Plotting with RStudio

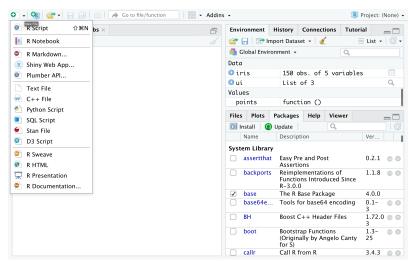


Objective of Exercise:

This lab introduces you to plotting in R with ggplot and GGally. GGally is an extension of ggplot2.

Exercise:

1. Click the plus symbol on the top left and click R Script to create a new R script, if you don't have one open already.



- 2. You will use the iris dataset. If you don't have it loaded, copy and paste the following into your R script file.
- 1. 1 2. 2
- library(datasets)
- data(iris)

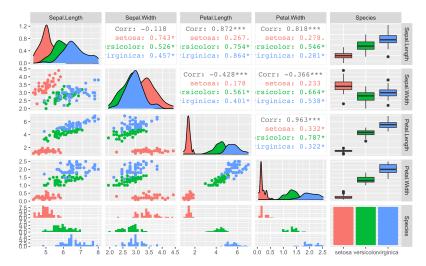
Copied!

3. In the previous lab, you installed the libraries necessary to create plots, let's execute the following commands:

- 1. 1 2. 2
- library(GGally)
- 2. ggpairs(iris, mapping=ggplot2::aes(colour = Species))

Copied!

- 4. Select the commands and click Run on the top. You'll see the following plot in the Plots window:
- 5. Click the **Zoom** icon on the plot window to zoom and see the plot.



6. This gives you a lot of information for a single line of code. First, you can see the data distributions per column and species on the diagonal. Then you see all the pair-wise scatter plots on the tiles left to the diagonal, again segregated by color. It is, for example, obvious that a line can be drawn to separate setosa against versicolor and virginica. In later courses, you will also learn how the overlapping species can be separated. This is called supervised machine learning using non-linear classifiers. You can also see the correlation between individual columns in the tiles on the right to the diagonal, which confirms that setose is more different, hence easier to distinguish, than versicolor and virginica. A correlation value close to one signifies high similarity, whereas a value closer to zero signifies less similarity. The remaining plots on the right are called box-plots, and the ones at the bottom are called histograms, but you will learn about this in a more advanced course in this series.

Author(s)

Romeo

Other Contributor(s)

Lavanya

Change log

Date	Version	Changed by	Change Description
2022-12-30	1.2	Steve Hord	QA pass edits
2020-12-10	1.1	Aije	Created simplified version of the lab
2020-12-10	1.0	Malika Singla	Migrated lab to Markdown

© IBM Corporation 2020. All rights reserved.