Loading required package: strucchange

Loading required package: zoo

Attaching package: ‘zoo’

The following objects are masked from ‘package:base’:

as.Date, as.Date.numeric

Loading required package: sandwich

> install.packages("party")

Error in install.packages : Updating loaded packages

Warning messages:

1: package ‘arules’ was built under R version 3.4.4

2: package ‘party’ was built under R version 3.4.4

3: package ‘mvtnorm’ was built under R version 3.4.4

4: package ‘strucchange’ was built under R version 3.4.3

5: package ‘zoo’ was built under R version 3.4.3

6: package ‘sandwich’ was built under R version 3.4.3

> install.packages("party")

Installing package into ‘T:/Documents/R/win-library/3.4’

(as ‘lib’ is unspecified)

Warning in install.packages :

package ‘party’ is in use and will not be installed

> set.seed(1234)

> ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.7, 0.3))

>

> trainData <- iris[ind==1,]

>

> trainData <- iris[ind==1]

Error in `[.data.frame`(iris, ind == 1) : undefined columns selected

>

> trainData <- iris[ind==1,]

>

> testData <- iris[ind==2,]

>

> View(iris)

> myFormula <- Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width

>

> iris\_ctree <- ctree(myFormula, data=trainData)

>

> print(iris\_ctree)

Conditional inference tree with 4 terminal nodes

Response: Species

Inputs: Sepal.Length, Sepal.Width, Petal.Length, Petal.Width

Number of observations: 112

1) Petal.Length <= 1.9; criterion = 1, statistic = 104.643

2)\* weights = 40

1) Petal.Length > 1.9

3) Petal.Width <= 1.7; criterion = 1, statistic = 48.939

4) Petal.Length <= 4.4; criterion = 0.974, statistic = 7.397

5)\* weights = 21

4) Petal.Length > 4.4

6)\* weights = 19

3) Petal.Width > 1.7

7)\* weights = 32

> plot(iris\_ctree)

> plot(iris\_ctree, type="simple")

>

> testPred <- predict(iris\_ctree, newdata = testData)

> ?predict

> ?predict%

Error: unexpected input in "?predict%"

> ?predict?

+ table(testPred, testData$Species)

Error in `?`(`?`(predict), table(testPred, testData$Species)) :

c("no documentation of type ‘T:/Documents/R/win-library/3.4/arules/help/predict’ and topic ‘table(testPred, testData$Species)’ (or error in processing help)", "no documentation of type ‘C:/Program Files/R/R-3.4.1/library/stats/help/predict’ and topic ‘table(testPred, testData$Species)’ (or error in processing help)")

In addition: Warning message:

In if (type == "package") package <- topic :

the condition has length > 1 and only the first element will be used

>

> testPred <- predict(iris\_ctree, newdata = testData)

> table(testPred, testData$Species)

testPred setosa versicolor virginica

setosa 10 0 0

versicolor 0 12 2

virginica 0 0 14

>

> install.packages(“rpart”)

Error: unexpected input in "install.packages(“"

>

> install.packages("rpart")

Error in install.packages : Updating loaded packages

>

Restarting R session...

Loading required package: arules

Loading required package: Matrix

Attaching package: ‘arules’

The following objects are masked from ‘package:base’:

abbreviate, write

> install.packages("rpart")

Error in install.packages : Updating loaded packages

Warning message:

package ‘arules’ was built under R version 3.4.4

> install.packages("rpart")

Installing package into ‘T:/Documents/R/win-library/3.4’

(as ‘lib’ is unspecified)

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/rpart\_4.1-13.zip'

Content type 'application/zip' length 950352 bytes (928 KB)

downloaded 928 KB

package ‘rpart’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\swen111\AppData\Local\Temp\RtmpkZpXXK\downloaded\_packages

> library(rpart)

Warning message:

package ‘rpart’ was built under R version 3.4.4

> set.seed(1234)

> ind <- sample(2, nrow(bodyfat), replace=TRUE, prob=c(0.7, 0.3))

>

> bodyfat.train <- bodyfat[ind==1,]

>

> bodyfat.test <- bodyfat[ind==2,]

>

> myFormula <- DEXfat ~ age + waistcirc + hipcirc + elbowbreadth + kneebreadth

>

> bodyfat\_rpart <- rpart(myFormula, data = bodyfat.train, control = rpart.control(minsplit = 10))

>

> printcp(bodyfat\_rpart)

Regression tree:

rpart(formula = myFormula, data = bodyfat.train, control = rpart.control(minsplit = 10))

Variables actually used in tree construction:

[1] age hipcirc waistcirc

Root node error: 7265/56 = 129.73

n= 56

CP nsplit rel error xerror xstd

1 0.672726 0 1.000000 1.01945 0.187244

2 0.093907 1 0.327274 0.44154 0.108530

3 0.060375 2 0.233367 0.42712 0.093629

4 0.034204 3 0.172992 0.38422 0.090305

5 0.017083 4 0.138787 0.30382 0.072956

6 0.016958 5 0.121705 0.27398 0.065996

7 0.010071 6 0.104747 0.26937 0.066136

8 0.010000 7 0.094676 0.26954 0.066207

> plotcp(bodyfat\_rpart)

> summary(bodyfat\_rpart)

Call:

rpart(formula = myFormula, data = bodyfat.train, control = rpart.control(minsplit = 10))

n= 56

CP nsplit rel error xerror xstd

1 0.67272638 0 1.00000000 1.0194546 0.18724382

2 0.09390665 1 0.32727362 0.4415438 0.10853044

3 0.06037503 2 0.23336696 0.4271241 0.09362895

4 0.03420446 3 0.17299193 0.3842206 0.09030539

5 0.01708278 4 0.13878747 0.3038187 0.07295556

6 0.01695763 5 0.12170469 0.2739808 0.06599642

7 0.01007079 6 0.10474706 0.2693702 0.06613618

8 0.01000000 7 0.09467627 0.2695358 0.06620732

Variable importance

waistcirc hipcirc kneebreadth elbowbreadth age

36 30 20 7 6

Node number 1: 56 observations, complexity param=0.6727264

mean=30.94589, MSE=129.7327

left son=2 (31 obs) right son=3 (25 obs)

Primary splits:

waistcirc < 88.4 to the left, improve=0.6727264, (0 missing)

hipcirc < 108.25 to the left, improve=0.6481678, (0 missing)

kneebreadth < 9.35 to the left, improve=0.5186401, (0 missing)

age < 38.5 to the left, improve=0.1736104, (0 missing)

elbowbreadth < 7.05 to the left, improve=0.1027717, (0 missing)

Surrogate splits:

hipcirc < 107.85 to the left, agree=0.911, adj=0.80, (0 split)

kneebreadth < 9.35 to the left, agree=0.821, adj=0.60, (0 split)

elbowbreadth < 7.05 to the left, agree=0.625, adj=0.16, (0 split)

age < 38.5 to the left, agree=0.607, adj=0.12, (0 split)

Node number 2: 31 observations, complexity param=0.06037503

mean=22.55645, MSE=30.9851

left son=4 (14 obs) right son=5 (17 obs)

Primary splits:

hipcirc < 96.25 to the left, improve=0.45664650, (0 missing)

waistcirc < 71.5 to the left, improve=0.41315090, (0 missing)

kneebreadth < 9.35 to the left, improve=0.30857320, (0 missing)

age < 53.5 to the left, improve=0.16883300, (0 missing)

elbowbreadth < 6.65 to the left, improve=0.05266785, (0 missing)

Surrogate splits:

waistcirc < 71.5 to the left, agree=0.710, adj=0.357, (0 split)

kneebreadth < 8.25 to the left, agree=0.677, adj=0.286, (0 split)

age < 31.5 to the left, agree=0.645, adj=0.214, (0 split)

elbowbreadth < 5.75 to the left, agree=0.581, adj=0.071, (0 split)

Node number 3: 25 observations, complexity param=0.09390665

mean=41.3488, MSE=56.68456

left son=6 (18 obs) right son=7 (7 obs)

Primary splits:

waistcirc < 104.75 to the left, improve=0.48142530, (0 missing)

kneebreadth < 11.05 to the left, improve=0.45932040, (0 missing)

hipcirc < 109.9 to the left, improve=0.44321140, (0 missing)

elbowbreadth < 6.35 to the left, improve=0.22817150, (0 missing)

age < 61.5 to the left, improve=0.05339468, (0 missing)

Surrogate splits:

hipcirc < 123.75 to the left, agree=0.88, adj=0.571, (0 split)

kneebreadth < 10.65 to the left, agree=0.80, adj=0.286, (0 split)

age < 45.5 to the right, agree=0.76, adj=0.143, (0 split)

elbowbreadth < 7.15 to the left, agree=0.76, adj=0.143, (0 split)

Node number 4: 14 observations, complexity param=0.01708278

mean=18.41143, MSE=15.87606

left son=8 (9 obs) right son=9 (5 obs)

Primary splits:

age < 60.5 to the left, improve=0.55837410, (0 missing)

waistcirc < 70.35 to the left, improve=0.52936660, (0 missing)

elbowbreadth < 6.65 to the left, improve=0.27100890, (0 missing)

hipcirc < 92.6 to the left, improve=0.22810830, (0 missing)

kneebreadth < 8.55 to the left, improve=0.09131885, (0 missing)

Surrogate splits:

elbowbreadth < 6.55 to the left, agree=0.857, adj=0.6, (0 split)

waistcirc < 71.5 to the left, agree=0.786, adj=0.4, (0 split)

Node number 5: 17 observations, complexity param=0.01695763

mean=25.97, MSE=17.62629

left son=10 (6 obs) right son=11 (11 obs)

Primary splits:

waistcirc < 77.75 to the left, improve=0.41114270, (0 missing)

kneebreadth < 9.5 to the left, improve=0.37807810, (0 missing)

hipcirc < 104.5 to the left, improve=0.36977980, (0 missing)

age < 53 to the left, improve=0.07801043, (0 missing)

elbowbreadth < 6.95 to the right, improve=0.04911615, (0 missing)

Surrogate splits:

elbowbreadth < 6.15 to the left, agree=0.765, adj=0.333, (0 split)

kneebreadth < 8.55 to the left, agree=0.765, adj=0.333, (0 split)

age < 32.5 to the left, agree=0.706, adj=0.167, (0 split)

hipcirc < 101.35 to the left, agree=0.706, adj=0.167, (0 split)

Node number 6: 18 observations, complexity param=0.03420446

mean=38.09111, MSE=18.36551

left son=12 (9 obs) right son=13 (9 obs)

Primary splits:

hipcirc < 109.9 to the left, improve=0.75170000, (0 missing)

elbowbreadth < 6.35 to the left, improve=0.39745500, (0 missing)

waistcirc < 98.75 to the left, improve=0.36088100, (0 missing)

kneebreadth < 9.9 to the left, improve=0.23541050, (0 missing)

age < 60.5 to the left, improve=0.07791805, (0 missing)

Surrogate splits:

elbowbreadth < 6.45 to the left, agree=0.833, adj=0.667, (0 split)

waistcirc < 98.75 to the left, agree=0.778, adj=0.556, (0 split)

kneebreadth < 9.3 to the left, agree=0.722, adj=0.444, (0 split)

age < 60.5 to the left, agree=0.667, adj=0.333, (0 split)

Node number 7: 7 observations

mean=49.72571, MSE=57.7572

Node number 8: 9 observations

mean=16.19222, MSE=7.431217

Node number 9: 5 observations

mean=22.406, MSE=6.255384

Node number 10: 6 observations

mean=22.325, MSE=5.122425

Node number 11: 11 observations, complexity param=0.01007079

mean=27.95818, MSE=13.2468

left son=22 (3 obs) right son=23 (8 obs)

Primary splits:

hipcirc < 99.5 to the left, improve=0.5021080, (0 missing)

kneebreadth < 9.5 to the left, improve=0.3645379, (0 missing)

age < 57 to the right, improve=0.2881438, (0 missing)

waistcirc < 84.25 to the left, improve=0.2865967, (0 missing)

elbowbreadth < 6.25 to the right, improve=0.1351710, (0 missing)

Surrogate splits:

age < 57 to the right, agree=0.818, adj=0.333, (0 split)

kneebreadth < 8.85 to the left, agree=0.818, adj=0.333, (0 split)

Node number 12: 9 observations

mean=34.37556, MSE=7.666625

Node number 13: 9 observations

mean=41.80667, MSE=1.453689

Node number 22: 3 observations

mean=23.74667, MSE=0.08562222

Node number 23: 8 observations

mean=29.5375, MSE=9.036669

> print(bodyfat\_rpart)

n= 56

node), split, n, deviance, yval

\* denotes terminal node

1) root 56 7265.0290000 30.94589

2) waistcirc< 88.4 31 960.5381000 22.55645

4) hipcirc< 96.25 14 222.2648000 18.41143

8) age< 60.5 9 66.8809600 16.19222 \*

9) age>=60.5 5 31.2769200 22.40600 \*

5) hipcirc>=96.25 17 299.6470000 25.97000

10) waistcirc< 77.75 6 30.7345500 22.32500 \*

11) waistcirc>=77.75 11 145.7148000 27.95818

22) hipcirc< 99.5 3 0.2568667 23.74667 \*

23) hipcirc>=99.5 8 72.2933500 29.53750 \*

3) waistcirc>=88.4 25 1417.1140000 41.34880

6) waistcirc< 104.75 18 330.5792000 38.09111

12) hipcirc< 109.9 9 68.9996200 34.37556 \*

13) hipcirc>=109.9 9 13.0832000 41.80667 \*

7) waistcirc>=104.75 7 404.3004000 49.72571 \*

> text(bodyfat\_rpart, use.n=T)

Error in rpartco(x) :

no information available on parameters from previous call to plot()

>

> opt <- which.min(bodyfat\_rpart$cptable[,"xerror"])

>

> cp <- bodyfat\_rpart$cptable[opt, "CP"]

>

> bodyfat\_prune <- prune(bodyfat\_rpart, cp = cp)

>

> print(bodyfat\_prune)

n= 56

node), split, n, deviance, yval

\* denotes terminal node

1) root 56 7265.02900 30.94589

2) waistcirc< 88.4 31 960.53810 22.55645

4) hipcirc< 96.25 14 222.26480 18.41143

8) age< 60.5 9 66.88096 16.19222 \*

9) age>=60.5 5 31.27692 22.40600 \*

5) hipcirc>=96.25 17 299.64700 25.97000

10) waistcirc< 77.75 6 30.73455 22.32500 \*

11) waistcirc>=77.75 11 145.71480 27.95818 \*

3) waistcirc>=88.4 25 1417.11400 41.34880

6) waistcirc< 104.75 18 330.57920 38.09111

12) hipcirc< 109.9 9 68.99962 34.37556 \*

13) hipcirc>=109.9 9 13.08320 41.80667 \*

7) waistcirc>=104.75 7 404.30040 49.72571 \*

> plot(bodyfat\_prune)

> DEXfat\_pred <- predict(bodyfat\_prune, newdata=bodyfat.test)

>

> table(DEXfat\_pred, bodyfat.test$DEXfat)

DEXfat\_pred 11.21 18.62 21.69 21.94 26.74 27.04 28.98 29.73 31.75 33.79 36.31 36.42 38.08 43.71 46.6

16.1922222222222 1 1 0 1 0 0 0 0 0 0 0 0 0 0 0

27.9581818181818 0 0 1 0 1 1 1 1 1 0 0 0 0 0 0

34.3755555555556 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0

41.8066666666667 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1

49.7257142857143 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0

>

> xlim <- range(bodyfat$DEXfat)

>

> plot(DEXfat\_pred ~ DEXfat, data=bodyfat.test, xlab="Observed",

+ + ylab="Predicted", ylim=xlim, xlim=xlim)

Error: unexpected '=' in:

"plot(DEXfat\_pred ~ DEXfat, data=bodyfat.test, xlab="Observed",

+ ylab="

>

> install.packages("e1071")

Installing package into ‘T:/Documents/R/win-library/3.4’

(as ‘lib’ is unspecified)

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/e1071\_1.6-8.zip'

Content type 'application/zip' length 895156 bytes (874 KB)

downloaded 874 KB

package ‘e1071’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\swen111\AppData\Local\Temp\RtmpkZpXXK\downloaded\_packages

>

> library(e1071)

Warning message:

package ‘e1071’ was built under R version 3.4.4

>

> model<-naiveBayes(iris[,1:4], iris[,5])

>

> table(predict(model, iris[,-5]), iris[,5])

setosa versicolor virginica

setosa 50 0 0

versicolor 0 47 3

virginica 0 3 47

>

> install.packages("caret")

Installing package into ‘T:/Documents/R/win-library/3.4’

(as ‘lib’ is unspecified)

also installing the dependencies ‘numDeriv’, ‘SQUAREM’, ‘abind’, ‘mnormt’, ‘lava’, ‘CVST’, ‘magic’, ‘psych’, ‘prodlim’, ‘DRR’, ‘sfsmisc’, ‘geometry’, ‘broom’, ‘ipred’, ‘dimRed’, ‘lubridate’, ‘timeDate’, ‘ddalpha’, ‘gower’, ‘RcppRoll’, ‘pls’, ‘ModelMetrics’, ‘recipes’

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/numDeriv\_2016.8-1.zip'

Content type 'application/zip' length 115375 bytes (112 KB)

downloaded 112 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/SQUAREM\_2017.10-1.zip'

Content type 'application/zip' length 272523 bytes (266 KB)

downloaded 266 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/abind\_1.4-5.zip'

Content type 'application/zip' length 40443 bytes (39 KB)

downloaded 39 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/mnormt\_1.5-5.zip'

Content type 'application/zip' length 102302 bytes (99 KB)

downloaded 99 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/lava\_1.6.1.zip'

Content type 'application/zip' length 2234291 bytes (2.1 MB)

downloaded 2.1 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/CVST\_0.2-2.zip'

Content type 'application/zip' length 57880 bytes (56 KB)

downloaded 56 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/magic\_1.5-8.zip'

Content type 'application/zip' length 505395 bytes (493 KB)

downloaded 493 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/psych\_1.8.4.zip'

Content type 'application/zip' length 5741480 bytes (5.5 MB)

downloaded 5.5 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/prodlim\_2018.04.18.zip'

Content type 'application/zip' length 238900 bytes (233 KB)

downloaded 233 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/DRR\_0.0.3.zip'

Content type 'application/zip' length 148544 bytes (145 KB)

downloaded 145 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/sfsmisc\_1.1-2.zip'

Content type 'application/zip' length 581748 bytes (568 KB)

downloaded 568 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/geometry\_0.3-6.zip'

Content type 'application/zip' length 683994 bytes (667 KB)

downloaded 667 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/broom\_0.4.4.zip'

Content type 'application/zip' length 1627973 bytes (1.6 MB)

downloaded 1.6 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/ipred\_0.9-6.zip'

Content type 'application/zip' length 298157 bytes (291 KB)

downloaded 291 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/dimRed\_0.1.0.zip'

Content type 'application/zip' length 331304 bytes (323 KB)

downloaded 323 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/lubridate\_1.7.4.zip'

Content type 'application/zip' length 1365335 bytes (1.3 MB)

downloaded 1.3 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/timeDate\_3043.102.zip'

Content type 'application/zip' length 805975 bytes (787 KB)

downloaded 787 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/ddalpha\_1.3.4.zip'

Content type 'application/zip' length 1541938 bytes (1.5 MB)

downloaded 1.5 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/gower\_0.1.2.zip'

Content type 'application/zip' length 122752 bytes (119 KB)

downloaded 119 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/RcppRoll\_0.3.0.zip'

Content type 'application/zip' length 616447 bytes (601 KB)

downloaded 601 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/pls\_2.6-0.zip'

Content type 'application/zip' length 1109351 bytes (1.1 MB)

downloaded 1.1 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/ModelMetrics\_1.1.0.zip'

Content type 'application/zip' length 592566 bytes (578 KB)

downloaded 578 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/recipes\_0.1.3.zip'

Content type 'application/zip' length 1056295 bytes (1.0 MB)

downloaded 1.0 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/caret\_6.0-80.zip'

Content type 'application/zip' length 5374764 bytes (5.1 MB)

downloaded 5.1 MB

package ‘numDeriv’ successfully unpacked and MD5 sums checked

package ‘SQUAREM’ successfully unpacked and MD5 sums checked

package ‘abind’ successfully unpacked and MD5 sums checked

package ‘mnormt’ successfully unpacked and MD5 sums checked

package ‘lava’ successfully unpacked and MD5 sums checked

package ‘CVST’ successfully unpacked and MD5 sums checked

package ‘magic’ successfully unpacked and MD5 sums checked

package ‘psych’ successfully unpacked and MD5 sums checked

package ‘prodlim’ successfully unpacked and MD5 sums checked

package ‘DRR’ successfully unpacked and MD5 sums checked

package ‘sfsmisc’ successfully unpacked and MD5 sums checked

package ‘geometry’ successfully unpacked and MD5 sums checked

package ‘broom’ successfully unpacked and MD5 sums checked

package ‘ipred’ successfully unpacked and MD5 sums checked

package ‘dimRed’ successfully unpacked and MD5 sums checked

package ‘lubridate’ successfully unpacked and MD5 sums checked

package ‘timeDate’ successfully unpacked and MD5 sums checked

package ‘ddalpha’ successfully unpacked and MD5 sums checked

package ‘gower’ successfully unpacked and MD5 sums checked

package ‘RcppRoll’ successfully unpacked and MD5 sums checked

package ‘pls’ successfully unpacked and MD5 sums checked

package ‘ModelMetrics’ successfully unpacked and MD5 sums checked

package ‘recipes’ successfully unpacked and MD5 sums checked

package ‘caret’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\swen111\AppData\Local\Temp\RtmpkZpXXK\downloaded\_packages

>

> library(caret)

Loading required package: lattice

Loading required package: ggplot2

Warning messages:

1: package ‘caret’ was built under R version 3.4.4

2: package ‘ggplot2’ was built under R version 3.4.3

> result <- confusionMatrix(predict(model, iris[1:4]), iris[,5])

>

> print(result)

Confusion Matrix and Statistics

Reference

Prediction setosa versicolor virginica

setosa 50 0 0

versicolor 0 47 3

virginica 0 3 47

Overall Statistics

Accuracy : 0.96

95% CI : (0.915, 0.9852)

No Information Rate : 0.3333

P-Value [Acc > NIR] : < 2.2e-16

Kappa : 0.94

Mcnemar's Test P-Value : NA

Statistics by Class:

Class: setosa Class: versicolor Class: virginica

Sensitivity 1.0000 0.9400 0.9400

Specificity 1.0000 0.9700 0.9700

Pos Pred Value 1.0000 0.9400 0.9400

Neg Pred Value 1.0000 0.9700 0.9700

Prevalence 0.3333 0.3333 0.3333

Detection Rate 0.3333 0.3133 0.3133

Detection Prevalence 0.3333 0.3333 0.3333

Balanced Accuracy 1.0000 0.9550 0.9550

> ?predict

> getwd()

[1] "T:/Documents"

> read.csv("car.csv")

Error in file(file, "rt") : cannot open the connection

In addition: Warning message:

In file(file, "rt") : cannot open file 'car.csv': No such file or directory

> read.csv("car.csv")

Error in file(file, "rt") : cannot open the connection

In addition: Warning message:

In file(file, "rt") : cannot open file 'car.csv': No such file or directory

> read.csv("car.csv")

Error in file(file, "rt") : cannot open the connection

In addition: Warning message:

In file(file, "rt") : cannot open file 'car.csv': No such file or directory

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Error in file(file, "rt") : cannot open the connection

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In file(file, "rt") : cannot open file 'car.csv': No such file or directory

> getwd()

[1] "T:/Documents"

> read.csv("car.csv")

Error in file(file, "rt") : cannot open the connection

In addition: Warning message:

In file(file, "rt") : cannot open file 'car.csv': No such file or directory

> read.table("car",",")

Error in file(file, "rt") : cannot open the connection

In addition: Warning message:

In file(file, "rt") : cannot open file 'car': No such file or directory

> read.table("car.data",",")

Error in !header : invalid argument type

> read.table("car.data",sep=",")

V1 V2 V3 V4 V5 V6 V7

1 vhigh vhigh 2 2 small low unacc

2 vhigh vhigh 2 2 small med unacc

3 vhigh vhigh 2 2 small high unacc

4 vhigh vhigh 2 2 med low unacc

5 vhigh vhigh 2 2 med med unacc

6 vhigh vhigh 2 2 med high unacc

7 vhigh vhigh 2 2 big low unacc

8 vhigh vhigh 2 2 big med unacc

9 vhigh vhigh 2 2 big high unacc

10 vhigh vhigh 2 4 small low unacc

11 vhigh vhigh 2 4 small med unacc

12 vhigh vhigh 2 4 small high unacc

13 vhigh vhigh 2 4 med low unacc

14 vhigh vhigh 2 4 med med unacc

15 vhigh vhigh 2 4 med high unacc

16 vhigh vhigh 2 4 big low unacc

17 vhigh vhigh 2 4 big med unacc

18 vhigh vhigh 2 4 big high unacc

19 vhigh vhigh 2 more small low unacc

20 vhigh vhigh 2 more small med unacc

21 vhigh vhigh 2 more small high unacc

22 vhigh vhigh 2 more med low unacc

23 vhigh vhigh 2 more med med unacc

24 vhigh vhigh 2 more med high unacc

25 vhigh vhigh 2 more big low unacc

26 vhigh vhigh 2 more big med unacc

27 vhigh vhigh 2 more big high unacc

28 vhigh vhigh 3 2 small low unacc

29 vhigh vhigh 3 2 small med unacc

30 vhigh vhigh 3 2 small high unacc

31 vhigh vhigh 3 2 med low unacc

32 vhigh vhigh 3 2 med med unacc

33 vhigh vhigh 3 2 med high unacc

34 vhigh vhigh 3 2 big low unacc

35 vhigh vhigh 3 2 big med unacc

36 vhigh vhigh 3 2 big high unacc

37 vhigh vhigh 3 4 small low unacc

38 vhigh vhigh 3 4 small med unacc

39 vhigh vhigh 3 4 small high unacc

40 vhigh vhigh 3 4 med low unacc

41 vhigh vhigh 3 4 med med unacc

42 vhigh vhigh 3 4 med high unacc

43 vhigh vhigh 3 4 big low unacc

44 vhigh vhigh 3 4 big med unacc

45 vhigh vhigh 3 4 big high unacc

46 vhigh vhigh 3 more small low unacc

47 vhigh vhigh 3 more small med unacc

48 vhigh vhigh 3 more small high unacc

49 vhigh vhigh 3 more med low unacc

50 vhigh vhigh 3 more med med unacc

51 vhigh vhigh 3 more med high unacc

52 vhigh vhigh 3 more big low unacc

53 vhigh vhigh 3 more big med unacc

54 vhigh vhigh 3 more big high unacc

55 vhigh vhigh 4 2 small low unacc

56 vhigh vhigh 4 2 small med unacc

57 vhigh vhigh 4 2 small high unacc

58 vhigh vhigh 4 2 med low unacc

59 vhigh vhigh 4 2 med med unacc

60 vhigh vhigh 4 2 med high unacc

61 vhigh vhigh 4 2 big low unacc

62 vhigh vhigh 4 2 big med unacc

63 vhigh vhigh 4 2 big high unacc

64 vhigh vhigh 4 4 small low unacc

65 vhigh vhigh 4 4 small med unacc

66 vhigh vhigh 4 4 small high unacc

67 vhigh vhigh 4 4 med low unacc

68 vhigh vhigh 4 4 med med unacc

69 vhigh vhigh 4 4 med high unacc

70 vhigh vhigh 4 4 big low unacc

71 vhigh vhigh 4 4 big med unacc

72 vhigh vhigh 4 4 big high unacc

73 vhigh vhigh 4 more small low unacc

74 vhigh vhigh 4 more small med unacc

75 vhigh vhigh 4 more small high unacc

76 vhigh vhigh 4 more med low unacc

77 vhigh vhigh 4 more med med unacc

78 vhigh vhigh 4 more med high unacc

79 vhigh vhigh 4 more big low unacc

80 vhigh vhigh 4 more big med unacc

81 vhigh vhigh 4 more big high unacc

82 vhigh vhigh 5more 2 small low unacc

83 vhigh vhigh 5more 2 small med unacc

84 vhigh vhigh 5more 2 small high unacc

85 vhigh vhigh 5more 2 med low unacc

86 vhigh vhigh 5more 2 med med unacc

87 vhigh vhigh 5more 2 med high unacc

88 vhigh vhigh 5more 2 big low unacc

89 vhigh vhigh 5more 2 big med unacc

90 vhigh vhigh 5more 2 big high unacc

91 vhigh vhigh 5more 4 small low unacc

92 vhigh vhigh 5more 4 small med unacc

93 vhigh vhigh 5more 4 small high unacc

94 vhigh vhigh 5more 4 med low unacc

95 vhigh vhigh 5more 4 med med unacc

96 vhigh vhigh 5more 4 med high unacc

97 vhigh vhigh 5more 4 big low unacc

98 vhigh vhigh 5more 4 big med unacc

99 vhigh vhigh 5more 4 big high unacc

100 vhigh vhigh 5more more small low unacc

101 vhigh vhigh 5more more small med unacc

102 vhigh vhigh 5more more small high unacc

103 vhigh vhigh 5more more med low unacc

104 vhigh vhigh 5more more med med unacc

105 vhigh vhigh 5more more med high unacc

106 vhigh vhigh 5more more big low unacc

107 vhigh vhigh 5more more big med unacc

108 vhigh vhigh 5more more big high unacc

109 vhigh high 2 2 small low unacc

110 vhigh high 2 2 small med unacc

111 vhigh high 2 2 small high unacc

112 vhigh high 2 2 med low unacc

113 vhigh high 2 2 med med unacc

114 vhigh high 2 2 med high unacc

115 vhigh high 2 2 big low unacc

116 vhigh high 2 2 big med unacc

117 vhigh high 2 2 big high unacc

118 vhigh high 2 4 small low unacc

119 vhigh high 2 4 small med unacc

120 vhigh high 2 4 small high unacc

121 vhigh high 2 4 med low unacc

122 vhigh high 2 4 med med unacc

123 vhigh high 2 4 med high unacc

124 vhigh high 2 4 big low unacc

125 vhigh high 2 4 big med unacc

126 vhigh high 2 4 big high unacc

127 vhigh high 2 more small low unacc

128 vhigh high 2 more small med unacc

129 vhigh high 2 more small high unacc

130 vhigh high 2 more med low unacc

131 vhigh high 2 more med med unacc

132 vhigh high 2 more med high unacc

133 vhigh high 2 more big low unacc

134 vhigh high 2 more big med unacc

135 vhigh high 2 more big high unacc

136 vhigh high 3 2 small low unacc

137 vhigh high 3 2 small med unacc

138 vhigh high 3 2 small high unacc

139 vhigh high 3 2 med low unacc

140 vhigh high 3 2 med med unacc

141 vhigh high 3 2 med high unacc

142 vhigh high 3 2 big low unacc

[ reached getOption("max.print") -- omitted 1586 rows ]

> df<-read.table("car.data",sep=",")

> set.seed(1234)

> ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.7, 0.3))

>

> View(df)

> trainData<-df[ind==1,]

> testData<-df[ind==2,]

> myFormula <- Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width

>

> df\_ctree<-ctree(myFormula, data=trainData)

Error in ctree(myFormula, data = trainData) :

could not find function "ctree"

>

> df\_ctree <- ctree(myFormula, data=trainData)

Error in ctree(myFormula, data = trainData) :

could not find function "ctree"

>

> ?ctree

> df\_ctree <- ctree(myFormula, data=trainData)

Error in ctree(myFormula, data = trainData) :

could not find function "ctree"

>

> library(party)

Loading required package: grid

Loading required package: mvtnorm

Loading required package: modeltools

Loading required package: stats4

Attaching package: ‘modeltools’

The following object is masked from ‘package:arules’:

info

Loading required package: strucchange

Loading required package: zoo

Attaching package: ‘zoo’

The following objects are masked from ‘package:base’:

as.Date, as.Date.numeric

Loading required package: sandwich

Warning messages:

1: package ‘party’ was built under R version 3.4.4

2: package ‘mvtnorm’ was built under R version 3.4.4

3: package ‘strucchange’ was built under R version 3.4.3

4: package ‘zoo’ was built under R version 3.4.3

5: package ‘sandwich’ was built under R version 3.4.3

>

> df\_ctree <- ctree(myFormula, data=trainData)

Error in eval(predvars, data, env) : object 'Species' not found

>

> myFormula <- Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width

>

> str(iris)

'data.frame': 150 obs. of 5 variables:

$ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...

$ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...

$ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...

$ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...

$ Species : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...

> str(df)

'data.frame': 1728 obs. of 7 variables:

$ V1: Factor w/ 4 levels "high","low","med",..: 4 4 4 4 4 4 4 4 4 4 ...

$ V2: Factor w/ 4 levels "high","low","med",..: 4 4 4 4 4 4 4 4 4 4 ...

$ V3: Factor w/ 4 levels "2","3","4","5more": 1 1 1 1 1 1 1 1 1 1 ...

$ V4: Factor w/ 3 levels "2","4","more": 1 1 1 1 1 1 1 1 1 2 ...

$ V5: Factor w/ 3 levels "big","med","small": 3 3 3 2 2 2 1 1 1 3 ...

$ V6: Factor w/ 3 levels "high","low","med": 2 3 1 2 3 1 2 3 1 2 ...

$ V7: Factor w/ 4 levels "acc","good","unacc",..: 3 3 3 3 3 3 3 3 3 3 ...

> myFormula <- V7 ~ V1 + V2 + V3 + V4 + V5 +V6

> df\_ctree <- ctree(myFormula, data=trainData)

>

> print(df\_ctree)

Conditional inference tree with 26 terminal nodes

Response: V7

Inputs: V1, V2, V3, V4, V5, V6

Number of observations: 1293

1) V6 == {high, med}; criterion = 1, statistic = 370.513

2) V4 == {2}; criterion = 1, statistic = 338.233

3)\* weights = 274

2) V4 == {4, more}

4) V1 == {low, med}; criterion = 1, statistic = 209.475

5) V2 == {high, vhigh}; criterion = 1, statistic = 116.769

6) V5 == {small}; criterion = 1, statistic = 39.052

7) V6 == {med}; criterion = 1, statistic = 20.444

8) V2 == {high}; criterion = 0.979, statistic = 8.474

9)\* weights = 10

8) V2 == {vhigh}

10)\* weights = 14

7) V6 == {high}

11)\* weights = 20

6) V5 == {big, med}

12) V6 == {med}; criterion = 0.986, statistic = 17.061

13) V3 == {3, 4, 5more}; criterion = 0.967, statistic = 12.594

14)\* weights = 29

13) V3 == {2}

15)\* weights = 10

12) V6 == {high}

16) V1 == {med}; criterion = 0.996, statistic = 11.652

17)\* weights = 26

16) V1 == {low}

18) V2 == {vhigh}; criterion = 0.999, statistic = 13.8

19)\* weights = 12

18) V2 == {high}

20)\* weights = 12

5) V2 == {low, med}

21) V6 == {high}; criterion = 1, statistic = 56.522

22) V5 == {small}; criterion = 1, statistic = 51.609

23)\* weights = 25

22) V5 == {big, med}

24) V5 == {med}; criterion = 0.994, statistic = 14.012

25)\* weights = 20

24) V5 == {big}

26)\* weights = 25

21) V6 == {med}

27) V5 == {small}; criterion = 1, statistic = 26.122

28)\* weights = 21

27) V5 == {big, med}

29) V1 == {med}; criterion = 0.989, statistic = 9.712

30) V2 == {med}; criterion = 1, statistic = 16.309

31)\* weights = 13

30) V2 == {low}

32)\* weights = 11

29) V1 == {low}

33)\* weights = 23

4) V1 == {high, vhigh}

34) V2 == {high, low, med}; criterion = 1, statistic = 104.584

35) V6 == {high}; criterion = 1, statistic = 26.93

36) V2 == {low, med}; criterion = 1, statistic = 23.595

37) V3 == {2}; criterion = 0.97, statistic = 12.8

38)\* weights = 17

37) V3 == {3, 4, 5more}

39)\* weights = 52

36) V2 == {high}

40) V1 == {vhigh}; criterion = 1, statistic = 34

41)\* weights = 16

40) V1 == {high}

42)\* weights = 19

35) V6 == {med}

43) V5 == {small}; criterion = 1, statistic = 42.521

44)\* weights = 31

43) V5 == {big, med}

45) V1 == {high}; criterion = 0.964, statistic = 12.38

46)\* weights = 35

45) V1 == {vhigh}

47) V2 == {high}; criterion = 0.996, statistic = 14.794

48)\* weights = 10

47) V2 == {low, med}

49)\* weights = 23

34) V2 == {vhigh}

50)\* weights = 73

1) V6 == {low}

51)\* weights = 472

> plot(df\_ctree)

> df<-read.table("car.data",sep=",")

> set.seed(1234)

> ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.7, 0.3))

>

> View(df)

> trainData<-df[ind==1,]

> testData<-df[ind==2,]

> library(party)

> myFormula <- V7 ~ V1 + V2 + V3 + V4 + V5 +V6

> df\_ctree <- ctree(myFormula, data=trainData)

> print(df\_ctree)

Conditional inference tree with 26 terminal nodes

Response: V7

Inputs: V1, V2, V3, V4, V5, V6

Number of observations: 1293

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2) V4 == {2}; criterion = 1, statistic = 338.233

3)\* weights = 274

2) V4 == {4, more}

4) V1 == {low, med}; criterion = 1, statistic = 209.475

5) V2 == {high, vhigh}; criterion = 1, statistic = 116.769

6) V5 == {small}; criterion = 1, statistic = 39.052

7) V6 == {med}; criterion = 1, statistic = 20.444

8) V2 == {high}; criterion = 0.979, statistic = 8.474

9)\* weights = 10

8) V2 == {vhigh}

10)\* weights = 14

7) V6 == {high}

11)\* weights = 20

6) V5 == {big, med}

12) V6 == {med}; criterion = 0.986, statistic = 17.061

13) V3 == {3, 4, 5more}; criterion = 0.967, statistic = 12.594

14)\* weights = 29

13) V3 == {2}

15)\* weights = 10

12) V6 == {high}

16) V1 == {med}; criterion = 0.996, statistic = 11.652

17)\* weights = 26

16) V1 == {low}

18) V2 == {vhigh}; criterion = 0.999, statistic = 13.8

19)\* weights = 12

18) V2 == {high}

20)\* weights = 12

5) V2 == {low, med}

21) V6 == {high}; criterion = 1, statistic = 56.522

22) V5 == {small}; criterion = 1, statistic = 51.609

23)\* weights = 25

22) V5 == {big, med}

24) V5 == {med}; criterion = 0.994, statistic = 14.012

25)\* weights = 20

24) V5 == {big}

26)\* weights = 25

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27) V5 == {small}; criterion = 1, statistic = 26.122

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31)\* weights = 13

30) V2 == {low}

32)\* weights = 11

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33)\* weights = 23

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44)\* weights = 31

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46)\* weights = 35

45) V1 == {vhigh}

47) V2 == {high}; criterion = 0.996, statistic = 14.794

48)\* weights = 10

47) V2 == {low, med}

49)\* weights = 23

34) V2 == {vhigh}

50)\* weights = 73

1) V6 == {low}

51)\* weights = 472

> plot(df\_ctree)

>

>

> trainData<-df[ind==1,]