

# Skills Network

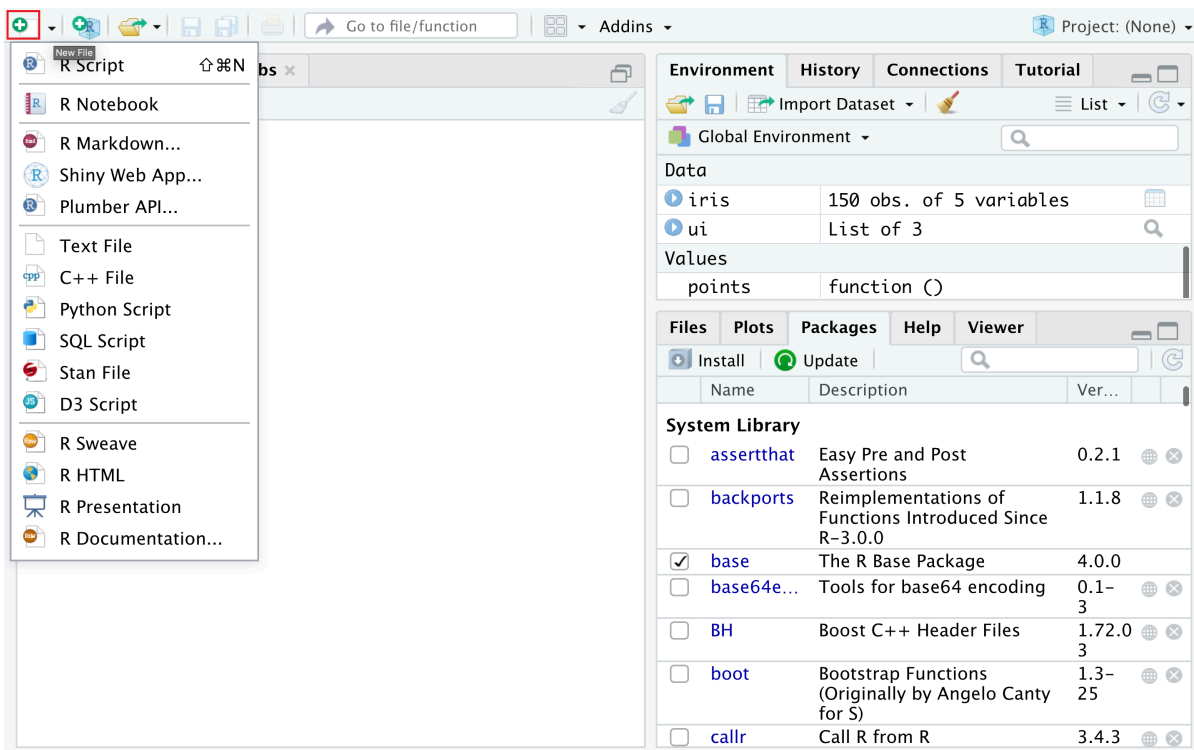
## Getting started with RStudio and Installing packages

### Objectives of Exercise:

After completing this lab, you will be able to:

- Load the datasets
- Install libraries

**Step 1** - Click the plus symbol on the top left and click R Script.



An untitled R Script panel opens. It would look like this.

The screenshot shows the RStudio IDE interface. The top toolbar has a red box around the 'Run' button (a green play icon). The editor window on the left shows a single line of code: '1'. The right-hand pane shows the 'Environment' tab with 'Global Environment' selected. It lists two objects: 'iris' (150 obs. of 5 variables) and 'ui' (List of 3). Below this is the 'Files' tab showing a list of installed R packages.

Name	Description	Ver...
<input type="checkbox"/> assertthat	Easy Pre and Post Assertions	0.2.1
<input type="checkbox"/> backports	Reimplementations of Functions Introduced Since R-3.0.0	1.1.8
<input checked="" type="checkbox"/> base	The R Base Package	4.0.0
<input type="checkbox"/> base64e...	Tools for base64 encoding	0.1-3
<input type="checkbox"/> BH	Boost C++ Header Files	1.72.0-3
<input type="checkbox"/> boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-25
<input type="checkbox"/> callr	Call R from R	3.4.3

**Step 2** - Now you load the iris dataset. Enter the following lines into the editor window that appears. Then select all the text, and click Run just above the editor window.

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

The screenshot shows the RStudio interface. The source editor on the left contains the following R code:

```
1 library(datasets)
2 data(iris)
3 View(iris)
```

The console at the bottom left is empty. The environment pane on the right shows the Global Environment with two objects: 'iris' (150 obs. of 5 variables) and 'ui' (List of 3). The 'Values' section shows 'points' as a function (). The 'System Library' pane lists installed packages, including 'base' (4.0.0), 'BH' (1.72.0), 'boot' (1.3-25), and 'callr' (3.4.3).

**Step 3** - You are taken to the data view tab to inspect your dataset. The dataset contains five columns and the first four are floating point type while the last column is a label of data type string which contains the category value. You can see there are total 150 entries of which you can see the first 7.

The screenshot shows the RStudio interface with the 'iris' dataset loaded. The source editor on the left contains the following R code:

```
> library(datasets)
> data(iris)
> View(iris)
> |
```

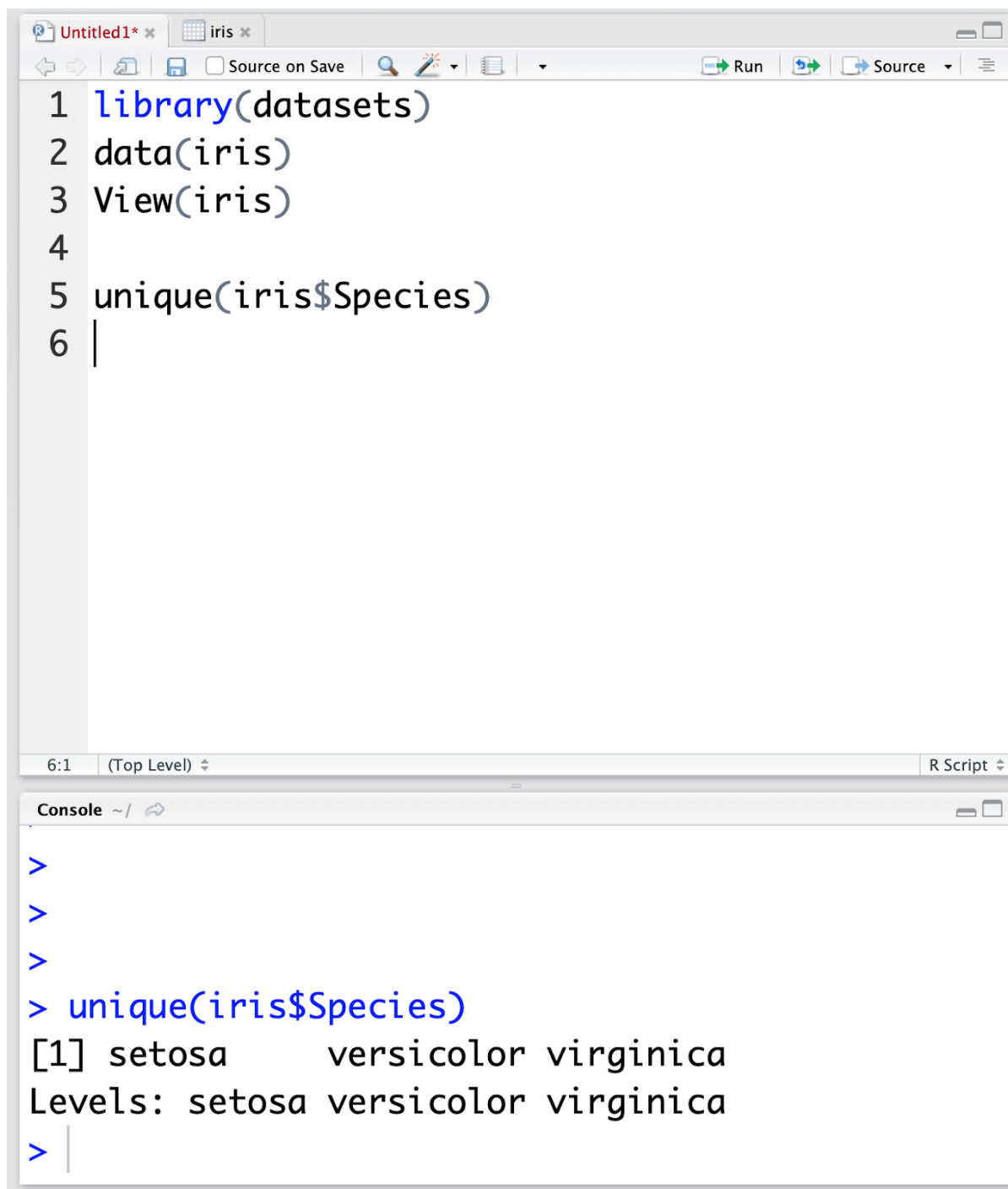
The console at the bottom left shows the execution of the commands. The environment pane on the right shows the Global Environment with two objects: 'iris' (150 obs. of 5 variables) and 'ui' (List of 3). The 'Values' section shows 'points' as a function (). The 'System Library' pane lists installed packages, including 'base' (4.0.0), 'BH' (1.72.0), 'boot' (1.3-25), and 'callr' (3.4.3).

The data view tab for the 'iris' dataset is displayed, showing the first 7 entries of the 150 total entries. The columns are Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, and Species. The data is as follows:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.5	3.0	1.6	0.4	setosa

**Step 4** - Now you can find the different species present in the data set. Enter the following command in the editor window and click Run.

```
unique(iris$Species)
```



The screenshot shows the RStudio environment. The top pane is the 'Source' editor, displaying an R script with the following code:

```
1 library(datasets)
2 data(iris)
3 View(iris)
4
5 unique(iris$Species)
6 |
```

The bottom pane is the 'Console' window, showing the output of the executed command:

```
>
>
>
> unique(iris$Species)
[1] setosa      versicolor virginica
Levels: setosa versicolor virginica
> |
```

In the Console window at the bottom you can see the result of the executed command and know that there are only three different species present in the dataset.

This concludes the lab; I hope you enjoyed it!

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