

# A Quick and focused overview of R data types and ggplot2 syntax

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INRA - MaIAGE

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## Plan

- 1 R and Rstudio
- 2 Simple Operations
- 3 Data
  - Elementary Modes
  - Data structures
  - Logical Filters
  - Import/export data
- 4 ggplot2

R is a **free and open** environment for computational statistics and graphics (Open source, Open development, under GNU General Public Licence).



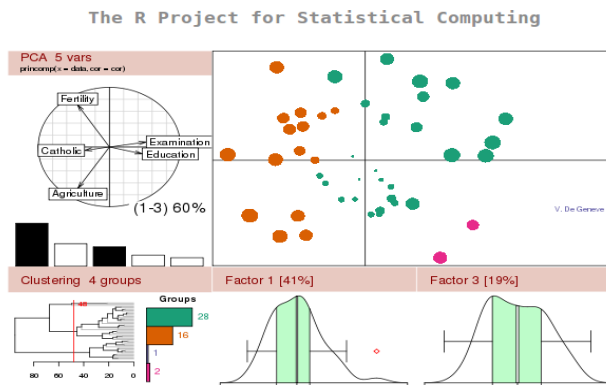
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#### Getting Started:

- R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To [download R](#), please choose your preferred [CRAN mirror](#).
- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

#### News:

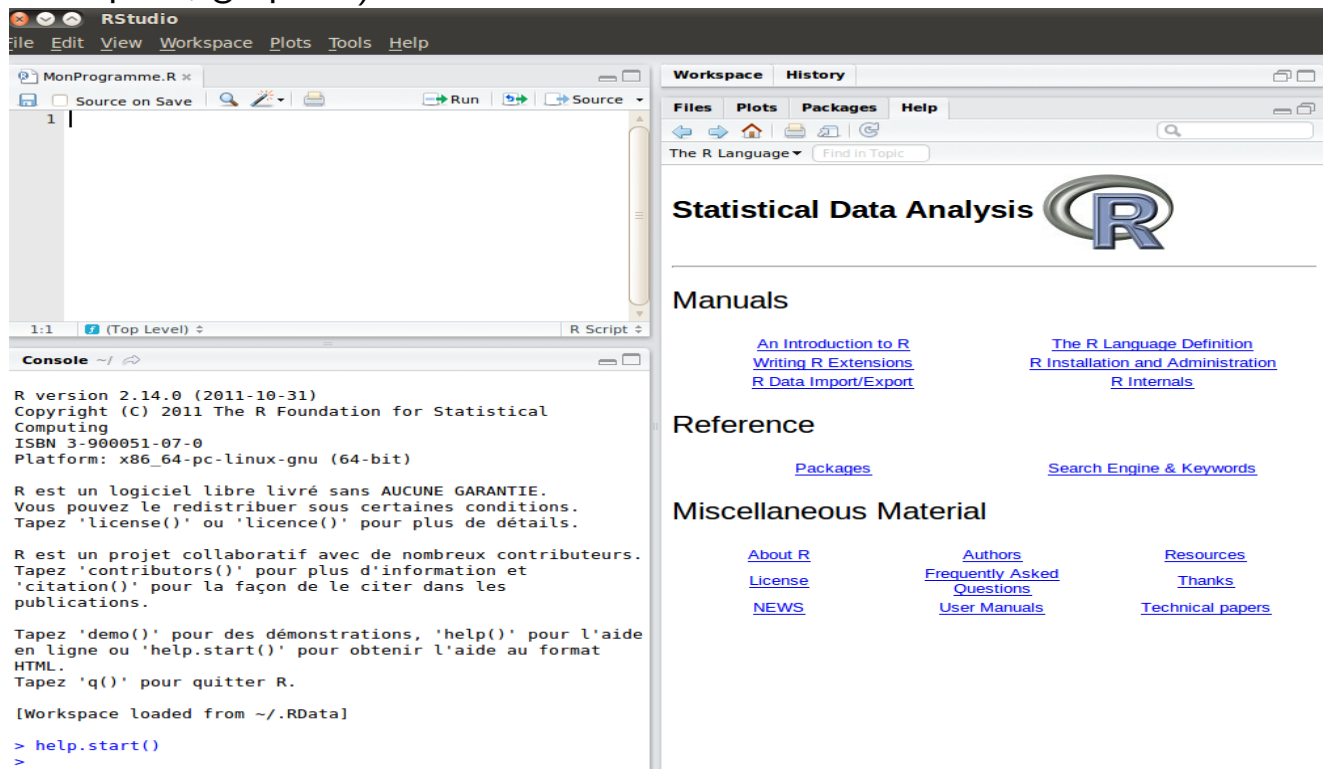
- [R 2.14.1 prerelease versions](#) will appear starting December 12. Final release is scheduled for December 22, 2011.
- [useR! 2012](#), will take place at Vanderbilt University, Nashville Tennessee, USA, June 12-15, 2012.
- [R version 2.14.0](#) (Great Pumpkin) has been released on 2011-10-31.
- [R version 2.13.2](#) has been released on 2011-09-30.
- [The R Journal Vol.3/1](#) is available.

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## Working environment

- R is an interpreted language
- There is no compilation
- One can work in the console (this tutorial) or in a script file (like the script associated with the training session)
- Good for interactive use of the language
- Bad for speed (when performing heavy computations)

Rstudio provides a nice front-end to R with 4 panels (script, console, workspace, graphics)



## Console

The console is a glorified calculator,

- you submit some R code and press Enter
- R evaluates the expression and returns the answers

```
2+2
```

```
## [1] 4
```

When using R-studio, you can use “CTRL + Enter” to execute some code *from the script* (as opposed to “Enter” to execute it *from the console*).

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# Getting help

- Widely used packages include detailed help files for the functions they provide.
- `help("function_name")` leads to the help page of `function_name`

```
help("mean") ## or  
?mean
```

# Installing and loading packages

The main strength of R comes from the thousands of **packages** that provide nice functions and utilities to the language. Most are available from the CRAN (Comprehensive R Archive Network) and easy to install:

```
install.packages("ggplot2")
```

Loading packages is equally easy:

```
library(ggplot2)
```

Most packages must be loaded at **each new session** (see the “Packages” tab in R-studio)

# Assigning a value to a variable

You can **save** the value of some R code using one of two ways:

- the “arrow operator”: `<-` (or more rarely `->`)
- the “equal” sign: `=` (we recommend `<-` over `=`)

The syntax is simple: **variable\_name <- value**.

```
a <- 2*4 ## or a = 2*4 (the # sign signals a comment)
```

And you can **access** and **manipulate** the value of that variable

```
a  
## [1] 8  
  
a/2  
## [1] 4
```

## Changing the value of a variable

The arrow is also used to change the value of an object:

```
a <- 4
a

## [1] 4
```

Modifications made to a copy do no impact the original object:

```
b <- a; b <- 8
a; b

## [1] 4
## [1] 8
```

## Removing a variable

The `rm()` function is used to remove an object from the workspace<sup>1</sup>:

```
a

## [1] 4

rm(a)
a ## a does not exist anymore

## Error in eval(expr, envir, enclos): objet 'a' introuvable
```

---

<sup>1</sup>Truth is a bit more complex, but it's a good enough approximation

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# Data in R

In R every *basic* object has four characteristics:

- a **name**
- a **mode**
- a **length**
- a **content**

The three main modes are **numeric**, **logical**, **character**.

## Elementary modes in R

There are several **basic** modes in R. The most common ones are illustrated below.

Numeric <sup>2</sup>	Character	Logical
<pre>x &lt;- 1 class(x)  ## [1] "numeric"</pre>	<pre>x &lt;- "hello" class(x)  ## [1] "character"</pre>	<pre>x &lt;- TRUE class(x)  ## [1] "logical"</pre>

- a **logical** can only take value **TRUE** or **FALSE**
- a **character** can be defined using simple (') or double (") quotes

---

<sup>2</sup>With a subtle difference between numeric and integer that we're going to ignore

## Data types conversion (I)

When possible, the functions **as.something** change a variable from one type to another:

```
as.numeric("5")
```

```
## [1] 5
```

```
as.logical(0.0)
```

```
## [1] FALSE
```

```
as.numeric(TRUE)
```

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

```
as.character(TRUE)
```

```
## [1] "TRUE"
```

```
as.numeric("5.56")
```

```
## [1] 5.56
```

```
as.logical(2)
```

```
## [1] TRUE
```

But sometimes fail (producing **NA**, Not Available) when the conversion is not properly defined:

```
as.numeric("INRA")
```

```
## Warning: NAs introduits lors de la conversion automatique
```

```
## [1] NA
```

Character is more general than numeric, itself more general than logical.



## Data types conversion (II)

Guess the results of the following commands and check your guesses in the console:

*## Numeric*

```
as.numeric(2/3)
as.numeric(5.67)
as.numeric(FALSE)
as.numeric(TRUE)
as.numeric("5.67")
as.numeric("MaIAGE")
```

*## Character*

```
as.character(2/3)
as.character(5.67)
as.character(FALSE)
as.character(TRUE)
as.character(5)
as.character(5+7)
```

*## Logical*

```
as.logical(2/3)
as.logical(0)
as.logical("45")
as.logical("MaIAGE")
```

Using the conversion rules from **logical** to **numeric**, guess the value of:

```
TRUE + TRUE + FALSE * TRUE + TRUE * TRUE
```

## Length

The **length()** function returns the length of an object:

```
a <- 2
length(a)

## [1] 1

a

## [1] 2
```

- In the previous example, **a** is a **vector** of **length** 1, with a single element
- Hence the mysterious **[1]** in the output of **a**

## Special values

There are two important **special values** in R : **NA** and **NULL**.

- **NA** stands for **N**ot **A**vailable and is a code for missing data.
- **NULL** is the R code for a null object. It has length 0.

```
a <- NA; length(a); is.na(a) ## NA
## [1] 1
## [1] TRUE

x <- NULL; length(x); is.null(x) ## NULL
## [1] 0
## [1] TRUE
```

## Data structures

R offers many **data structures** to organize data. The main ones are

- vector (1D array)
- factor
- matrix (2D array)
- list
- data.frame

# Vectors

Multiple elements of the **same** mode (numeric, character, logical) can be collected in a vector (1D array) using the `c` command:

```
x <- c(2, 4, 8, 9, 0)
x ## prints x

## [1] 2 4 8 9 0
```

Elements of `x` can be accessed with the indexing operations:

```
x[1] ## first element      x[c(3, 5)] ## third and fifth elements
## [1] 2                  ## [1] 8 0
```

Elements of different types are coerced to the most general mode before collection:

```
c(3.4, 2, TRUE)          c(3.4, "MaIAGE", TRUE)
## [1] 3.4 2.0 1.0      ## [1] "3.4"      "MaIAGE" "TRUE"
```

## Named Vectors (I)

If `x` is a **named vector**, elements can be accessed by **name** rather than by **position**:

```
x <- c("first" = 1, "second" = 4, "third" = 9)
x

## first second third
##      1      4      9
```

```
x[1]

## first
##      1
```

```
x["first"]

## first
##      1
```

# Named Vectors (I)

Names can be set or changed after creating a vector using **names**

```
x <- c(1, 4, 9)
x

## [1] 1 4 9

names(x) <- c("first", "second", "third")
x

## first second third
##      1      4      9
```

## Logical Indexing

A vector **x** can be indexed by a **logical vector** index specifying which elements should be kept. In that case, **index** and **x** should have the **same length**...

```
x <- 1:6
index <- c(TRUE, FALSE, TRUE, TRUE, FALSE, FALSE)
x[index] ## = x[c(1, 3, 4)]

## [1] 1 3 4
```

...otherwise strange things can happen.

```
index <- c(TRUE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE)
x[index] ## = x[c(1, 3, 4, 7)] but x[7] does not exist

## [1] 1 3 4 NA
```

## Vectors: exercise

Guess the result of the following code, check your guess in the console:

```
## Indexing
x <- c("0", "0", "H", "L", "Q")
x[c(4, 3, 1, 2, 5)] ## following Marcel Duchamp
## Type conversion
y <- c(4.5, 3, TRUE, "0.5")
class(y[3])
y[3]
## Conversion and indexing
z <- as.logical(c(4.5, 3, FALSE)) ## converts the whole vector
z
z[c(3, 1, 1)]
```

## Matrices

Matrices are essentially 2-D vectors: all elements must have the same mode. Indexing works the same way than for vectors but with **two** indices: the first for rows, the second for columns.

```
x <- matrix(1:18, nrow = 3, ncol = 6)
x

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]    1    4    7   10   13   16
## [2,]    2    5    8   11   14   17
## [3,]    3    6    9   12   15   18

x[2, 4] ## element in 2nd row, 4th column

## [1] 11
```

```
x[, 2] ## 2nd column
```

```
## [1] 4 5 6
```

```
x[2, ] ## 2nd row
```

```
## [1] 2 5 8 11 14 17
```

# Matrices indexing

Try to guess what the following commands do, check in the console

```
x[ , c(1, 4, 6)]  
x[c(1, 3), ]  
x[c(1, 3), c(1, 4, 6)]
```

## Factor (I)

Factors are used for **categorical** variables that only take a finite number of values (also called **levels**)

```
x <- factor(c("a", "a", "b", "a", "c"))  
class(x)  
  
## [1] "factor"
```

Levels can be accessed with `levels`

```
levels(x)  
  
## [1] "a" "b" "c"
```

Internally, R treats `x` as a integer<sup>3</sup> vector and associates each level to a value: here 1 = "a", 2 = "b" and 3 = "c" (**alphabetical order** by default) so that `x = c(1, 1, 2, 1, 3)`.

<sup>3</sup>just think of them as numeric values

## Factor (II)

Sometimes it's convenient to impose a different ordering with the argument `levels` of the `factor` function.

```
y <- factor(x, levels = c("b", "a", "c"))
levels(y)

## [1] "b" "a" "c"
```

Finally since factors are internally coded as integer vectors, conversions can be surprising:

```
as.numeric(x) ## 1="a", 2="b"
```

```
## [1] 1 1 2 1 3
```

```
as.character(x)
```

```
## [1] "a" "a" "b" "a" "c"
```

```
as.integer(y) ## 1="b", 2="a"
```

```
## [1] 2 2 1 2 3
```

```
as.character(y)
```

```
## [1] "a" "a" "b" "a" "c"
```

## Factor (Exercise)

Compare the two different codes and try to guess the results. Check with the console.

```
x <- c("a" = 1, "b" = 2, "c" = 3)
y <- c("a", "b", "c")
x[y]
z1 <- factor(y, levels = c("a", "b", "c"))
z2 <- factor(y, levels = c("b", "a", "c"))
```

```
z1
x[z1]
x[as.character(z1)]
```

```
z2
x[z2]
x[as.character(z2)]
```

Did you guess right? If not, remember that factors are coded as **integer** vectors and try to guess the representation of **z1** and **z2** as numeric vectors.

## data.frame (I)

A `data.frame` is a **table-like** structure (created with `data.frame()` used to store contextual data of different modes. Technically a `data.frame` is a **list** of equal-length **vectors** and/or **factors**.

```
x <- data.frame(number = c(1:4),
                 group = factor(c("A", "A", "B", "B")),
                 desc = c("riri", "fifi", "lulu", "picsou"))
```

```
x

##   number group  desc
## 1      1     A   riri
## 2      2     A   fifi
## 3      3     B   lulu
## 4      4     B picsou
```

```
class(x)

## [1] "data.frame"
```

```
class(x[, 1])
```

```
## [1] "integer"
```

```
class(x[, 2])
```

```
## [1] "factor"
```

```
x[2, "desc"] ## or x[2, 3]
```

```
## [1] "fifi"
```

## data.frame (II)

A **data.frame** has two dimensions: rows and columns (just like a matrix)

```
dim(x);nrow(x);ncol(x)
```

```
## [1] 4 3
```

```
## [1] 4
```

```
## [1] 3
```

Its columns are names and can be accessed with the special operator **\$**.

```
x$group
```

```
## [1] A A B B
```

```
## Levels: A B
```



## data.frame (exercice)

Guess what the following code does and check in the console.

x

```
##      ID group      value
## 1    1      A  1.29891241
## 2    2      A -0.06922655
## 3    3      A -0.21717540
## 4    4      A -0.23028309
## 5    5      A -0.17481615
## 6    6      B -1.30304922
## 7    7      B -1.27979172
## 8    8      B -1.54874545
## 9    9      B -0.64328443
## 10  10      B  0.20690014
```

```
ii <- 1:5
df <- x[ii, c("ID", "value")]
df
df[, 2]
class(df[, 2])
df[2, ]
class(df[2, ])
```

## Fundamental data types: summary

- vector (and matrix): 1-D (and 2-D) **array** of basic data, all of the same type (integer, numeric, logical, character)
- list: indexed **collection** of objects that need not be of the same type and can be arbitrarily complex
- factor: used for **categorical** data, collection of elementary variables that can only take a finite number of values (e.g. small, medium, large)
- data.frame: used for experimental results, a **table-like** structure (technically, a list of equal-length vectors). All elements in a column have the same type but different columns may have different types.

## Indexing: summary

- **position** index elements by position in a vector/factor (`x[i]`) or positions (row, column) in a matrix/data.frame (`x[i, j]`)
- **name**: index elements by name in a vector/factor (`x["first"]`) or positions (row, column) in a matrix/data.frame (`x["row", "column"]`)
- **logical index**: use a **logical mask** index the same size as `x` that specifies which elements to keep (`x[index]`)
- **name with \$ (for list)**: use a component's name to extract it from a list. Works for data.frame which are a special kind of list (`x$name`)

More than one element (or row, column) can be indexed at the same time:  
`x[c(i1, i2, ..., in)]`

## Building logical filters (I)

R provides a built-in way to build **logical indexes** using logical operations (e.g. to filter data)

```
x <- 1:5
z <- (x < 3); z ## the first command returns a logical vector

## [1] TRUE TRUE FALSE FALSE FALSE

z <- (x < 4) & (x > 1); z ## logical AND

## [1] FALSE TRUE TRUE FALSE FALSE

z <- (x < 2) | (x > 4); z ## logical OR

## [1] TRUE FALSE FALSE FALSE TRUE

!z ## logical NOT

## [1] FALSE TRUE TRUE TRUE FALSE
```

## Building logical filters (II)

The logical indexes can be transformed to integer indexes using **which**

```
which(z)

## [1] 1 5
```

and used to **extract** part of the data

```
z <- (x < 4)
x[z]

## [1] 1 2 3

## or equivalently
x[x < 4]

## [1] 1 2 3
```

## Import data

The simplest way to import a tabulated text file<sup>4</sup> is **read.table()**. **read.table()** outputs a **data.frame** and is very flexible. Its main arguments are:

Argument	Description
<b>file</b>	File name, or complete path to file (can be an URL)
<b>header</b>	First line = variable names? ( <b>FALSE</b> by default)
<b>sep</b>	Field separator character (white character by default)
<b>dec</b>	Character used for decimal points ("," by default)
<b>na.strings</b>	Character vector of strings to be interpreted as <b>NA</b> ( <b>NA</b> by default)
<b>row.names</b>	Column number (or name) where the rownames are stored.

---

<sup>4</sup>think excel worksheet, but in text format

## Export data

Matrix-like objects (matrices, data.frame) can be exported as tabulated text files (**human-readable** with **write.table()**). The typical use is:

```
## for tsv
write.table(matrix_object, file = "my_file.tsv", sep = "\t")
```

To save **general** objects as R -readable objects (more compact), use **save()** (and **load()** to load them back).

```
save(object1, object2, file = "data.Rdata")
load("data.Rdata")
```

Finally, **save.image()** is a shortcut to save the complete workspace.

## A few pointers for beginners

- <http://www.r-project.org/>
- <http://www.bioconductor.org/help/publications/>
- [cran.r-project.org/doc/contrib/Paradis-rdebuts\\_fr.pdf](http://cran.r-project.org/doc/contrib/Paradis-rdebuts_fr.pdf)

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## ggplot2

- ggplot2 is a powerful package by Hadley Wickham to produce **elegant statistical graphics**
- it has relatively **simple** syntax
- gg stands for *grammar of graphics* (Leland Wilkinson, 2005)
- the plot is built one component at a time with smart **defaults settings**

```
library(ggplot2)
```

# The different components of a plot

- ① **data**: must be stored as a `data.frame`
- ② **aesthetics**: Visual characters that represent the data (position, size, color, fill, etc.)
- ③ **scales**: For each aesthetic, the conversion from data to display value (color scale, size scale, transparency scales, log-transformation of continuous values, etc)
- ④ **geoms**: Type of geometric objects used to represent the data (points, line, bar, etc.)
- ⑤ **coord**: 2D coordinate systems used to represent the data (cartesian, polar, etc.)
- ⑥ **stat**: data-smoothing, statistical transformation used to summarize the data
- ⑦ **facets**: a way to split the data into subsets (e.g. male only/female only) and represent the data as *small multiple plots*

## Foreword

These slides are not a complete introduction to ggplot2. They only intend to **introduce** elements used in the phyloseq training session and therefore to

- present the *syntax* of a ggplot
- present simple *examples* of ggplot graphs
- illustrate the *data to visual characteristics* mapping
- show how to *modify* a graph by:
  - adding a custom color scale
  - changing the color scale
  - subdividing the data to draw small multiple plots

# Learning by doing: building a plot

The `ggplot` function is used to build the plot **layer** by **layer**. The general syntax is

```
## p stands for plot
p <- ggplot(data, aes(x, y)) + layer1 + layer2 + ...
```

We'll work with the built-in `diamonds` dataset (10 attributes of almost 54000 diamonds, see `?diamonds` for details)

```
data(diamonds) ## import datasets
class(diamonds) ## data.frame

## [1] "data.frame"

names(diamonds) ## documented properties

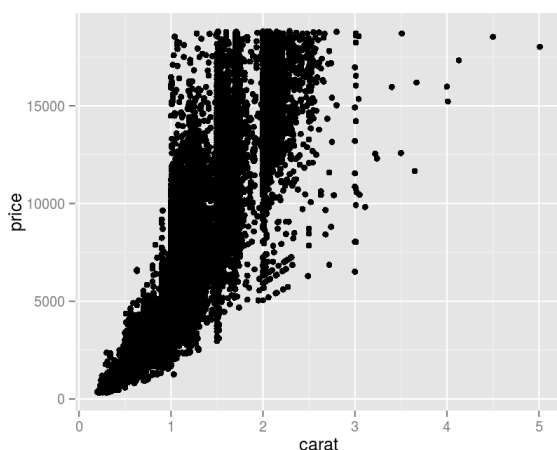
## [1] "carat" "cut" "color" "clarity" "depth" "table"
## [8] "x" "y" "z"
```

"pri

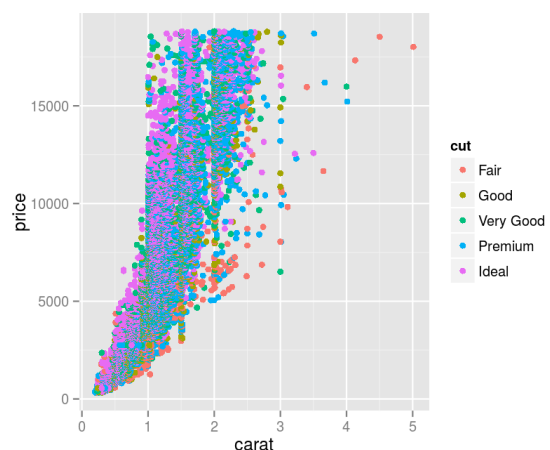
## First plot: price vs. carat

```
## set base plot, x coordinate is carat, y is price
p <- ggplot(diamonds, mapping = aes(x = carat, y = price))
```

```
## Add a layer to represent
## data as point
p1 <- p + geom_point()
plot(p1)
```



```
## Add a layer to represent
## data as point, colored by cut
p2 <- p + geom_point(aes(color = cut))
plot(p2)
```



# Understanding the plot

The first command tells ggplot that

- **data** is stored in the diamonds dataframe
- **global aesthetics** (set with `aes`) are as follows : `carat` is mapped to x coordinate, `price` to y coordinate

The second one adds a **layer** in which data are represented by **points** (`geom_point`). The **aesthetics** are extracted from global aesthetics `aes(x = carat, y = price)`.

The variant `aes(color = cut)` adds a new local aesthetic for the point layer. `cut` value is mapped to the color of the points and both a legend and a color scale are automatically constructed.

## More about aesthetics

We played with `color` but with `geom_point` we can also play with

- `shape`
- `size`
- `alpha` (transparency)
- `fill`.

The value of each aesthetic can be either

- identical for all observation: the argument must be given **outside** of `aes` (e.g. `geom_point(color = "black")`)
- mapped to a variable value (here `cut`): the argument must be given **inside** of `aes` (e.g. `geom_point(aes(color = cut))`)

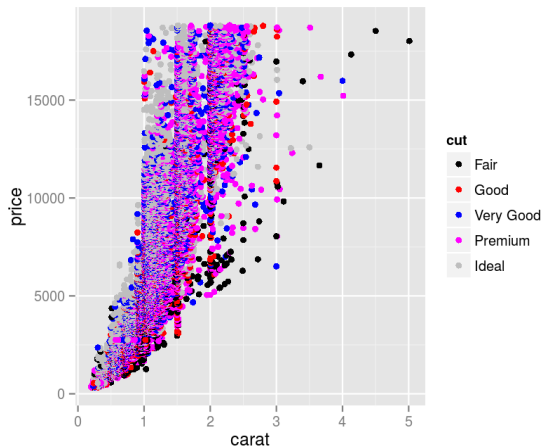


## Changing scales

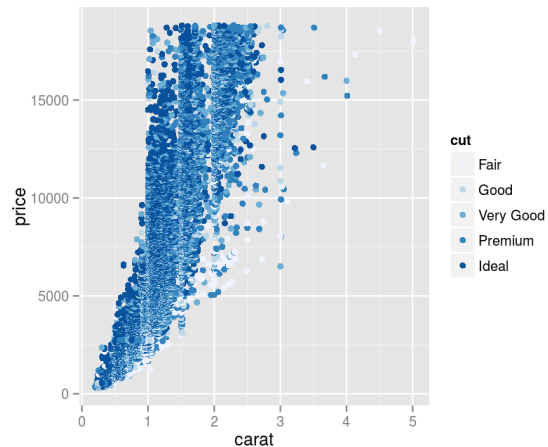
cut is a factor, with a discrete number of values. We can change the color scale manually with the family of functions `scale_color_something`

```
palette <- c("black", "red", "blue", "magenta", "gray")
names(palette) <- c("Fair", "Good", "Very Good", "Premium", "Ideal")
```

```
## Manual color scale
p2.1 <- p2 +
  scale_color_manual(values = palette)
plot(p2.1)
```



```
## Use built-in color palette
p2.2 <- p2 +
  scale_color_brewer()
plot(p2.2)
```



## More about scales

- Each aesthetic is associated with a scale
- Whenever possible, `ggplot2` will try to merge the scales (like `color` and `fill`)
- For aesthetics mapped to a variable, the scale will vary depending on the nature of the variable: `numeric` (continuous) or `factor`, `logical` (discrete)
- every scale is build in the following way
  - they all begin with `scale_`
  - continue with the aesthetic name (`linetype`, `fill`, `color`)
  - and end with the name of the scale (`manual`, `discrete`, `brewer`)

## More about geom

Here we used `geom_point` to represent data as points. We could have used other geometric representations of the data:

- `geom_point`
- `geom_line`
- `geom_bar`
- `geom_density`
- `geom_boxplot`
- `geom_histogram`

Each geometry expects and accepts different aesthetics (e.g `linetype` is useful for lines but useless for points)

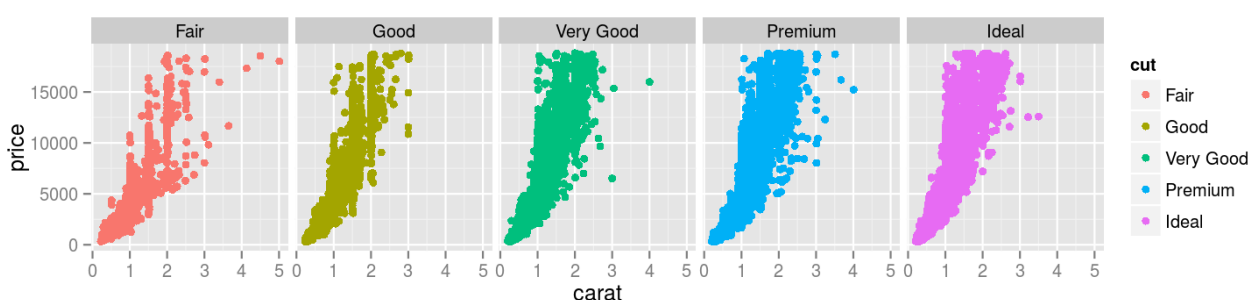
## Small multiple plots: facet\_grid

We can split the data in subsets to draw *small multiple plots* using **facetting**. There are two variants of facetting:

- `facet_wrap` if only one variable is used for facetting
- `facet_grid`, usually used for two or more variables (but can be used for one)

```
## facet along cut, only points from a given cut appear in a facet
```

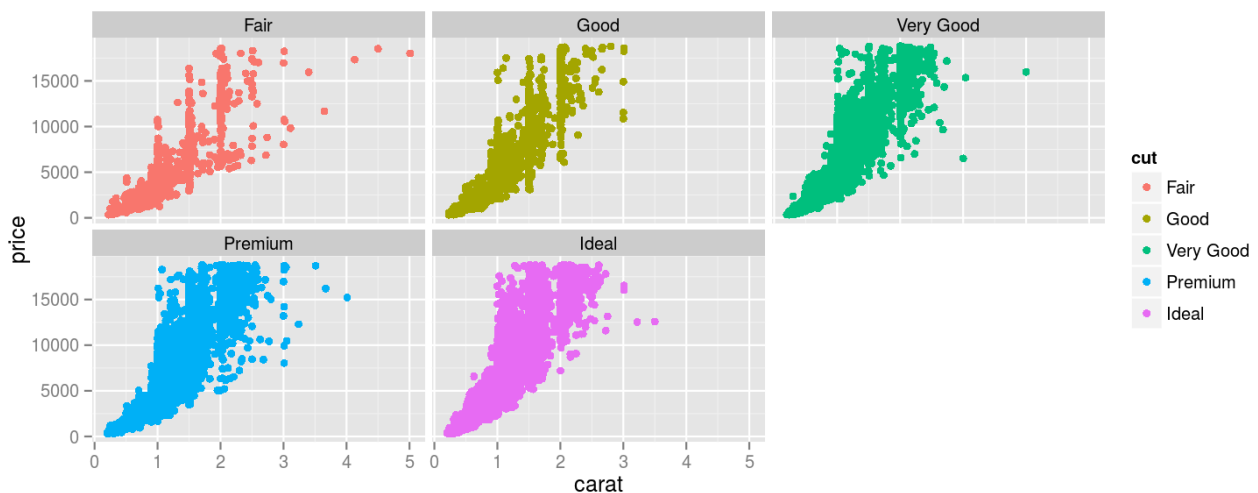
```
p3 <- p2 + facet_grid(~ cut)
plot(p3)
```



## Small multiple plots: facet\_grid

Compare `facet_wrap` and `facet_grid` when using only **one** variable for facetting: facets are organized differently

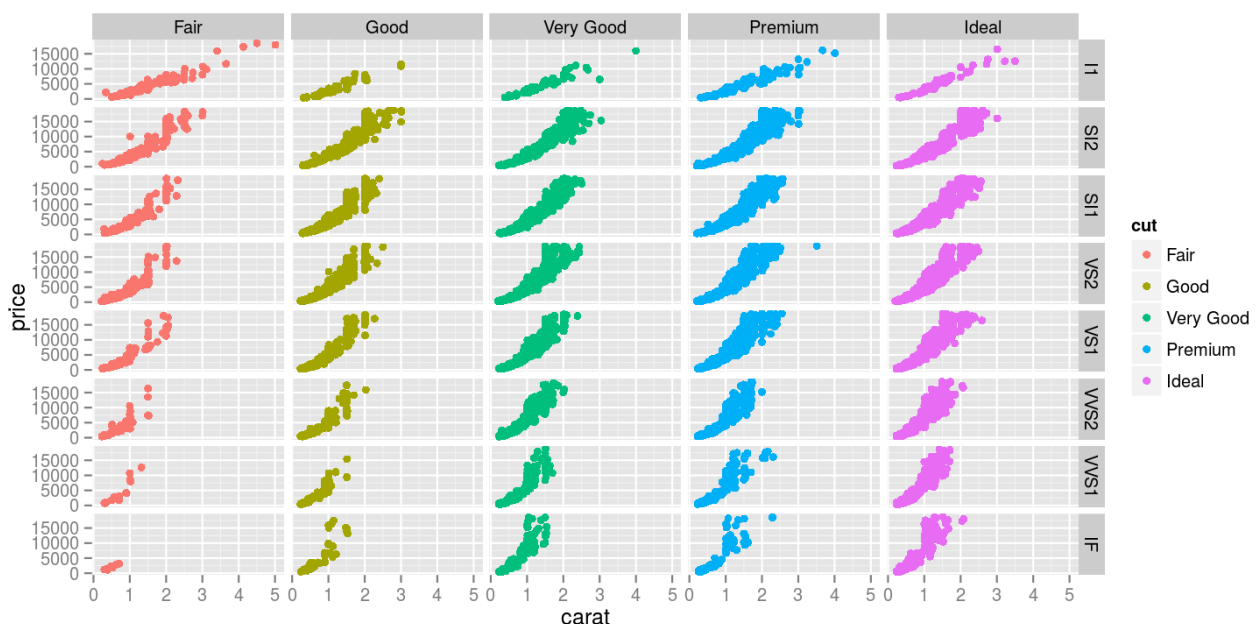
```
## facet along cut
p3 <- p2 + facet_wrap(~ cut)
plot(p3)
```



## Small multiple plots: facet\_grid

`facet_grid` is most useful when splitting the data along two factors

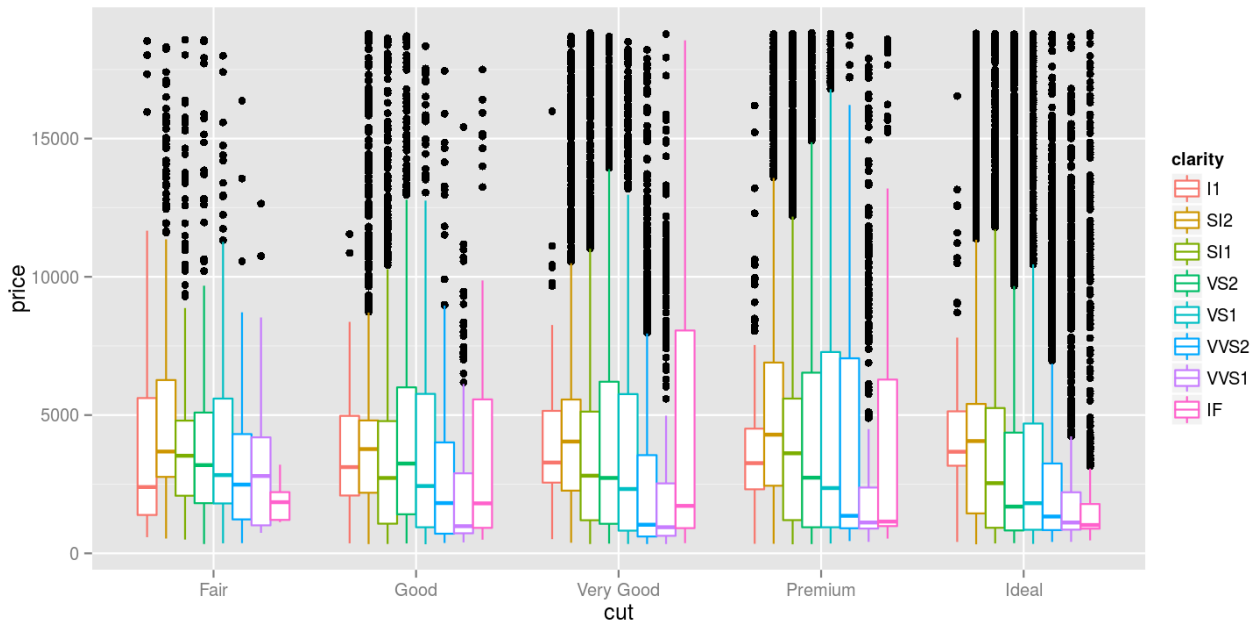
```
## facet along clarity (rows) * cut (column)
p3 <- p2 + facet_grid(clarity ~ cut)
plot(p3)
```



## Small multiple plots (I)

Sometimes, facetting wastes spaces. Imagine we want to compare the distribution (using boxplot) of prices (y) for different cuts (x) and highlight (with color) the differences between different clarities.

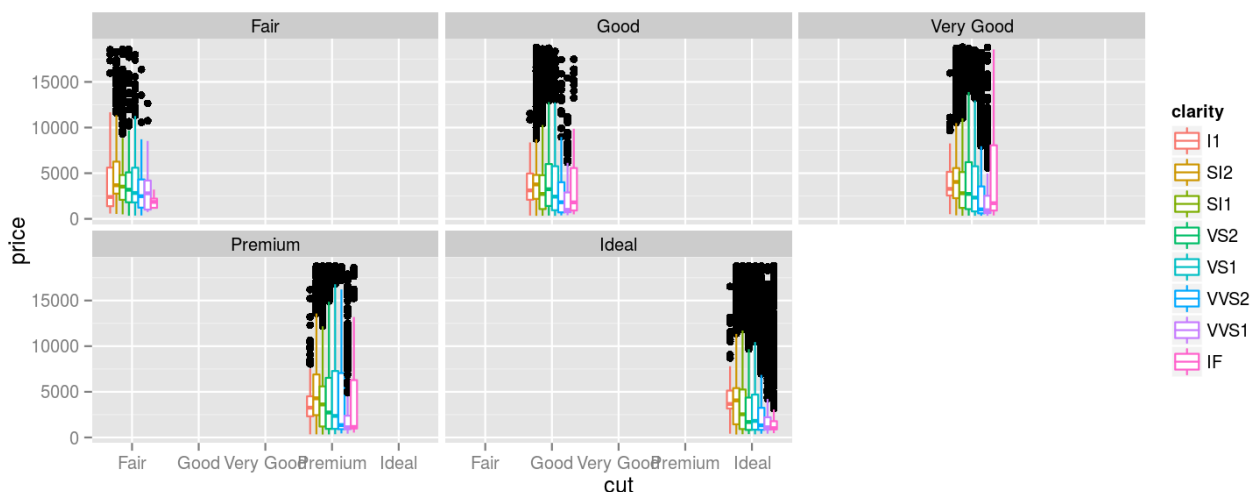
```
p <- ggplot(diamonds, aes(x = cut, y = price, color = clarity)) + geom_boxplot()  
plot(p)
```



## Small multiple plots (II)

We may want to facet by cut to make the plot easier to read

```
p1 <- p + facet_wrap(~cut)  
plot(p1)
```

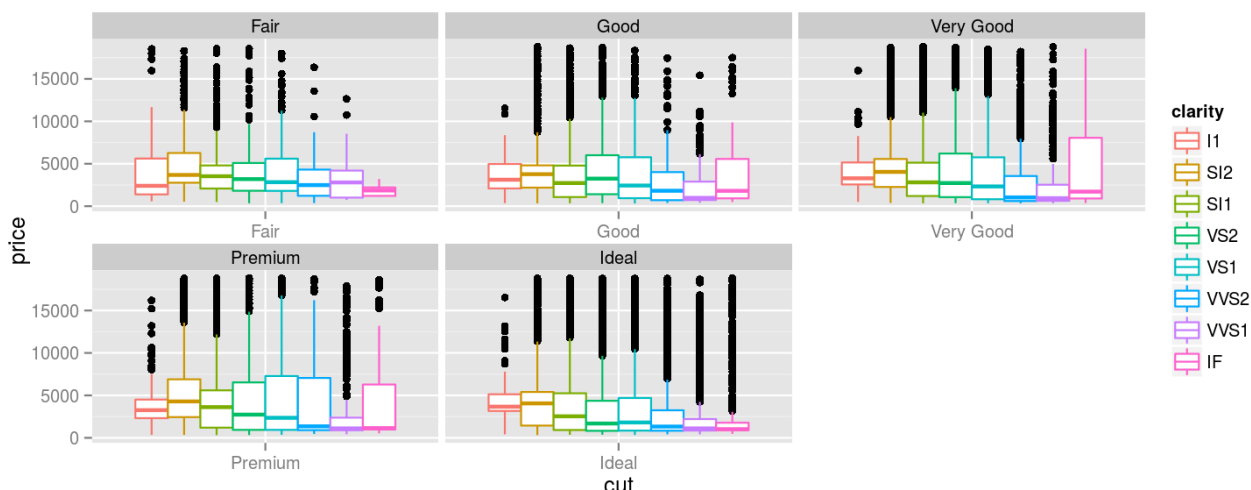


Each cut is represented in only one facet and the **common** x-scale **wastes** a lot of space.

## Small multiple plots (III)

We facet by cut but do not impose a common x-scale which leads to a much better use of space.

```
p2 <- p + facet_wrap(~cut, scales = "free_x")  
plot(p2)
```



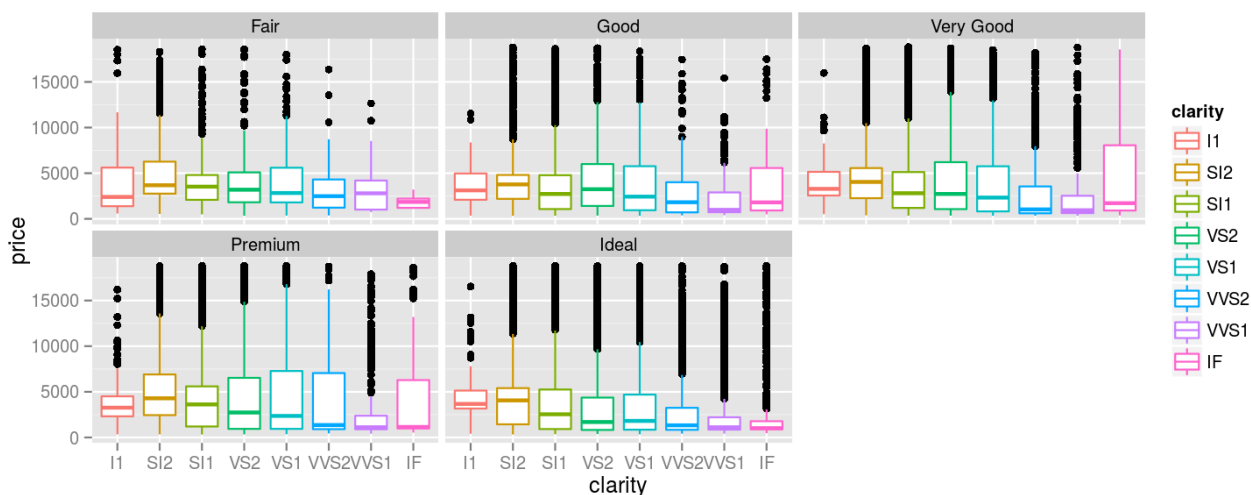
scales = "free\_y" would lead to one y-scale per facet

scales = "free" to one y-scale and one x-scale per facet

## Small multiple plots (IV)

Finally, note that the same graph can be obtained in many different ways.

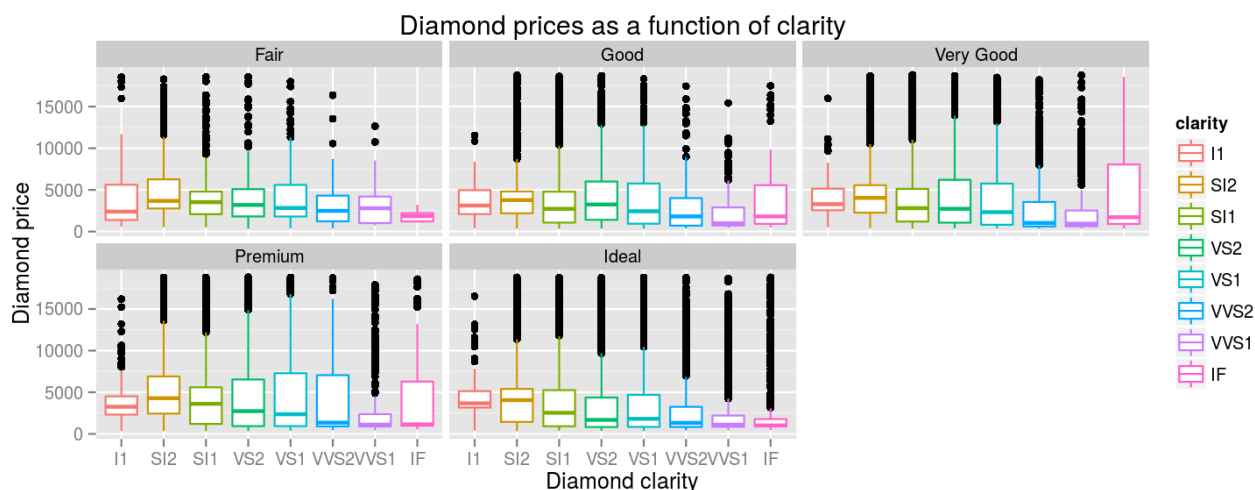
```
p <- ggplot(diamonds, aes(x = clarity, y = price, color = clarity)) +  
  geom_boxplot() + facet_wrap(~cut)  
plot(p)
```



## Adding title and axis labels

You can add (or change) title and axis labels with the commands `ggtitle`, `xlab` and `ylab`

```
p <- p + ggtitle("Diamond prices as a function of clarity") +  
  xlab("Diamond clarity") + ylab("Diamond price")  
plot(p)
```



## Exporting plots

- You can save graphics using `ggsave`
- it guesses the `filetype` from the filename extension.
- By default, it saves the `last plot` with its current dimensions
- but you can `override` the dimensions at will

```
## the last three arguments are optional  
ggsave("myplot.png", plot = p, width = 10, height = 4)
```

- <http://had.co.nz/ggplot2/>
- <http://groups.google.com/group/ggplot2>
- <http://cran.r-project.org/web/packages/ggplot2/index.html>
- Wickman, H. 2009 – *ggplot2. Elegant graphics for data analysis*. Springer, 212p.