



COURS M1 IA
PROMOTION 16
« SYSTÈMES INTELLIGENTS & MULTIMÉDIA »

useR!



- Open source, development-flexible, extensible**
- Large number of statistical and numerical methods**
- High quality visualization and graphical tools**
- Extended by a very large collection of rapidly developing packages**



/Volumes/DataHD/Users/jdz

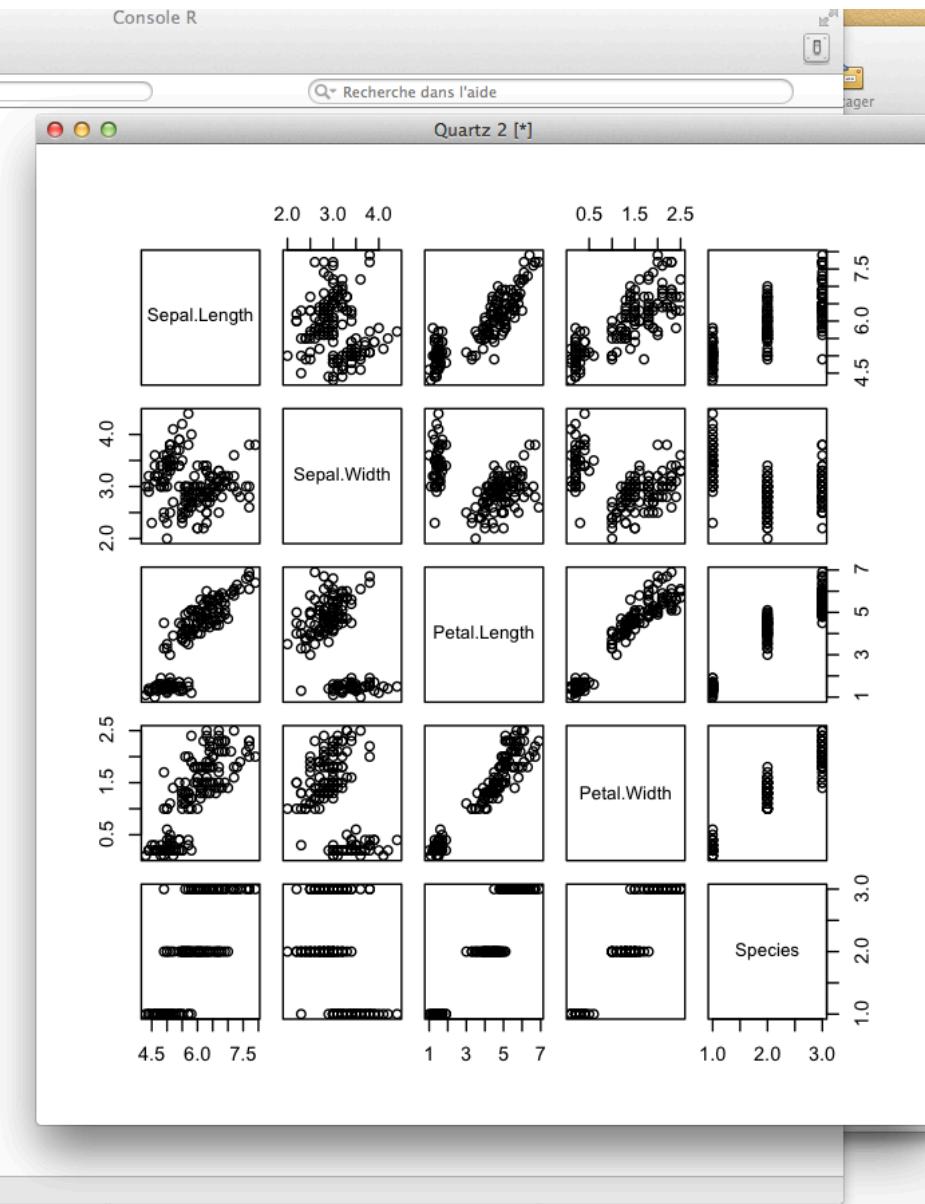
Console R

Recherche dans l'aide



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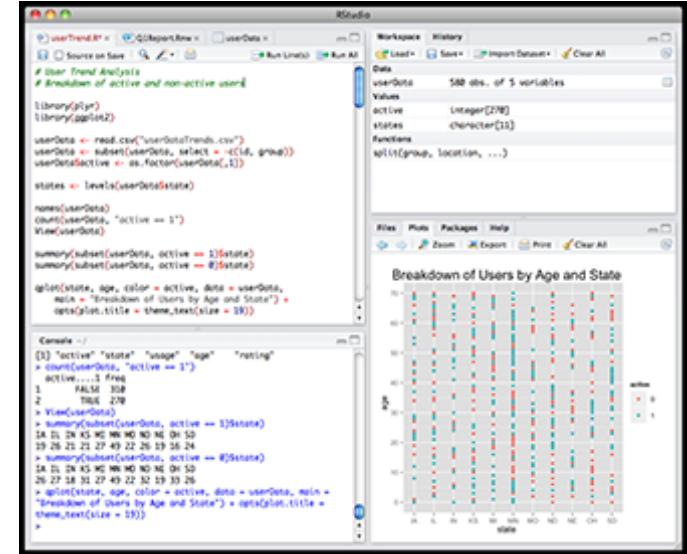
```
data(iris)  
plot(iris)
```

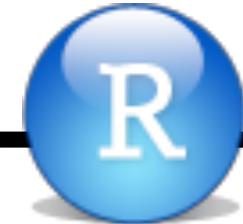




RSTUDIO

- **4 windows**
 - **Editor**,
 - **Console**,
 - **History**,
 - **Files/plots**
- **Code completion**
- **Easy access to help (F1)**
- **One step Sweave (latex/R) pdf generation**
- **Searchable history**
- **Keyboard Shortcuts**
 - http://www.rstudio.org/docs/using/keyboard_shortcuts





RSTUDIO

RStudio

Project: (None)

Workspace

- Boston 506 obs. of 14 variables
- HouseVotes84 435 obs. of 17 variables
- data 150 obs. of 4 variables
- dendat 100x1 double matrix
- iris 150 obs. of 5 variables
- z 150x3 double matrix

Values

- BOTTOM 1
- Delta 0.01
- F10 ecdfGamma

Files

Plots

Packages

Help

Console

Platform: x86_64-apple-darwin9.8.0/x86_64 (64-bit)

R est un logiciel libre livré sans AUCUNE GARANTIE.
Vous pouvez le redistribuer sous certaines conditions.
Tapez 'license()' ou 'licence()' pour plus de détails.

R est un projet collaboratif avec de nombreux contributeurs.
Tapez 'contributors()' pour plus d'information et
'citation()' pour la façon de le citer dans les publications.

Tapez 'demo()' pour des démonstrations, 'help()' pour l'aide en ligne ou 'help.start()' pour obtenir l'aide au format HTML.
Tapez 'q()' pour quitter R.

[Workspace loaded from ~/.RData]

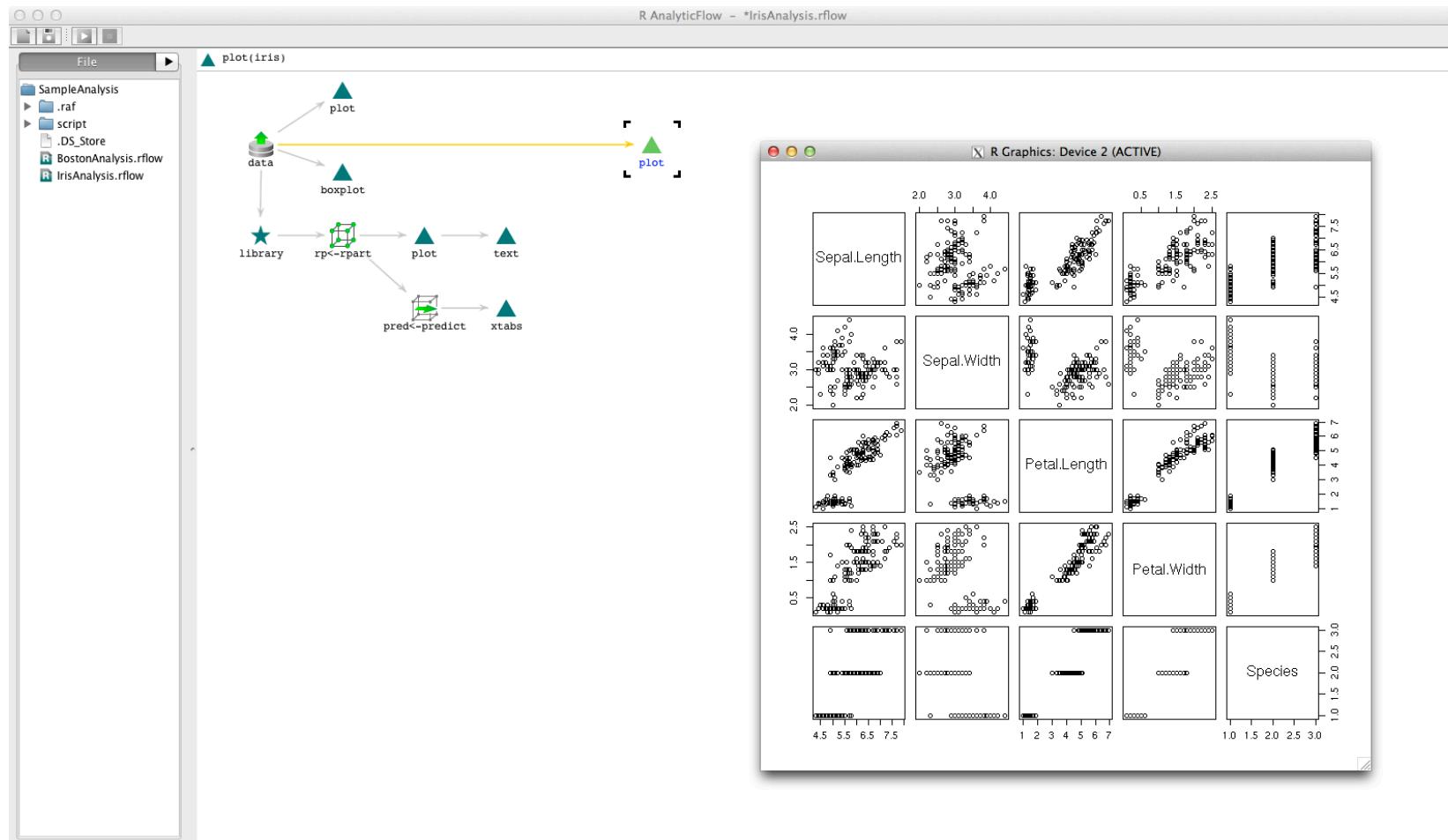
```
> data(iris)
> View(iris)
> plot(iris)
>
```

Figure: Iris flower dataset analysis

A 4x4 grid of plots showing relationships between Iris flower species based on Sepal.Length, Sepal.Width, Petal.Length, and Petal.Width.

- Row 1: Sepal.Length vs Sepal.Length (Diagonal), Sepal.Length vs Petal.Length, Sepal.Length vs Petal.Width, Sepal.Length vs Species.
- Row 2: Sepal.Length vs Sepal.Width, Sepal.Width vs Petal.Length, Sepal.Width vs Petal.Width, Sepal.Width vs Species.
- Row 3: Sepal.Length vs Sepal.Length (Diagonal), Sepal.Length vs Petal.Length, Sepal.Length vs Petal.Width, Sepal.Length vs Species.
- Row 4: Sepal.Length vs Sepal.Width, Sepal.Width vs Petal.Length, Sepal.Width vs Petal.Width, Sepal.Width vs Species.

The Species column shows three distinct clusters corresponding to the Iris setosa, Iris virginica, and Iris versicolor species.



Descriptive Statistics in R

Mean	> <code>mean(x);</code> > <code>mean(x,trim=a)</code>
Median	> <code>median(x)</code>
Mode	> <code>sort(table(x))</code>
Standard deviation	> <code>sd(x)</code>
Variance	> <code>var(x)</code>
the median absolute deviation	> <code>mad(c(x))</code>
interquartile range	> <code>IQR(x)</code>
Range	> <code>range(x)</code>

SCATTERPLOT MATRIX

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	6.5	2.8	4.6	1.5	versicolor
5	5.7	2.8	4.5	1.3	versicolor
6	6.3	3.3	4.7	1.6	versicolor
7	6.7	2.5	5.8	1.8	virginica
8

- Iris dataset
- 150 flowers
- 5 variables



(cc) BY

Goingslo, [flickr](#)

LES DONNÉES DES INDIENS PIMA

- The National Institute of Diabetes and Digestive and Kidney Diseases conducted a study on 768 adult female Pima Indians living near Phoenix.
- **9 Variables (8 continuous, 1 categorical)**
 - 1) pregnant: Number of times pregnant
 - 2) Glucose : Plasma glucose concentration at 2 hours in an oral glucose tolerance test
 - 3) Diastolic : Diastolic blood pressure (mm Hg)
 - 4) Triceps : Triceps skin fold thickness (mm)
 - 5) Insulin : 2-Hour serum insulin (mu U/ml)
 - 6) Bmi : Body mass index (weight in kg/(height in metres squared))
 - 7) Diabetes : Diabetes pedigree function
 - 8) Age : Age (years)
 - 9) Test : diabetes (coded 0 if negative, 1 if positive)

INTERMEDE EN R : QUANTILES

```
# Chargement de la librairie
library(faraway)
# Chargement des données PIMA
data(pima)
?pima
str(pima)
summary(pima)
pima$diastolic
# Calcul la somme des femmes qui ont 0
# pour la variable diastolic
sum(pima$diastolic == 0)

# On remplace les valeurs nuls par NA
pima$diastolic[ pima$diastolic == 0 ] <-
NA
pima$glucose[ pima$glucose == 0 ] <- NA
pima$triceps [ pima$triceps == 0 ] <- NA
pima$insulin [ pima$insulin == 0 ] <- NA
pima$bmi [ pima$bmi == 0 ] <- NA
```

INTERMEDE EN R : SCATTERPLOT

```
# Modification des facteurs
pima$test <- factor(pima$test)
levels(pima$test) <- c("negativ", "positiv")
summary(pima$test)

#some boxplot
boxplot(pima$triceps, main="Skin at triceps in mm")

#parallel boxplots
boxplot(diabetes ~ test , pima, main="Parallel
Boxplots")

### scatterplot
plot(diastolic ~ bmi,pima)

### scatterplotmatrix
plot(pima, pch= "+",main="Scatterplotmatrix")
```

INTERMEDE EN R : PCA

```
# The ground data are set to be the pima data
MyData <- pima

# Performs a principal components analysis on
# GroundData
MyData.pca <- prcomp(MyData[,-9])
# Display the coefficients of the two first
# components
signif(MyData.pca$rotation[,1],digits = 2)
signif(MyData.pca$rotation[,2],digits = 2)

# The Data2D is built from the two first components
# and the column result of the test
class <- MyData[,9]
Data2D <- data.frame(cbind(MyData.pca$x[,1:2],
class))
names(Data2D) <- c("PC1","PC2","test")
```