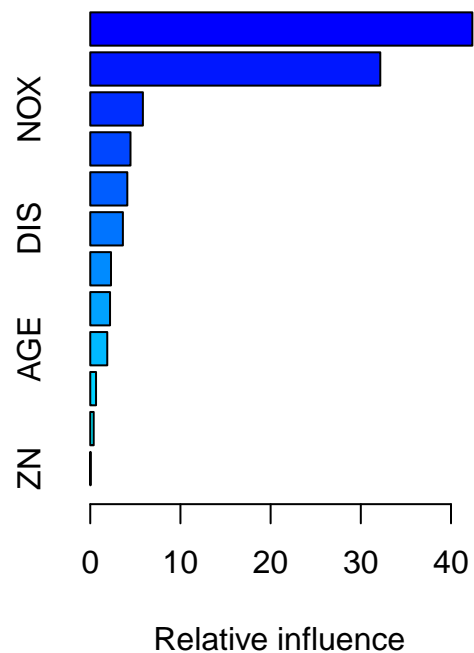
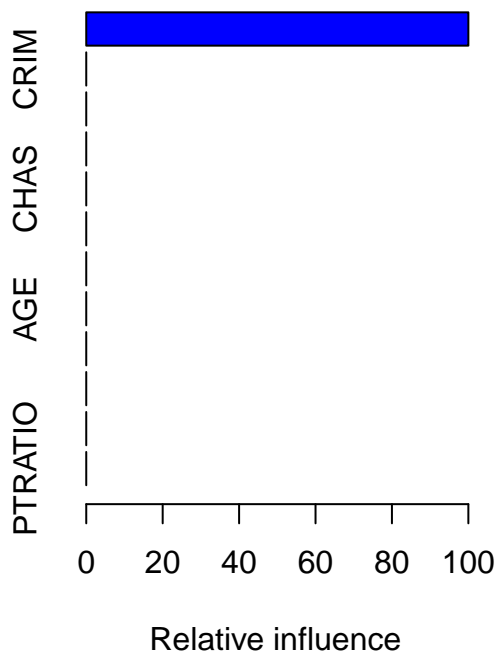
```



```
par(mfrow = c(1, 2))
summary(mod_boosted, n.trees = 1) # based on the first tree
```

```
##          var rel.inf
## LSTAT    LSTAT    100
## CRIM     CRIM      0
## ZN       ZN        0
## INDUS    INDUS      0
## CHAS     CHAS       0
## NOX      NOX        0
## RM       RM         0
## AGE      AGE        0
## DIS      DIS        0
## RAD      RAD        0
## TAX      TAX        0
## PTRATIO  PTRATIO    0
```

```
summary(mod_boosted, n.trees = best.iter) # based on the estimated best number of trees
```

```
##      var      rel.inf
## RM      RM 42.36820423
## LSTAT    LSTAT 32.15865779
## NOX      NOX  5.83833014
## CRIM     CRIM  4.46132510
## PTRATIO  PTRATIO 4.10908279
## DIS      DIS  3.61888325
## TAX      TAX  2.30171792
## INDUS    INDUS 2.19312476
## AGE      AGE  1.88764093
## RAD      RAD  0.64305519
## CHAS     CHAS  0.38004279
## ZN       ZN   0.03993511
```

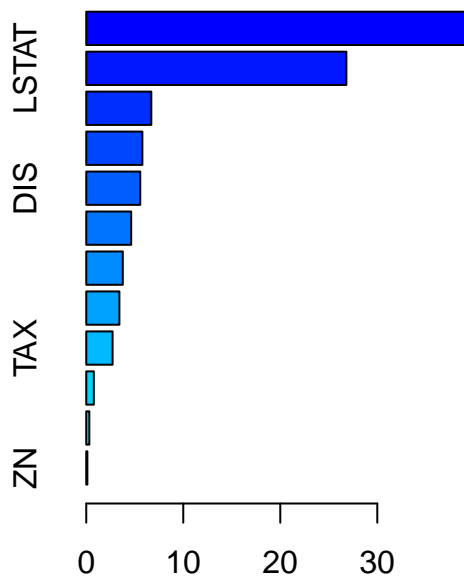
```
summary(mod_boosted, n.trees = 3000) # based on something
```

```
##      var      rel.inf
## RM      RM 39.3864807
## LSTAT    LSTAT 26.8133470
## CRIM     CRIM  6.7066555
## NOX      NOX  5.7859931
## DIS      DIS  5.5650171
## PTRATIO  PTRATIO 4.6317920
## AGE      AGE  3.7671004
## INDUS    INDUS 3.4174186
```

```
## TAX          TAX  2.7119535
## RAD          RAD  0.7809762
## CHAS         CHAS 0.3185178
## ZN           ZN   0.1147481
```

```
#print(pretty.gbm.tree(mod_boosted,1))
#print(pretty.gbm.tree(mod_boosted,mod_boosted$n.trees))
f.predict1 <- predict(mod_boosted, housing.test[, -p], 1)
f.predict2 <- predict(mod_boosted, housing.test[, -p], 3000)
f.predict3 <- predict(mod_boosted, housing.test[, -p], best.iter)
RMSE_b1 = RMSE(housing.test[, p], f.predict1)
RMSE_b2 = RMSE(housing.test[, p], f.predict2)
RMSE_b3 = RMSE(housing.test[, p], f.predict3)
c(RMSE_b1, RMSE_b2, RMSE_b3)
```

```
## [1] 9.618313 5.024867 4.853227
```



Relative influence

bagging = seleccionar aleatoriamente conjunto de linhas dos dados de treino, para treinar modelos em sequencia
boosting = seleccionar priorizando dados que foram pior preditos, para treinar modelos em sequencia

On construit maintenant une procédure de bagging. L'idée est de moyennner des arbres CART construits sur des échantillons bootstrap des données de départ. Un échantillon Bootstrap est un tirage avec remise de N points parmi les N points de l'échantillon initial.

```
#modèle arbre bagging
cont = rpart.control(minsplit = 2, cp = 0.0001)
B = 2000
Y <- matrix(0, nrow(housing.test), B)
```

```
for (i in 1:B) {
  u = sample(1:nrow(housing.train), nrow(housing.train), replace = TRUE)
  appren <- housing.train[u, ]
  mod_tree <- rpart(class ~., data = appren, control = cont)
  Y[, i] <- predict(mod_tree, newdata = housing.test)
}
```

```
#Y est de taille 206*B, 206 etant le nombre de points tests
#a completer :
Y_pred_bag = apply(Y, 1, mean) # mean of each tree's result
#a completer :
RMSE_bag = RMSE(housing.test[, p], Y_pred_bag)
RMSE_bag
```

Bagging is an ensemble algorithm that fits multiple models on different subsets of a training dataset, then combines the predictions from all models.

```
## [1] 4.864175
```

Random forest is an extension of bagging that also randomly selects subsets of features used in each data sample.

Construire un modèle de Type Random Forest. - quelle est la différence entre un modèle type bagging et un modèle de forêts aléatoires ?

```
#modèle arbres random forest
library(randomForest)
```

```
## randomForest 4.7-1.1
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
mod_RF <- randomForest(class~., data = housing.train, ntree = 300, sampsize = nrow(housing.train))
summary(mod_RF)
```

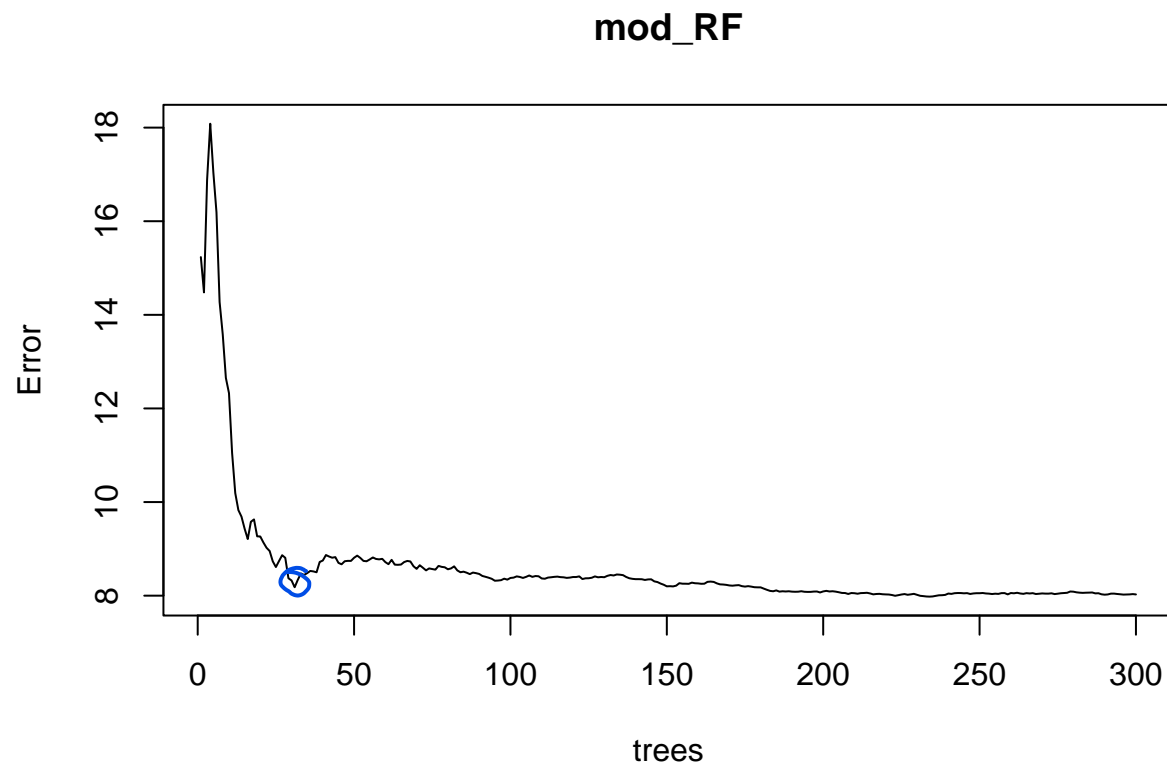
```
##           Length Class  Mode
## call           5    -none- call
## type            1    -none- character
## predicted      300    -none- numeric
## mse            300    -none- numeric
## rsq            300    -none- numeric
## oob.times      300    -none- numeric
## importance      12    -none- numeric
## importanceSD     0    -none- NULL
## localImportance  0    -none- NULL
## proximity        0    -none- NULL
## ntree            1    -none- numeric
## mtry             1    -none- numeric
```

```
## forest      11    -none- list
## coefs       0    -none- NULL
## y          300    -none- numeric
## test       0    -none- NULL
## inbag       0    -none- NULL
## terms      3    terms  call
```

```
importance(mod_RF)
```

```
##      IncNodePurity
## CRIM      1289.00260
## ZN        194.06135
## INDUS     1409.38286
## CHAS       41.82852
## NOX       1309.59676
## RM        7471.05953
## AGE        656.74447
## DIS       1036.39422
## RAD        144.51651
## TAX       1059.09902
## PTRATIO   1306.87398
## LSTAT     5852.45326
```

```
plot(mod_RF)
```



errado, precisava ter pegado o minimo do erro

```
which(mod_RF$trees == min(mod_RF$trees), arr.ind = TRUE)
```

```
## Warning in min(mod_RF$trees): no non-missing arguments to min; returning Inf
```

```
## integer(0)
```

```
#a completer :  
Y_pred_RF <- predict(mod_RF, housing.test) talvez esteja errado porque precisava especificar qual árvore  
#a completer : usar  
RMSE_RF = RMSE(housing.test[, p], Y_pred_RF)  
RMSE_RF
```

```
## [1] 4.931825
```

Méthode de réduction de dimension par orthogonalisation

On s'intéresse maintenant aux modèles PCR et PLS construits à partir de la matrice augmentée des interactions.

```
library(pls)
```

```
##
```

```
## Attaching package: 'pls'
```

```
## The following object is masked from 'package:caret':
```

```
##
```

```
## R2
```

```
## The following object is masked from 'package:DiceEval':
```

```
##
```

```
## R2
```

```
## The following object is masked from 'package:stats':
```

```
##
```

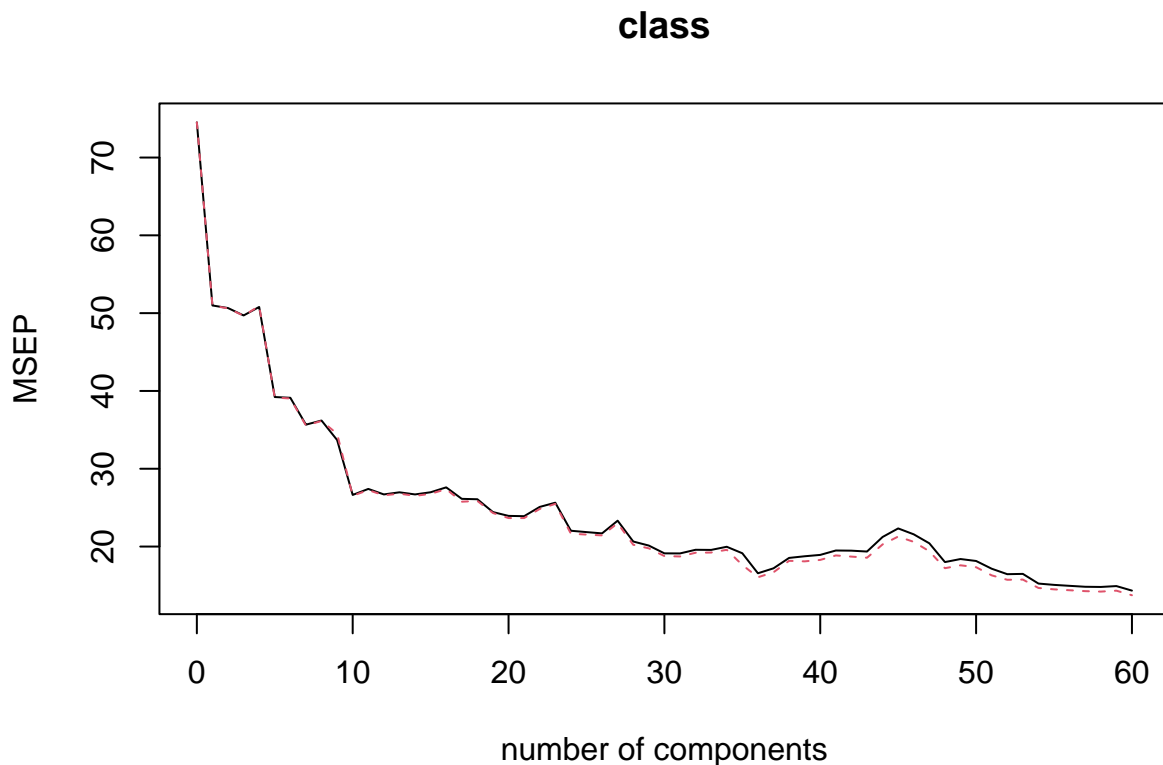
```
## loadings
```

```
#PCR
```

```
housing.pcr <- pcr(class ~ .^2, 60, data = housing.train)
```

Faire le choix du nombre de composantes par validation croisée en utilisant la routine crossval.

```
#a completer :  
housing.cv <- crossval(housing.pcr, segments = 10)  
plot(MSEP(housing.cv))
```



Faire la prédiction du modèle pour le nombre de composantes sélectionnées.

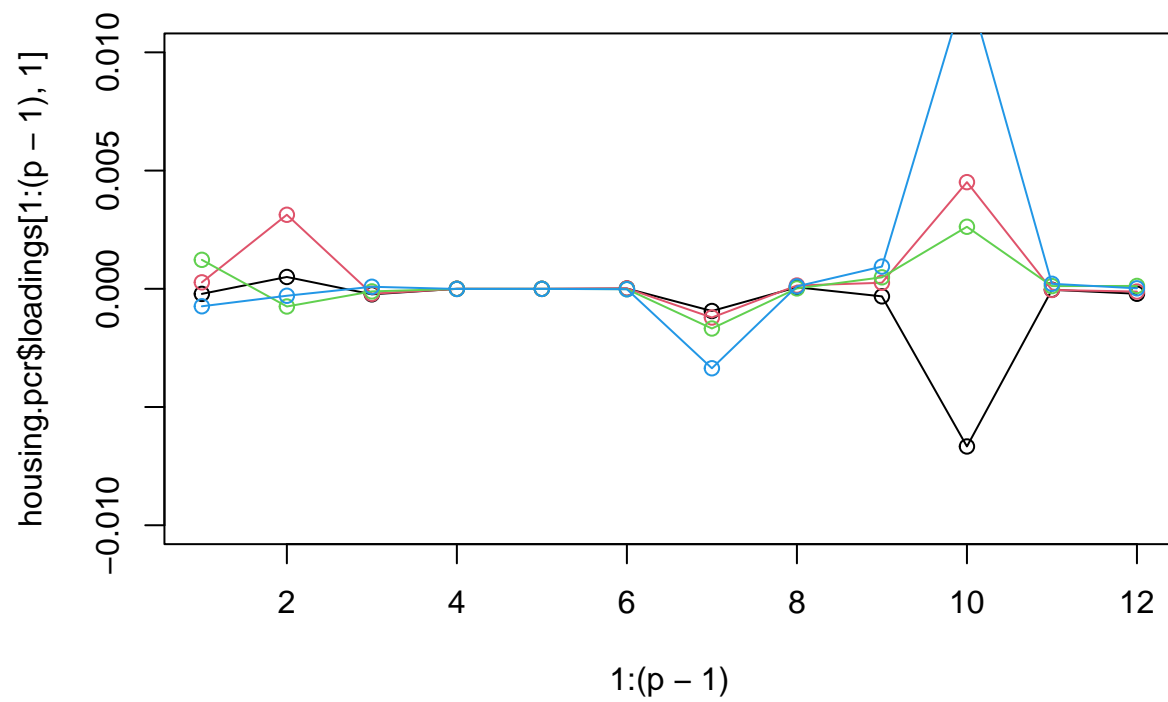
```
#a completer :
nbcomp = 36
Y_PCR = predict(housing.pcr, newdata = housing.test, ncomp = nbcomp, type = "response")
#a completer :
RMSE_PCR = RMSE(housing.test[, p], Y_PCR)
RMSE_PCR
```

```
## [1] 5.487672
```

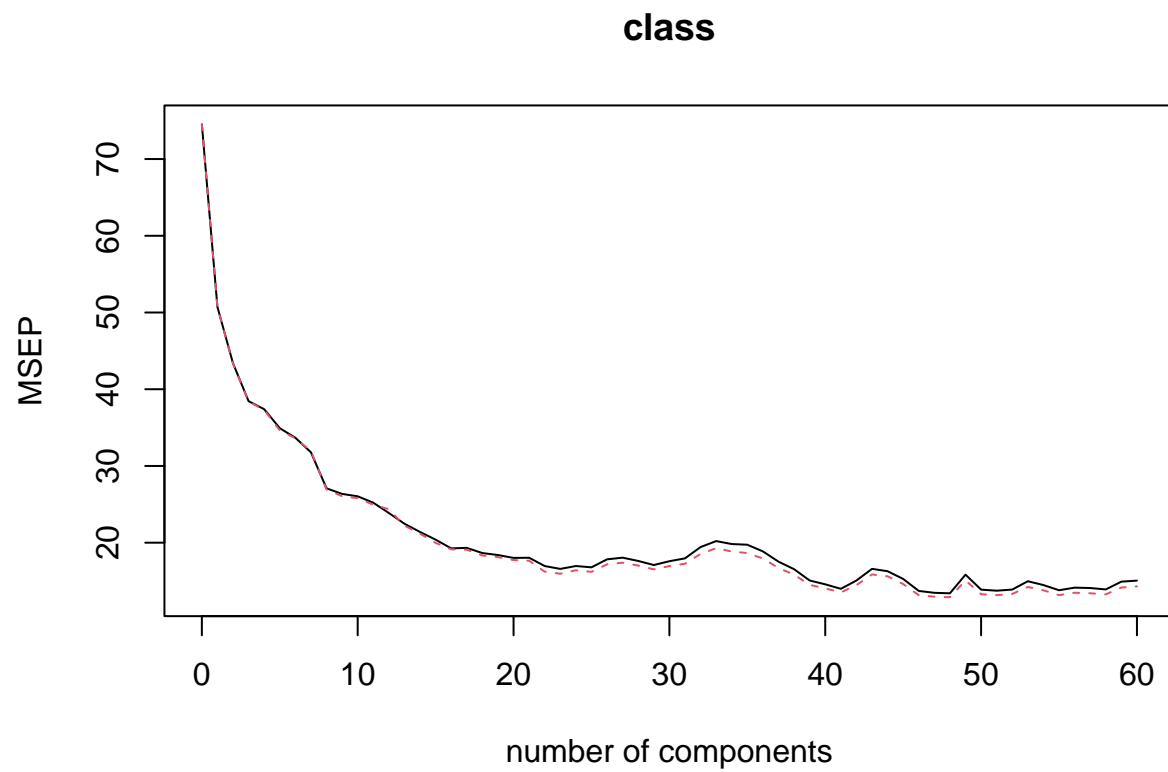
Tracer les premières fonctions propres et interpréter.

```
housing.pcr <- pcr(class ~ .^2, nbcomp, data = housing.train)
#coef(housing.pcr)

#tracer des premières fonctions propres
par(mfrow = c(1,1))
plot(1:(p-1),housing.pcr$loadings[1:(p-1),1],type = "l",col = 1,ylim = c(-0.01,0.01))
points(1:(p-1),housing.pcr$loadings[1:(p-1),1],col = 1)
for (i in 2:4)
{
  points(1:(p-1),housing.pcr$loadings[1:(p-1),i],col = i)
  lines(1:(p-1),housing.pcr$loadings[1:(p-1),i],col = i)
}
```



```
#PLS
housing.pls <- pls(class ~ .^2, 60, data = housing.train)
housing.pls.cv <- crossval(housing.pls, segments = 10)
plot(MSEP(housing.pls.cv))
```



```
#a completer :  
Y_PLS = predict(housing.pls, newdata = housing.test, ncomp = nbcomp, type = "response")  
#a completer :  
RMSE_PLS = RMSE(housing.test[, p], Y_PLS)  
RMSE_PLS
```

```
## [1] 4.993442
```