Plotting with RStudio
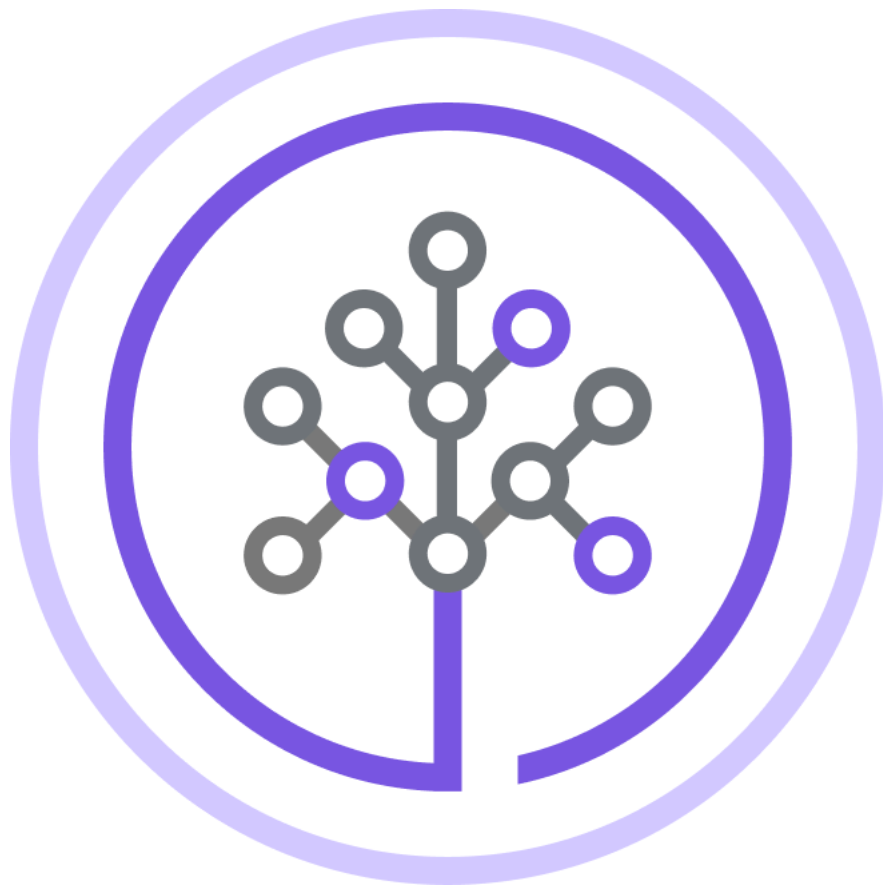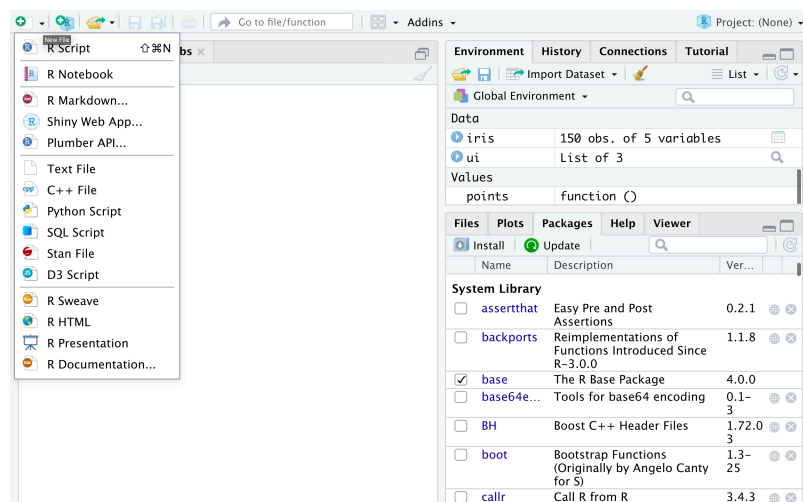

Objective of Exercise:

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
```

```
1. library(datasets)
2. data(iris)
```
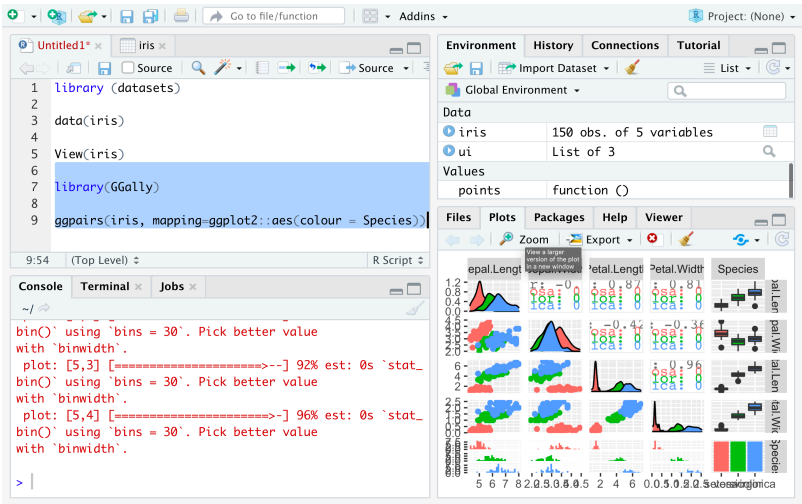
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3. In the previous lab, you installed the libraries necessary to create plots, let's execute the following commands:
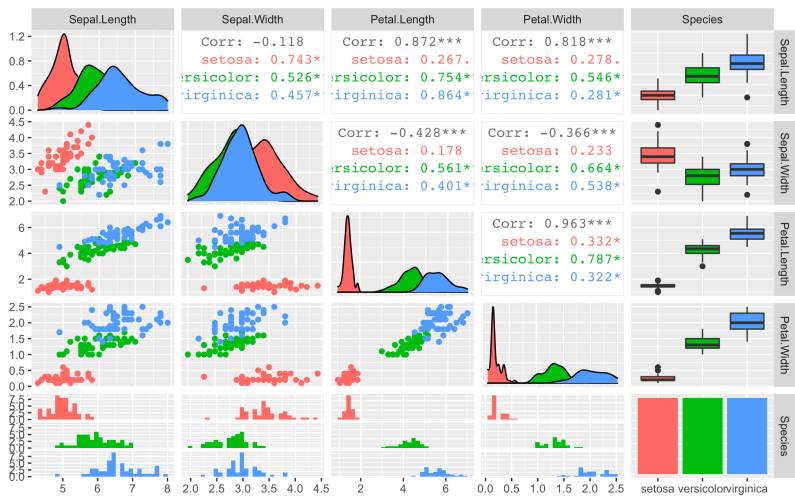
```
1. 1
2. 2
```

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

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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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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