Science des données I : module 2

Travaux pratiques

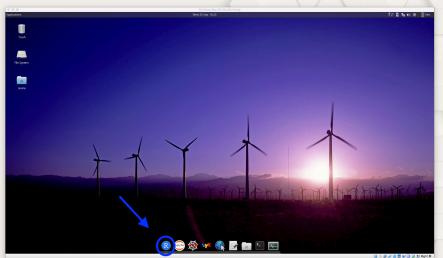


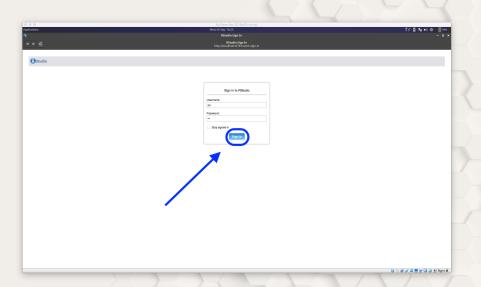
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http://biodatascience-course.sciviews.org/
Guyliann.Engels@umons.ac.be Philippe,Grosjean@umons.ac.be

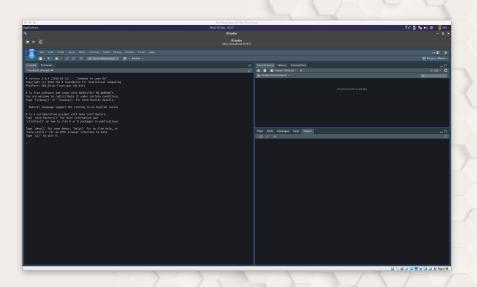


Découverte du logiciel R

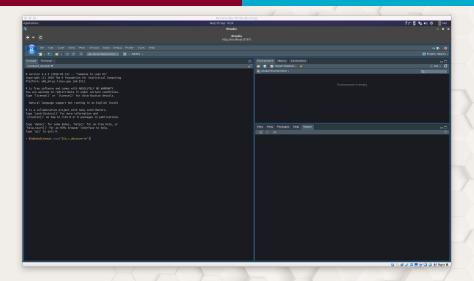








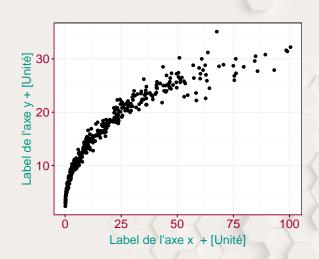




Insérez les instructions suivantes dans la console R

BioDataScience::run("02a_r_decouverte")

Réalisation de nuage de points

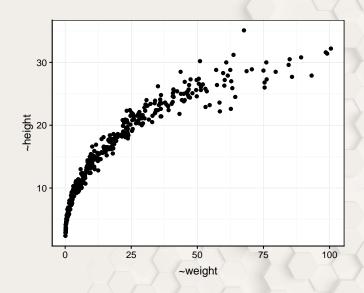


Les éléments indispensables :

- Les axes avec les graduations (en rouge)
- les labels et les unités des axes (en bleu)



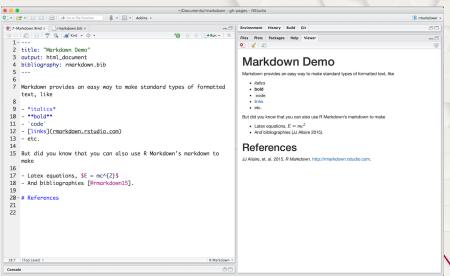
chart(ub, formula = height ~ weight) + geom_point()





Utilisation de R Markdown

Markdown: language très simples



R.: suite d'instructions

```
® Untitled1*
   🕨 📗 📗 🖪 Source on Save 🛮 🔍 🎢 🗸 📗
                                                     Run Source - 3
     #.Importation.des.packages.indispensables.à.l'analyse.des.données-
     SciViews::R
     ub <- read("urchin_bio", package = "data.io")-
     chart(ub, formula = height ~ weight) +-
10:1 (Top Level) $
                                                                          R Script :
```



title: "Example" author: "John Doe" date: "21 September 2016" output: pdf_document

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

Including Plots

You can also embed plots, for example:

Note that the <code>'echo</code> = <code>FALSE'</code> parameter was added to the code chunk to prevent printing of the R code that generated the plot.

Description

- Préambule (Rouge)
- Markdown (Bleu)
- Chunks, R code (Vert)
- Markdown (Bleu)
- Chunks, R code (Vert)
- Markdown (Bleu)



Comparaison de workflow



- biometry_2014_ew
- biometry_2016_ew

R Markdown



- biometry_2014
- biometry_2016

Quel format d'analyse vous semble le plus approprié dans la recherche scientifique et collaborative ?

