

# Skills Network

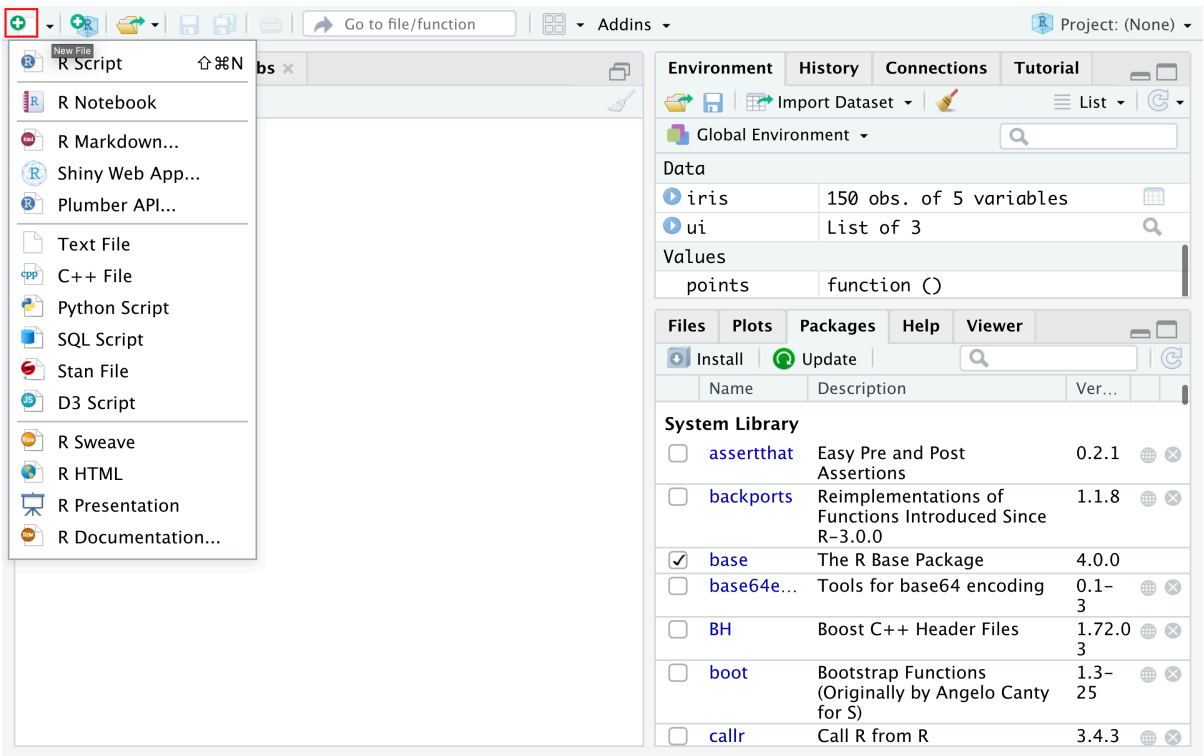
## Getting started with RStudio and Installing packages

### Objectives of Exercise:

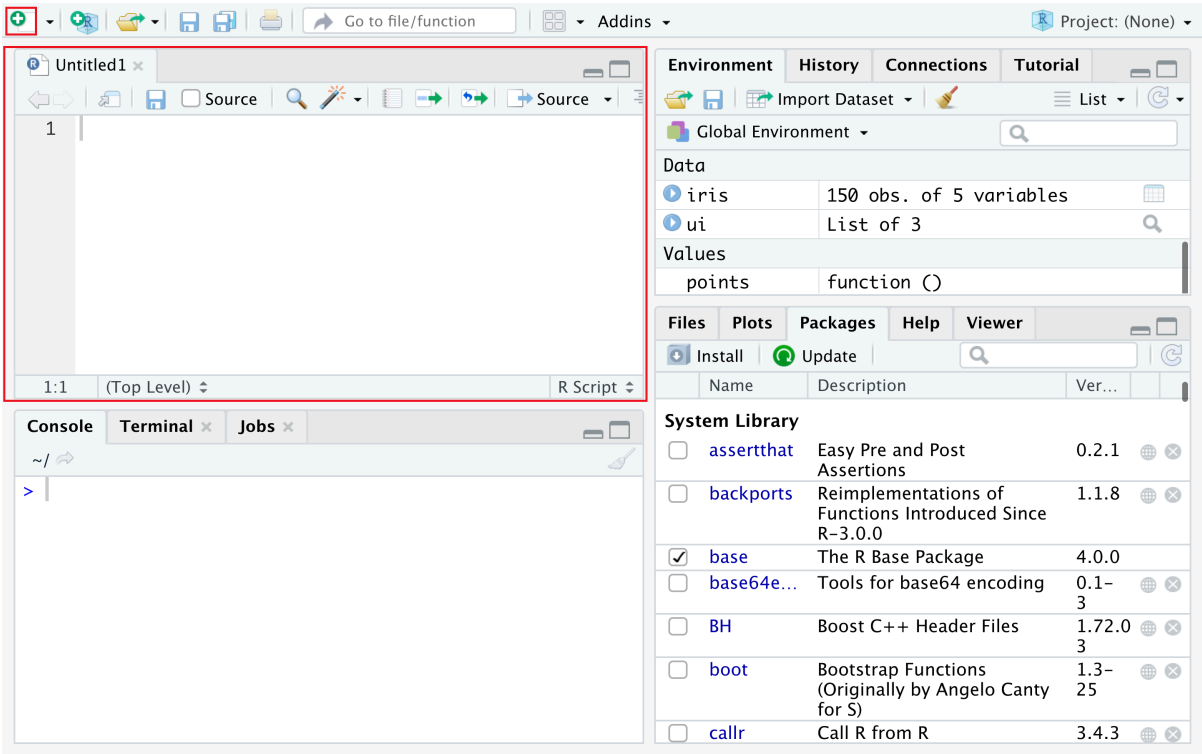
After completing this lab, you will be able to:

- Load the datasets
- Install libraries

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



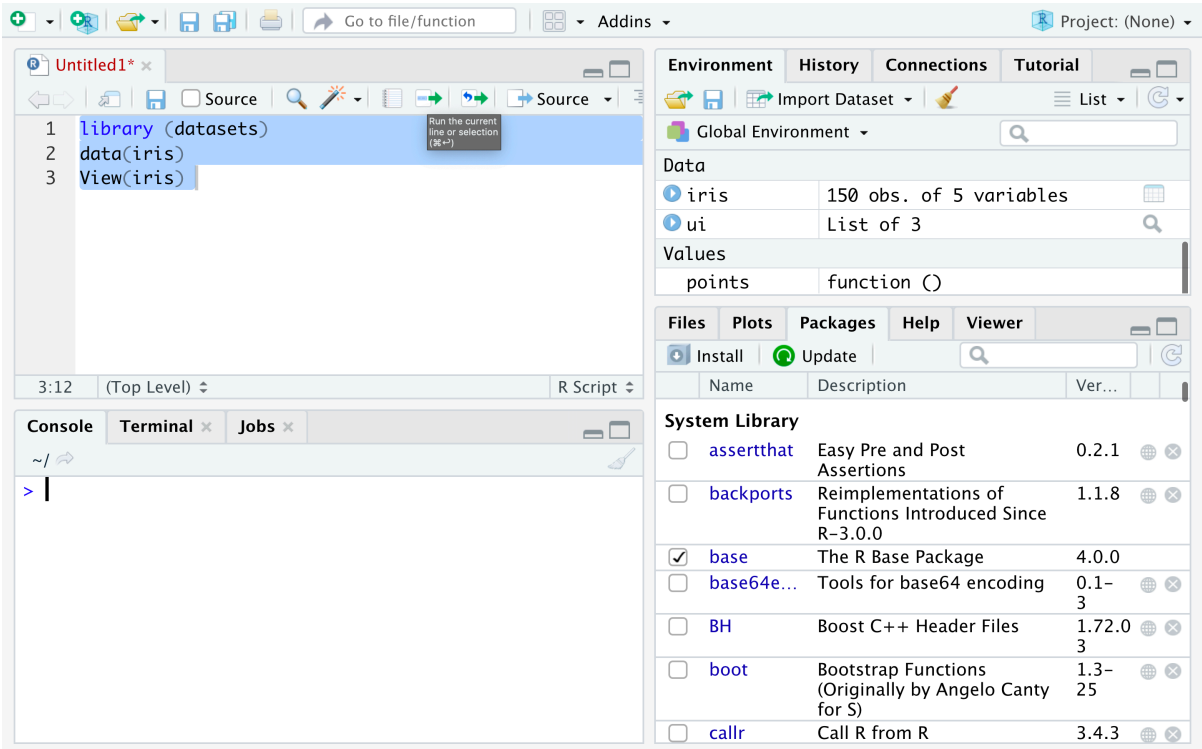
An untitled R Script panel opens. It would look like this.



**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.

- 1.
  - 2.
  - 3.
- 
1. library (datasets)
  2. data(iris)
  3. View(iris)

Copied!



**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.

Go to file/function

Addins

Project: (None)

Untitled1\* iris

Filter

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

Showing 1 to 7 of 150 entries, 5 total columns

Console Terminal Jobs

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

Environment History Connections Tutorial

Import Dataset

Global Environment

Data

iris 150 obs. of 5 variables

ui List of 3

Values

points function ()

Files Plots Packages Help Viewer

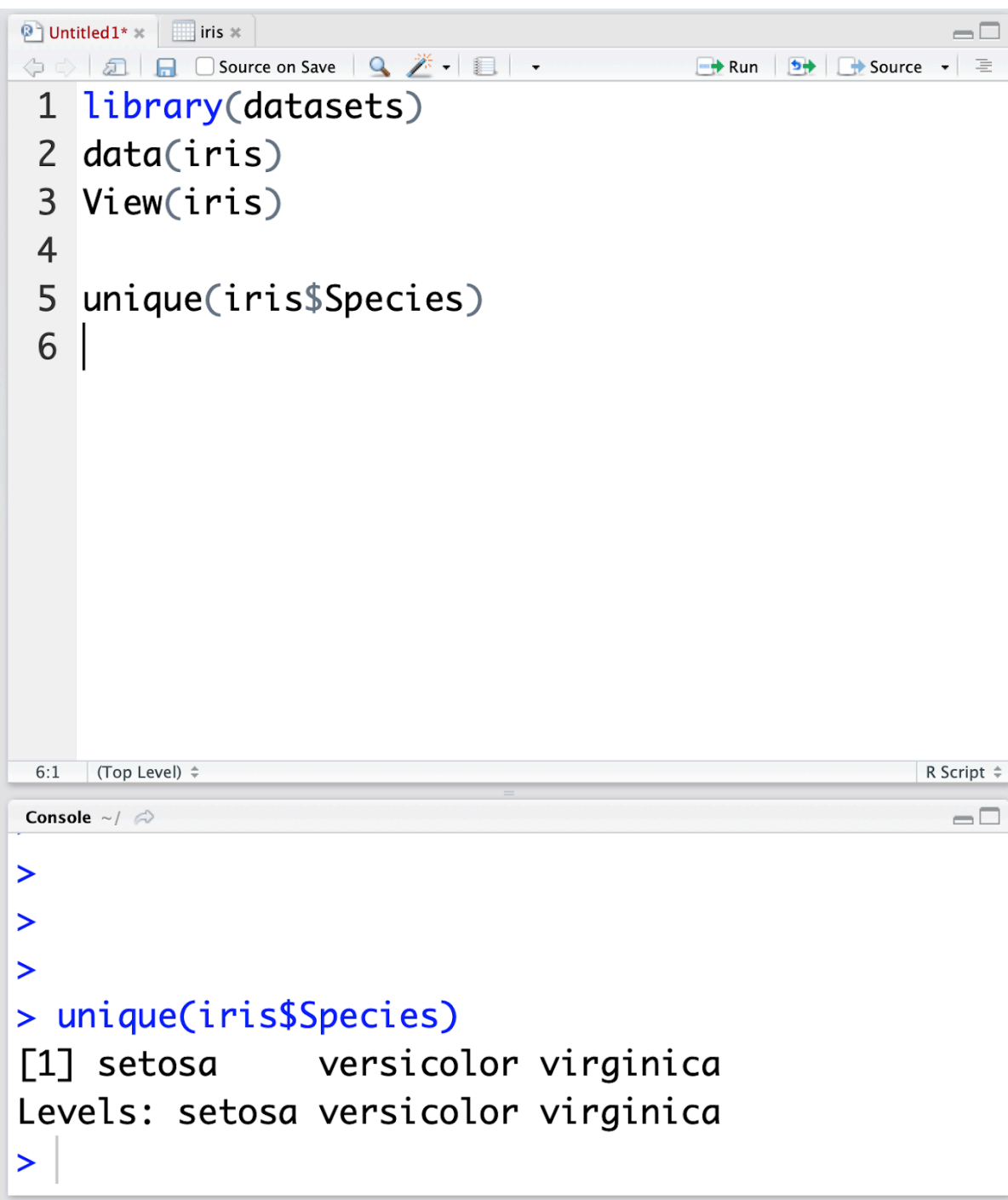
Install Update

Name	Description	Ver...
System Library		
<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 4** - Now you can find the different species present in the data set. Enter the following command in the editor window and click Run.

1. 1
1. `unique(iris$Species)`

Copied!



The image shows a screenshot of the RStudio interface. The top pane is the 'Source' editor, which contains an R script with the following code:

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

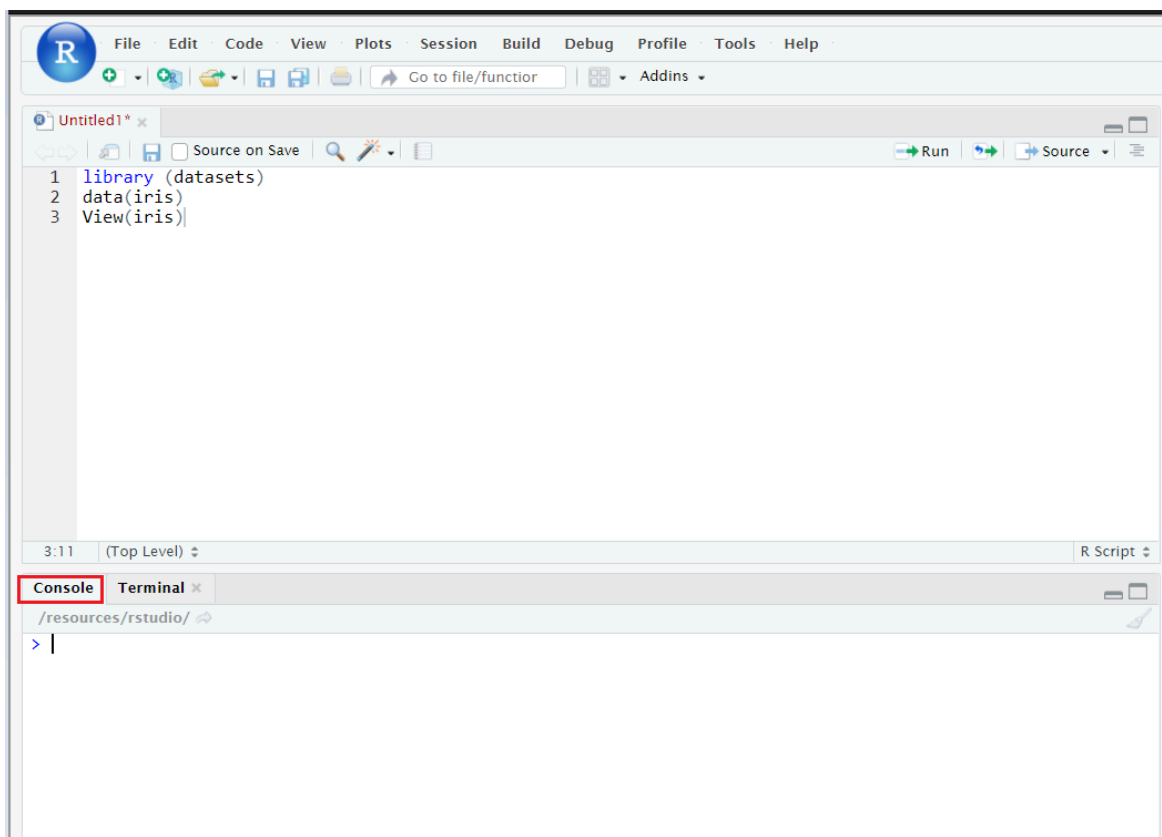
The bottom pane is the 'Console' window, which shows the output of the executed commands:

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

The console output indicates that there are three distinct species in the iris dataset: setosa, versicolor, and 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 data set.

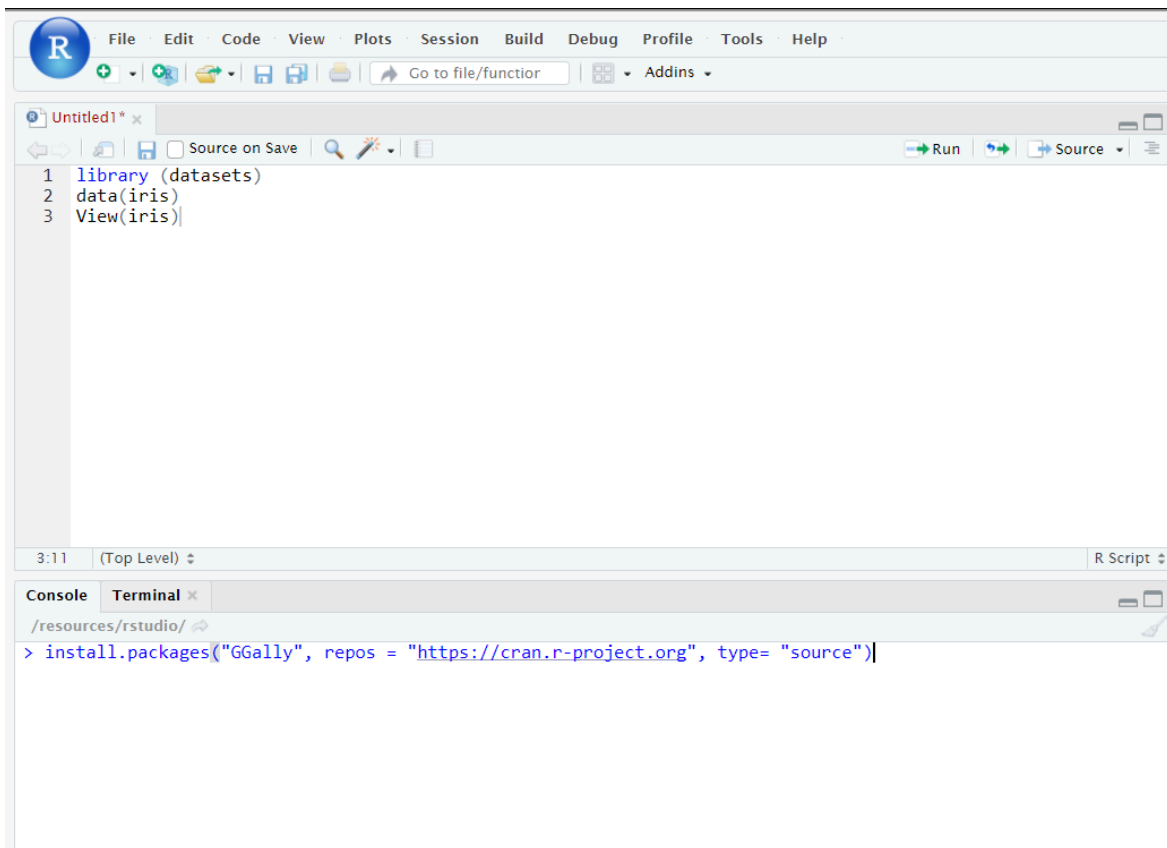
**Step 5** - Next you will look into the data set in more detail. Open a Console.



**Step 6** - Run the following command in the console.

- 1
1. `install.packages("GGally", repos = "https://cran.r-project.org", type = "source")`

Copied!



**Step 7** - Click *Enter* to install the packages.

This concludes the lab; I hope you enjoyed it!

# Author(s)

Romeo

# Other Contributor(s)

Lavanya

# Change log

Date	Version	Changed by	Change Description
2023-07-09	3.0	Anita Verma	Changed to RStudio lab
2021-13-01	2.4	Malika Singla	Update the installation for R packages
2020-12-10	2.3	Aije	Moved plot steps to a new lab
2020-12-10	2.2	Malika Singla	Update the installation for R packages
2020-12-07	2.1	Aije	Changed instructions to use Skills Network Lab
2020-08-25	2.0	Lavanya	Migrated Lab to Markdown and added to course repo in GitLab

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