Plotting with RStudio

Skills Network

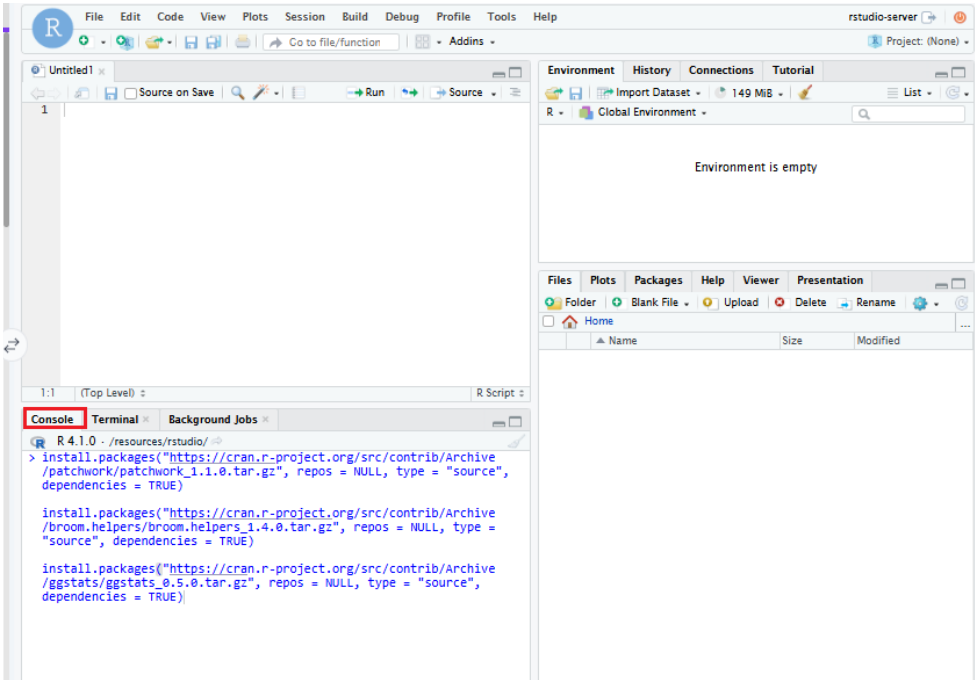
Objective of Exercise:

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

Pre Requisite:

Before loading the GGAlly package, ensure its dependencies are installed. Run the following commands in the Console window, as shown in the screenshot below, and then continue with the steps in the Exercise.

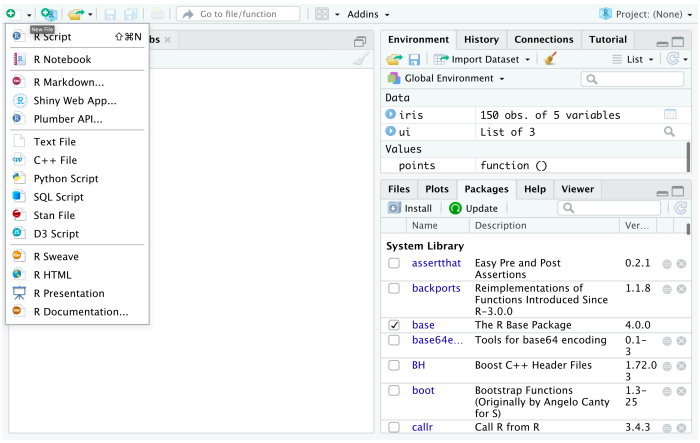
▸ See Screenshot




```
install.packages("https://cran.r-project.org/src/contrib/Archive/patchwork/patchwork_1.1.0.tar.gz", repos = NULL, type = "source", dependencies = TRUE)
install.packages("https://cran.r-project.org/src/contrib/Archive/broom.helpers/broom.helpers_1.4.0.tar.gz", repos = NULL, type = "source", dependencies = TRUE)
install.packages("https://cran.r-project.org/src/contrib/Archive/ggstats/ggstats_0.5.0.tar.gz", repos = NULL, type = "source", dependencies = TRUE)
```

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.



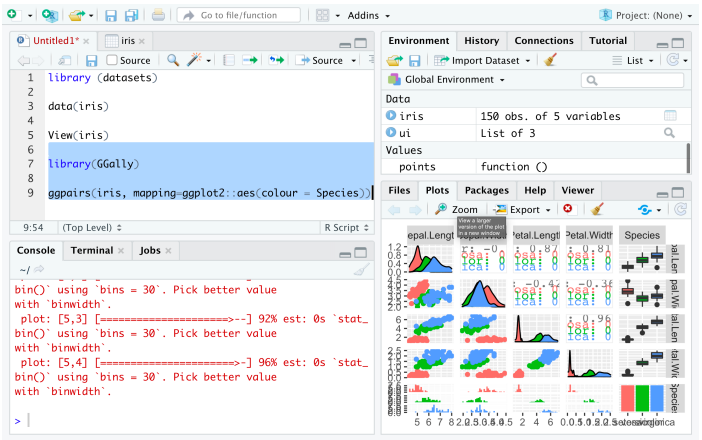
2. You will use the iris dataset. If you don't have it loaded, copy and paste the following into your R script file.

```
library(datasets)
data(iris)
```

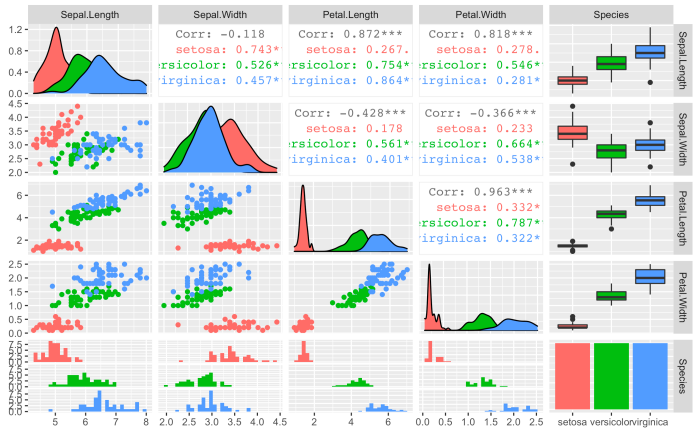
3. In the previous lab, you installed the libraries necessary to create plots, let's execute the following commands:

```
library(GGally)
ggpairs(iris, mapping=ggplot2::aes(colour = Species))
```

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.

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