

Introdução à Linguagem de Programação em R

Dia 2

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Contents

Graphs

Basic Graphs

`lattice` Package

Contents

Graphs

Basic Graphs

`lattice` Package

Functions

Introduction

Iterations and Loops

Basic Graphs

One of the main reasons data analysts turn to R is for its strong graphic capabilities.

In R, graphs are typically created interactively.

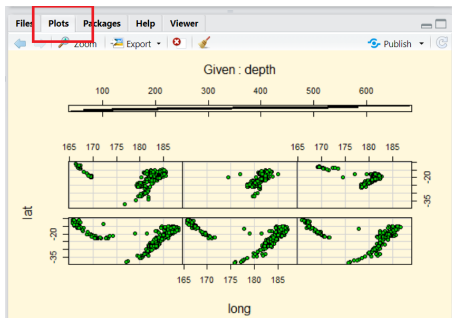
```
# Creating a Graph  
>attach(mtcars)  
>plot(wt, mpg)  
>abline(lm(mpg~wt))  
>title("Regression of MPG on Weight")
```

The `plot()` function opens a graph window and plots weight vs. miles per gallon. The next line of code adds a regression line to this graph. The final line adds a title.

Basic Graphs

You can run the function `>demo(graphics)` to see several options.

When you produce a plot it will be seen in a window called *plots*:



Basic graphs

The function `plot()` is generic. The graph depends on the first argument of the function `plot()`.

Data base: CO2

- ▶ `data(CO2)`
- ▶ `plot(CO2$Type)`
- ▶ `plot(CO2$uptake)`
- ▶ `plot(CO2$Type, CO2$conc)`

Graph Functions

Graphics commands can be grouped into three categories:

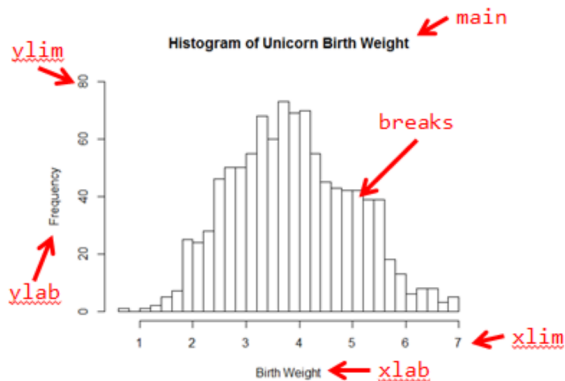
- ▶ High-level graphics functions: create new graphics in the graphic window, axes, labels, titles, etc.
- ▶ Low-level graphical functions: allow new information to be added to graphs already existing.
- ▶ Interactive graphic functions: allow adding or removing information in existing graphics.

Basic Graphs

The next arguments are very used in most graphical functions:

<code>main=""</code> <code>xlab="", ylab=""</code> <code>xlim=,ylim=</code> <code>type=""</code> <code>col=</code> <code>lty=</code>	<code>title</code> variables labels specifies the lower and upper limits of the axes "l" lines "p" points connected by lines "o" lines over points "h" vertical lines "s" steps controls the color controls the type of lines
---	--

Basic graphs



Legends

`legend()`

```
>plot(rnorm(10), type = "l")  
>lines(rnorm(10), col = "red", lty = 2)  
>title("Random numbers")  
>legend("topright", c("1a série", "2a série"), lty =  
+1:2,col = 1:2)
```

Several graphs on the same page

The argument `mfrow` is used to define line by line of the page where the graphs are putted. You could define column by column instead using `mfcol()` argument.

```
>par(mfrow=c(1,2))  
>hist(CO2$uptake)  
>pie(table(CO2$Plant))
```

Several graphs on the same page

You could split the window device by several sizes using the function `layout()`, where the principal argument is a matrix whose dimensions defines how the device will be divided.

```
layout(matrix(1:4, 2, 2))
```

You can use the function `layout.show()` to visualize the information.

```
layout.show(4)
```

Saving Graphs

You could save your graphs in several formats: .pdf, jpeg, ps:

Example:

```
>jpeg(file="plot.jpeg")  
>plot(Plant)  
>dev.off()
```

The image will be saved in your working directory.

Saving Graphs

To save a graphic:

- ▶ Click the Plots Tab window
- ▶ Click the Export button
- ▶ Choose your desired format
- ▶ Modify the export settings as you desire
- ▶ Click Save

Exercises



- ▶ Go to https://github.com/CarinaSilva/Introducao-Linguagem-de-Programacao-em-R/tree/main/Dia_2
- ▶ exercises_day2: Do exercise 1 to 8

lattice Package

Lattice is a powerful and elegant data visualization package for R programming, with an emphasis on multivariate data.

```
# Install
install.packages("lattice")

# Load
library("lattice")
```


lattice Package

The lattice package has a number of different functions to create different types of plot. For example, to create a scatterplot, use the `xypplot()` function. Notice that this is different from base graphics, where the `plot()` function creates a variety of different plot types.

lattice Package

The typical format is

```
graph_type(formula, data=)
```

formula: This is a formula typically of the form $y \sim x \mid z$. It means to create a plot of y against x , conditional on z . In other words, create a plot for every unique value of z . Each of the variables in the formula has to be a column in the data frame that you specify in the data argument.

data: A data frame that contains all the columns that you specify in the formula argument.

lattice Package

`graph_type` is selected from the listed below:

graph_type	description	formula examples
barchart	bar chart	$x \sim A$ or $A \sim x$
bwplot	boxplot	$x \sim A$ or $A \sim x$
cloud	3D scatterplot	$z \sim x * y A$
contourplot	3D contour plot	$z \sim x * y$
densityplot	kernal density plot	$\sim x A * B$
dotplot	dotplot	$\sim x A$
histogram	histogram	$\sim x$
levelplot	3D level plot	$z \sim y * x$
parallel	parallel coordinates plot	data frame
splom	scatterplot matrix	data frame
stripplot	strip plots	$A \sim x$ or $x \sim A$
xyplot	scatterplot	$y \sim x A$
wireframe	3D wireframe graph	$z \sim y * x$

lattice Package

- ◇ $\sim x | A$ for each level of factor (A), it displays a numerical variable which is x;
- ◇ $y \sim x | A * B$ for every combination of factor A and B, there exists a relationship between the variables x and y.
- ◇ $\sim x$ means display numeric variable x alone.

lattice Package

```
>my_data <- iris
>head(my_data)
# Default plot
>xyplot(Sepal.Length~ Petal.Length, data = my_data)
# Color by groups
>xyplot(Sepal.Length ~ Petal.Length, group = Species,
data = my_data, auto.key = TRUE)
```

lattice Package

```
# Show points ("p"), grids ("g") and smoothing line
# Change xlab and ylab
>xyplot(Sepal.Length ~ Petal.Length, data = my_data,
+ type = c("p", "g", "smooth"),
+ xlab = "Miles/(US) gallon", ylab = "Weight (1000
lbs)")
```

lattice Package

Multiple panels by groups: $y \sim x \mid \text{group}$

```
>xyplot(Sepal.Length ~Petal.Length | Species,  
+ group = Species, data = my_data,  
+ type = c("p", "smooth"),  
+ scales = "free")
```

lattice Package

```
>bwplot( Petal.Length ~ Species, data = my_data,  
+ layout = c(4, 1), xlab = "Length")  
  >bwplot( Petal.Length ~ Species, data = my_data,  
+ layout = c(4, 1), xlab = "Length")  
>bwplot( ~Petal.Length | Species, data = my_data,  
+ layout = c(4, 1), xlab = "Length")
```


Exercises



- ▶ Go to https://github.com/CarinaSilva/Introducao-Linguagem-de-Programacao-em-R/tree/main/Dia_2
- ▶ `exercises_day2`: Do exercise 9 to 11.

ggplot2 Package



<https://ggplot2.tidyverse.org/reference/>

Functions

A function is a set of statements organized together to perform a specific task. R has a large number of in-built functions and the user can create their own functions.

An R function is created by using the keyword `function`. The basic syntax of an R function definition is as follows

```
function_name <- function(arg_1, arg_2, ...) {  
  Function body  
}
```

Functions

The different parts of a function are

- ▶ **Function Name** - This is the actual name of the function. It is stored in R environment as an object with this name.
- ▶ **Arguments** - An argument is a placeholder. When a function is invoked, you pass a value to the argument. Arguments are optional, that is, a function may contain no arguments. Also arguments can have default values.
- ▶ **Function Body** - The function body contains a collection of statements that defines what the function does.
- ▶ **Return Value** - The return value of a function is the last expression in the function body to be evaluated.

Functions

Example:

```
pow <- function(x, y) {  
  # function to print x raised to the power y  
  result <- x^y  
  print(paste(x,"raised to the power", y, "is", result))  
}
```

Functions

How to call a function

```
> pow(8, 2)
[1] "8 raised to the power 2 is 64"
> pow(2, 8)
[1] "2 raised to the power 8 is 256"
```

Exercises



- ▶ Go to `https://github.com/CarinaSilva/Introducao-Linguagem-de-Programacao-em-R/tree/main/Dia_2`
- ▶ `exercises_day2`: Do exercise 12 to 14.

Iterations/Loops

Sometimes, iteration can not be avoided. The R commands `for` or `while` are useful in this situation. Here is an example of using `for` inside a function:

```
> Jsum <- function(x)      {  
+   jsum <- 0  
+   for(i in 1:length(x)) { jsum <- jsum + x[i] }  
+   return(jsum)           }
```

Note: R has its own function that performs this task, called `sum`. It will work MUCH faster than this one, especially on large vectors.

Iterations/Loops

When writing your own function, **avoid iteration** if you can; take advantage of R **vectorized math** and functions such as **apply**. It successively applies the function of your choice to each row (or column) of a matrix.

```
> x <- matrix(1:12, 3, 4)
> apply(x, 2, mean)  # returns the mean of each column.
> apply(x, 1, mean)  # returns the mean of each row.
```