

Psi Chi Honor Society & Psychology Club

 Studio® /  Workshop

Introduction
March 3rd, 2021

<https://joshmgarciaa.github.io/PsiChiDASW1/Introduction.html>

UH PSI CHI & PSYCHOLOGY CLUB
VOLUNTEER EVENT

LETTERS OF HOPE

Join UH Psi Chi & Psychology Club as we support Letters of Hope-CLE. Letters of Hope collects anonymous stories and letters and share them through multiple platforms, building community throughout the county and world. We will write a handwritten Letter of Hope in response to a story. Letters of Hope can be words of connection, encouragement, support, or gratitude. All the information can be found at their website through the link below.

<https://www.neverevergiveupcle.com/how-to-write-a-letter-of-hope>

For volunteering credit, please write one letter of hope and send a screenshot of your submission confirmation page and your ID number to uh.psichi@gmail.com by March 14th. Earn 50 points for volunteering!



ONGOING EVENT OPEN

MARCH 1 - 14, 2021

****50 POINTS FOR PARTICIPATING!****

3rd General Meeting

Presentation about diversity, equity, and inclusion in psychology from APA's Committee of State Leaders Diversity Liaison Dr. Erin Alexander.

Earn 20 points for attending.

The meeting will be held on Microsoft Teams. The meeting link can be found under the "General" channel on the UH Psi Chi & Psychology Club Teams page.

Alternatively, follow this link: <https://tinyurl.com/3rdGMPsiChi>

Wednesday, March 24th

5:45 - 6:45 PM

jamovi download link

- <https://www.jamovi.org/download.html>

R & R Studio download links

1. <https://cran.microsoft.com/>
2. <https://rstudio.com/products/rstudio/download/>

You need both R and R Studio

Agenda

- 1. What are R Studio and jamovi?**
- 2. Introduction & Descriptive Statistics in jamovi**
- 3. Introduction & Descriptive Statistics in R Studio**
- 4. Creating an html report in R Studio**

R / R Studio

R is an integrated suite of software facilities for data manipulation, calculation and graphical display.

The screenshot displays the RStudio environment with the following components:

- Script Editor:** Contains R code for loading packages, connecting to a database, and calling an API.
- Environment:** Shows the current session's environment with a connection string for SQLite.
- Jobs Panel:** Displays the execution status of the script and its components.

```
1 # Load packages ----
2 library(repurrrsive)
3 library(tidyverse)
4 library(httr)
5 library(stringr)
6 library(here)
7
8 # Call the API ----
9 pov <- set_names(map_int(got_chars, "id"),
10                  map_chr(got_chars, "name"))
11 ice <- pov %>%
12   enframe(value = "id")
13
14 ice_and_fire_url <- "https://anapioficeandfire.com/"
15 ice <- ice %>%
16   mutate(
17     response = map(id,
18                   ~ GET(ice_and_fire_url,
19                       path = c("api", "characters", .x))),
20     stuff = map(response, ~ content(.x, as = "parsed",
21                                   simplifyVector = TRUE))
22   ) %>%
```

Environment: data/chinook.db (SQLite)

```
library(odbc)
con <- dbConnect(odbc::odbc(), .connection_string = "Driver={SQLite
Driver};Database=data/chinook.db",
  timeout = 10)
```

(Not connected)

System Library:

Name	Description	Version
<input type="checkbox"/> altparsers	Use alternative parsers for R code	0.1
<input type="checkbox"/> altstringiside	'ALTREP' example	0.0.0.90C
<input type="checkbox"/> assertthat	Easy Pre and Post Assertions	0.2.0
<input type="checkbox"/> backports	Reimplementations of Functions Introduced Since R-3.0.0	1.1.2
<input checked="" type="checkbox"/> base	The R Base Package	3.5.1
<input type="checkbox"/> base64enc	Tools for base64 encoding	0.1-3
<input type="checkbox"/> BH	Boost C++ Header Files	1.69.0-1
<input type="checkbox"/> bindr	Parametrized Active Bindings	0.1.1
<input type="checkbox"/> bindrcpp	An 'Rcpp' Interface to Active Bindings	0.2.2
<input type="checkbox"/> bit	A Class for Vectors of 1-Bit Booleans	1.1-14
<input type="checkbox"/> bit64	A S3 Class for Vectors of 64bit Integers	0.9-7
<input type="checkbox"/> bitops	Bitwise Operations	1.0-6
<input type="checkbox"/> blob	A Simple S3 Class for Representing Vectors of Binary Data ('BLOBS')	1.1.1
<input type="checkbox"/> blogdown	Create Blogs and Websites with R Markdown	0.8.5
<input type="checkbox"/> bookdown	Authoring Books and Technical	0.7

R packages

“Packages are the fundamental units of reproducible R code. They include reusable R functions, the documentation that describes how to use them, and sample data.”
(Wickham and Bryan, 2021)

They are like collections of formulas where you can input your data and select specific options to run analyses.

Example code for loading packages:

```
library(jtools)
```

```
library(jmv)
```

```
library(tidyverse)
```

For more info:

<https://r-pkgs.org/index.html>

jamovi



ANALYSES

jamovi provides a complete suite of analyses for (not just) the social sciences; t-tests, ANOVAs, correlation and regression, non-parametric tests, contingency tables, reliability and factor analysis. Need more analyses? then see [the jamovi library](#) – a library of additional analyses contributed by experts in their field.



STATISTICAL SPREADSHEET

jamovi is a fully functional spreadsheet, immediately familiar to anyone. Enter, copy/paste data, filter rows, compute new values, perform transforms across many columns at once – jamovi provides a streamlined spreadsheet experience, optimised for statistical data.



R SYNTAX

Love R? Check out jamovi's “syntax mode”, where the underlying R syntax for each analysis is made available. Just copy and paste this into R for a seamless transition. Alternatively, run R code directly inside jamovi with [the Rj Editor](#).

How are R and Jamovi connected?

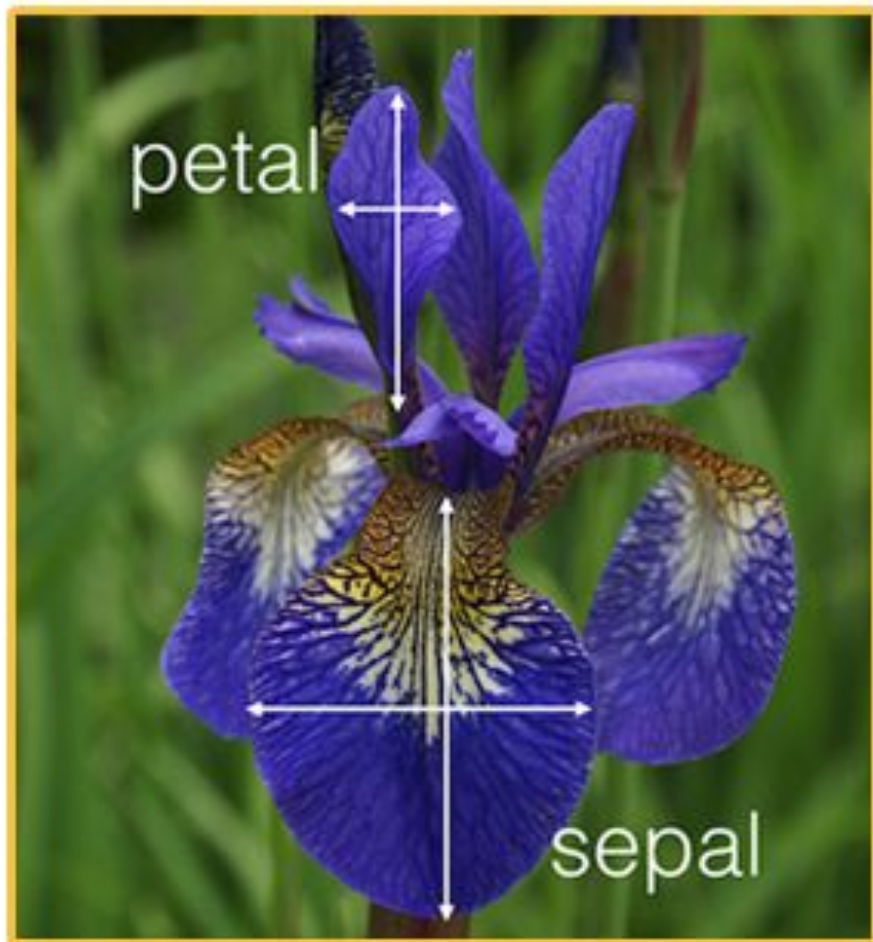
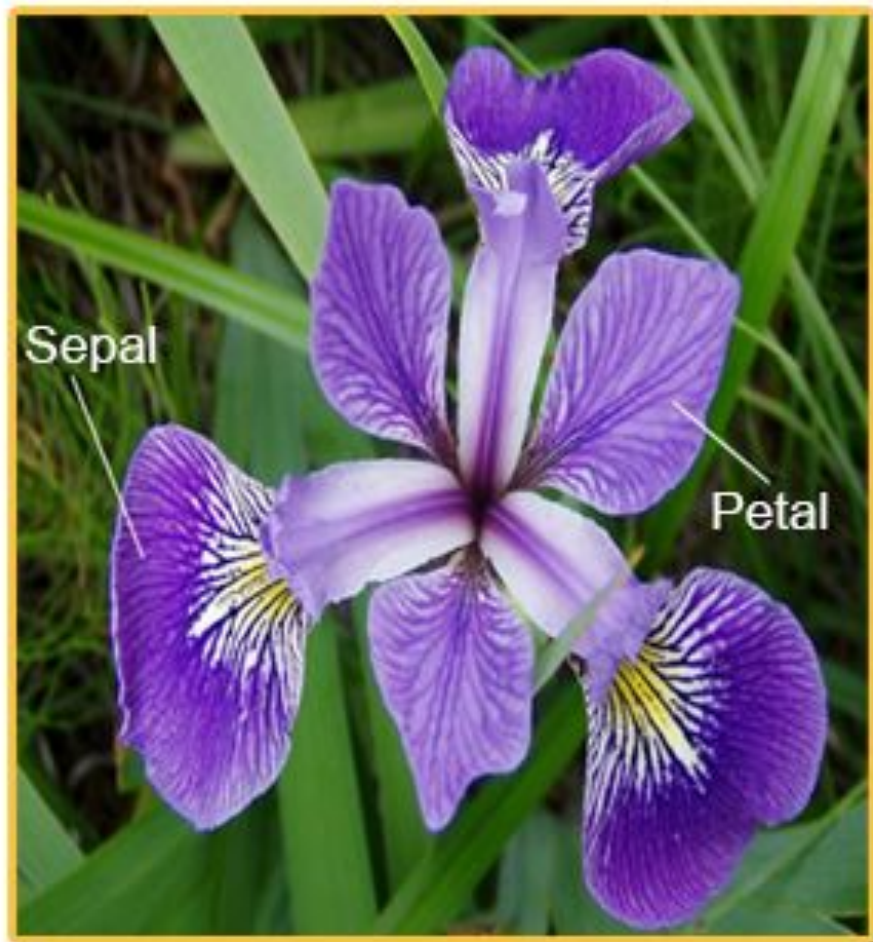
JMV R PACKAGE

`jmv` is the jamovi R package. All the analyses included with jamovi are available from within R using this package. For examples on how to use `jmv`, jamovi can be placed in 'syntax mode' (available from the top right menu). Syntax mode produces the R syntax required to reproduce jamovi analyses in R.

`jmv` is available from CRAN [here](#), and can be installed in R with:

```
install.packages('jmv')
```





The screenshot shows the jamovi software interface. The top menu bar includes 'Data', 'Analyses', and 'Edit'. Below the menu bar is a toolbar with icons for various statistical analyses: Exploration, T-Tests, ANOVA, Regression, Frequencies, Factor, and R. The main workspace is divided into two panes. The left pane contains a data grid with columns labeled A, B, and C, and rows numbered 1 to 31. The right pane is titled 'Results' and contains a 'References' section with two entries: [1] The jamovi project (2021). *jamovi*. (Version 1.6) [Computer Software]. Retrieved from [2] R Core Team (2020). *R: A Language and environment for statistical computing*. (Version 4.0.2) Retrieved from <https://cran.r-project.org>. (R packages retrieved from MRAN snapshot of 2020-09-14)

In the top right corner, the 'Modules' button (a plus sign icon) is circled in red. A dropdown menu is open, showing the 'jamovi library' option, which is also circled in red. The dropdown menu lists the following installed modules:

- jmv
Analyses bundled with jamovi
- jmvbaseR
Base R
- jpower
Power Analysis for Common Research Designs
- Rj
Editor to run R code inside jamovi

At the bottom of the interface, there is a status bar with the following information: Ready, Filters 0, Row count 0, Filtered 0, Deleted 0, Added 0, Cells edited 0.

Click Modules -> jamovi library in the top right



Data

Analyses

Edit



Exploration



T-Tests



ANOVA



Regression



jamovi



Modules

Scroll down to
r-data sets and
press install

Installed

Available

Sideload

INSTALL

**Isj-data - learning statistics with jamovi 1.0.1**

Danielle Navarro, David Foxcroft

This module provides examples data sets to accompany the book [learning statistics with jamovi](https://www.jamovi.org).

INSTALL

**r-datasets - R data sets 1.0.1**

The R Core Team

This module provides the example data sets from R

INSTALL

**Statkat - Method Selection Tool 1.0.2**

Rivka M. de Vries

This tool will help you to find an appropriate statistical method given your research question and the measurement level of your data.

INSTALL





Data

Analyses

Edit



Exploration



T-Tests



ANOVA



Regression



Frequencies



Factor



R



Modules

	A	B	C		
1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
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28					
29					
30					
31					

Results

References

- [1] The jamovi project (2021). *jamovi*. (Version 1.6) [Computer Software]. Retrieved from <https://www.jamovi.org>.
- [2] R Core Team (2020). *R: A Language and environment for statistical computing*. (Version 4.0) [Computer software]. Retrieved from <https://cran.r-project.org>. (R packages retrieved from MRAN snapshot 2020-08-24).

Click the 3 bars in the top left

New

Open

This PC

Data Library

Import

Save

Save As

Export

Recent

data.csv

data.RData

↑ Data Library

Q |



Big 5 (Dolan, Oort, Steel & Wicherts, 2009)
A nice correlation data set



Tooth Growth
An uninspiring ANOVA data set



Bugs (Ryan, Wilde & Crist, 2013)
A repeated measures ANOVA data set



Anderson's Iris Data
The 'iris' data set from R

Click Open then select Anderson's
Iris Data

project (2021). *jamovi*. (Version 1.6) [Computer Software]. Retrieved from <https://www.jamovi.org>.

language and environment for statistical computing. (Version 4.0) [Computer software].
[r-project.org](https://www.r-project.org). (R packages retrieved from MRAN snapshot 2020-08-24).



Data

Analyses

Edit



Exploration



T-Tests



ANOVA



Regression



Frequencies



Factor



R



Modules

	Sepal.Len...	Sepal.Wid...	Petal.Len...	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	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa
11	5.4	3.7	1.5	0.2	setosa
12	4.8	3.4	1.6	0.2	setosa
13	4.8	3.0	1.4	0.1	setosa
14	4.3	3.0	1.1	0.1	setosa
15	5.8	4.0	1.2	0.2	setosa
16	5.7	4.4	1.5	0.4	setosa
17	5.4	3.9	1.3	0.4	setosa
18	5.1	3.5	1.4	0.3	setosa
19	5.7	3.8	1.7	0.3	setosa
20	5.1	3.8	1.5	0.3	setosa
21	5.4	3.4	1.7	0.2	setosa
22	5.1	3.7	1.5	0.4	setosa
23	4.6	3.6	1.0	0.2	setosa
24	5.1	3.3	1.7	0.5	setosa
25	4.8	3.4	1.9	0.2	setosa
26	5.0	3.0	1.6	0.2	setosa
27	5.0	3.4	1.6	0.4	setosa
28	5.2	3.5	1.5	0.2	setosa
29	5.2	3.4	1.4	0.2	setosa

Now, we should be here with the data opened.

There are 4 continuous variables:

- Sepal.Length
- Sepal.Width,
- Petal.Length
- Petal.Width

version 1.6.16

There is 1 nominal variable:

- Species

What is the other type of variable that data are often classified as?



Data

Analyses

Edit



Exploration



T-Tests



ANOVA



Regression



Frequencies



Factor



R



Modules

	Sepal.Len...	Sepal.Wid...	Petal.Len...	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	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa
11	5.4	3.7	1.5	0.2	setosa
12	4.8	3.4	1.6	0.2	setosa
13	4.8	3.0	1.4	0.1	setosa
14	4.3	3.0	1.1	0.1	setosa
15	5.8	4.0	1.2	0.2	setosa
16	5.7	4.4	1.5	0.4	setosa
17	5.4	3.9	1.3	0.4	setosa
18	5.1	3.5	1.4	0.3	setosa
19	5.7	3.8	1.7	0.3	setosa
20	5.1	3.8	1.5	0.3	setosa
21	5.4	3.4	1.7	0.2	setosa
22	5.1	3.7	1.5	0.4	setosa
23	4.6	3.6	1.0	0.2	setosa
24	5.1	3.3	1.7	0.5	setosa
25	4.8	3.4	1.9	0.2	setosa
26	5.0	3.0	1.6	0.2	setosa
27	5.0	3.4	1.6	0.4	setosa
28	5.2	3.5	1.5	0.2	setosa
29	5.2	3.4	1.4	0.2	setosa

Results

References

- [1] The jamovi project (2021). *jamovi*. (Version 1.6) [Computer Software]. Retrieved from <https://www.jamovi.org>.
- [2] R Core Team (2020). *R: A Language and environment for statistical computing*. (Version 4.0) [Computer software]. Retrieved from <https://cran.r-project.org>. (R packages retrieved from MRAN snapshot 2020-08-24).

Click the 3 dots in the top right





	Sepal.Len...	Sepal.Wid...	Petal.Len...	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	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa
11	5.4	3.7	1.5	0.2	setosa
12	4.8	3.4	1.6	0.2	setosa
13	4.8	3.0	1.4	0.1	setosa
14	4.3	3.0	1.1	0.1	setosa
15	5.8	4.0	1.2	0.2	setosa
16	5.7	4.4	1.5	0.4	setosa
17	5.4	3.9	1.3	0.4	setosa
18	5.1	3.5	1.4	0.3	setosa
19	5.7	3.8	1.7	0.3	setosa
20	5.1	3.8	1.5	0.3	setosa
21	5.4	3.4	1.7	0.2	setosa
22	5.1	3.7	1.5	0.4	setosa
23	4.6	3.6	1.0	0.2	setosa
24	5.1	3.3	1.7	0.5	setosa
25	4.8	3.4	1.9	0.2	setosa
26	5.0	3.0	1.6	0.2	setosa
27	5.0	3.4	1.6	0.4	setosa
28	5.2	3.5	1.5	0.2	setosa
29	5.2	3.4	1.4	0.2	setosa

Turn on Syntax Mode

This will allow you to see the R Syntax when working in jamovi.

This can be copy and pasted to R.

Zoom

- 100% +

Results

Number format

3 sf ▾

p-value format

3 dp ▾

References

Visible ▾

Syntax mode ☒

Plots

Plot theme

Default ▾

Color palette

jmv ▾

Import

Default missing

NA

Screen Capture Tool

Developer mode ☐

Version 1.6.16.0

jamovi - iris

Data

Analyses

Edit

Exploration

T-Tests

ANOVA

Regression

Frequencies

Factor

R

Modules

Descriptives

Sepal.Wid...

Petal.Leng...

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	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa
11	5.4	3.7	1.5	0.2	setosa
12	4.8	3.4	1.6	0.2	setosa
13	4.8	3.0	1.4	0.1	setosa
14	4.3	3.0	1.1	0.1	setosa
15	5.8	4.0	1.2	0.2	setosa
16	5.7	4.4	1.5	0.4	setosa
17	5.4	3.9	1.3	0.4	setosa
18	5.1	3.5	1.4	0.3	setosa
19	5.7	3.8	1.7	0.3	setosa
20	5.1	3.8	1.5	0.3	setosa
21	5.4	3.4	1.7	0.2	setosa
22	5.1	3.7	1.5	0.4	setosa
23	4.6	3.6	1.0	0.2	setosa
24	5.1	3.3	1.7	0.5	setosa
25	4.8	3.4	1.9	0.2	setosa
26	5.0	3.0	1.6	0.2	setosa
27	5.0	3.4	1.6	0.4	setosa
28	5.2	3.5	1.5	0.2	setosa
29	5.2	3.4	1.4	0.2	setosa

Results

References

[1] The jamovi project (2021). *jamovi*. (Version 1.6) [Computer Software]. Retrieved from <https://www.jamovi.org>.

[2] R Core Team (2020). *R: A Language and environment for statistical computing*. (Version 4.0) [Computer software]. Retrieved from <https://cran.r-project.org>. (R packages retrieved from MRAN snapshot 2020-08-24).

Exploration -> descriptives

Descriptives



Sepal.Length

Sepal.Width

Petal.Length

Petal.Width

Species



Variables



Split by

☐ Frequency tables

> | Statistics

> | Plots

Results

Descriptives

Descriptives

N
Missing
Mean
Median
Standard deviation
Minimum
Maximum

References

- [1] The jamovi project (2021). *jamovi*. (Version 1.6) [Computer Software]. Retrieved from <https://www.jamovi.org>.
- [2] R Core Team (2020). *R: A Language and environment for statistical computing*. (Version 4.0) [Computer software]. Retrieved from <https://cran.r-project.org>. (R packages retrieved from MRAN snapshot 2020-08-24).

Descriptives

Species

←

Variables

Sepal.Length

Petal.Width

Petal.Length

Sepal.Width

Split by

→

☐ Frequency tables

Statistics

Sample Size

☒ N ☒ Missing

Central Tendency

☒ Mean

Results

Descriptives

Descriptives

	Sepal.Length	Petal.Width	Petal.Length	Sepal.Width
N	150	150	150	150
Missing	0	0	0	0
Mean	5.84	1.20	3.76	3.06
Median	5.80	1.30	4.35	3.00
Standard deviation	0.828	0.762	1.77	0.436
Minimum	4.30	0.100	1.00	2.00
Maximum	7.90	2.50	6.90	4.40
Skewness	0.315	-0.103	-0.275	0.319
Std. error skewness	0.198	0.198	0.198	0.198
Kurtosis	-0.552	-1.34	-1.40	0.228
Std. error kurtosis	0.394	0.394	0.394	0.394

I select all of the continuous variables for descriptives

I select the following to create a table with:

- Number of data points
- Number of missing data points
- Standard deviation
- Minimum value
- Maximum value
- Mean
- Median
- Skew
- Kurtosis

I also get the following plots for each variable:

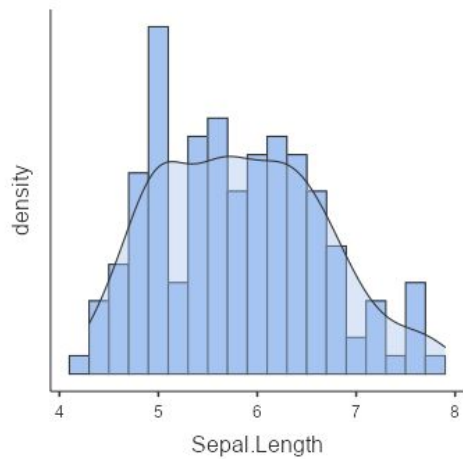
- Histograms
- Box plots

Sample Size <input checked="" type="checkbox"/> N <input checked="" type="checkbox"/> Missing		Central Tendency <input checked="" type="checkbox"/> Mean <input checked="" type="checkbox"/> Median <input type="checkbox"/> Mode <input type="checkbox"/> Sum
Percentile Values <input type="checkbox"/> Cut points for <input type="text" value="4"/> equal groups <input type="checkbox"/> Percentiles <input type="text" value="25,50,75"/>		
Dispersion <input checked="" type="checkbox"/> Std. deviation <input checked="" type="checkbox"/> Minimum <input type="checkbox"/> Variance <input checked="" type="checkbox"/> Maximum <input type="checkbox"/> Range <input type="checkbox"/> S. E. Mean <input type="checkbox"/> IQR		Distribution <input checked="" type="checkbox"/> Skewness <input checked="" type="checkbox"/> Kurtosis
		Normality <input type="checkbox"/> Shapiro-Wilk
<div>▼ Plots</div>		
Histograms <input checked="" type="checkbox"/> Histogram <input checked="" type="checkbox"/> Density	Box Plots <input checked="" type="checkbox"/> Box plot <input checked="" type="checkbox"/> Violin <input checked="" type="checkbox"/> Data <div><input type="text" value="Jittered"/> ▼</div> <input type="checkbox"/> Mean	Bar Plots <input type="checkbox"/> Bar plot
Q-Q Plots <input type="checkbox"/> Q-Q		

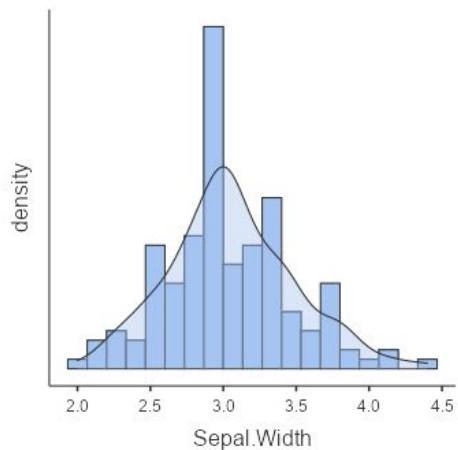
```
jmv::descriptives(  
  data = data,  
  vars = vars(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width),  
  hist = TRUE,  
  dens = TRUE,  
  box = TRUE,  
  violin = TRUE,  
  dot = TRUE,  
  boxMean = TRUE,  
  skew = TRUE,  
  kurt = TRUE)
```

Sample Size		Central Tendency
<input checked="" type="checkbox"/> N	<input checked="" type="checkbox"/> Missing	<input checked="" type="checkbox"/> Mean
Percentile Values		<input checked="" type="checkbox"/> Median
<input type="checkbox"/> Cut points for	<input type="text" value="4"/> equal groups	<input type="checkbox"/> Mode
<input type="checkbox"/> Percentiles	<input type="text" value="25,50,75"/>	<input type="checkbox"/> Sum
Dispersion		Distribution
<input checked="" type="checkbox"/> Std. deviation	<input checked="" type="checkbox"/> Minimum	<input checked="" type="checkbox"/> Skewness
<input type="checkbox"/> Variance	<input checked="" type="checkbox"/> Maximum	<input checked="" type="checkbox"/> Kurtosis
<input type="checkbox"/> Range	<input type="checkbox"/> S. E. Mean	
<input type="checkbox"/> IQR		
Normality		
<input type="checkbox"/> Shapiro-Wilk		
Plots		
Histograms	Box Plots	Bar Plots
<input checked="" type="checkbox"/> Histogram	<input checked="" type="checkbox"/> Box plot	<input type="checkbox"/> Bar plot
<input checked="" type="checkbox"/> Density	<input checked="" type="checkbox"/> Violin	
Q-Q Plots	<input checked="" type="checkbox"/> Data	
<input type="checkbox"/> Q-Q	<input type="text" value="Jittered"/>	
	<input type="checkbox"/> Mean	

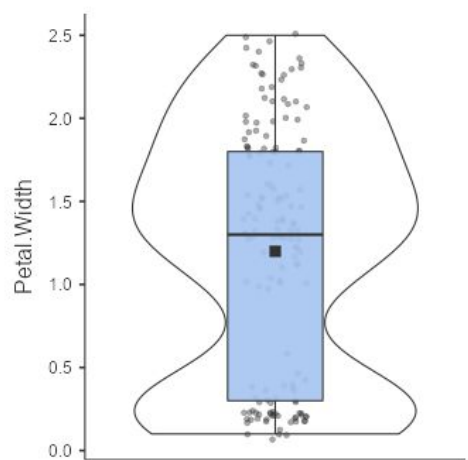
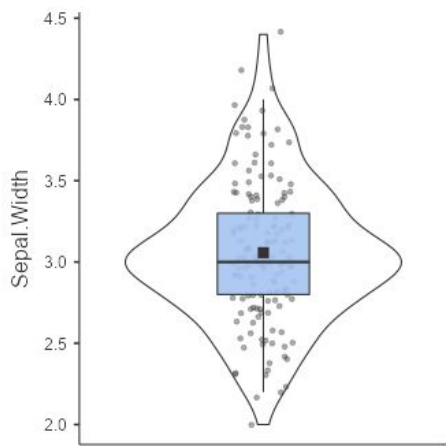
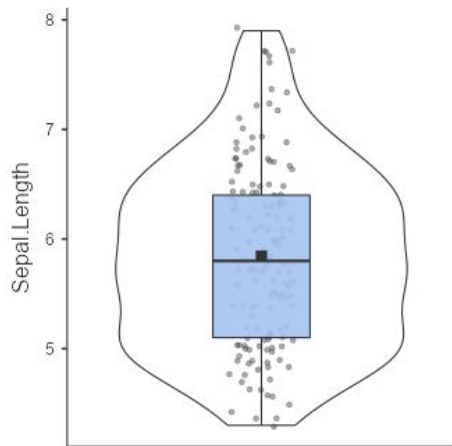
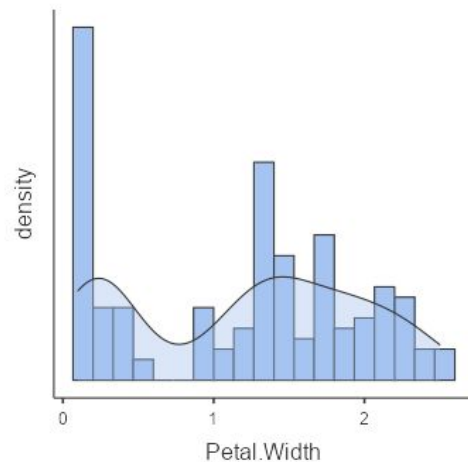
Sepal.Length



Sepal.Width



Petal.Width



jamovi - iris

Menu: Data, Analyses, Edit

Tools: Exploration, T-Tests, ANOVA, Regression, Frequencies, Factor, R

Modules: +

Descriptives

Variables:

- Sepal.Length
- Sepal.Width
- Petal.Length
- Petal.Width

Split by:

- Species

☐ Frequency tables

Statistics:

Sample Size

☒ N ☒ Missing

Percentile Values

☐ Cut points for 4 equal groups

☐ Percentiles 25,50,75

Dispersion

☒ Std. deviation ☒ Minimum

☐ Variance ☒ Maximum

☐ Range ☐ S. E. Mean

☐ IQR

Central Tendency

☒ Mean

☒ Median

☐ Mode

☐ Sum

Distribution

☒ Skewness

☒ Kurtosis

Normality

☐ Shapiro-Wilk

Descriptives

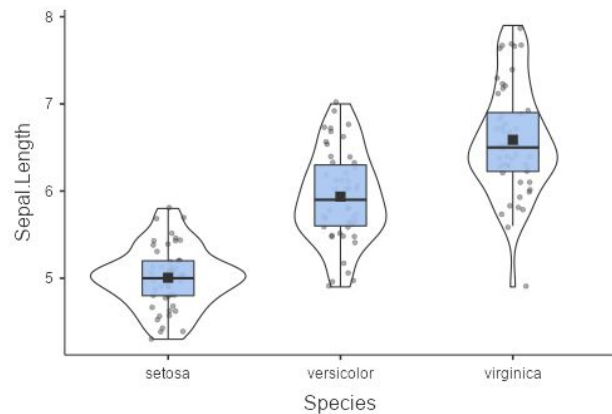
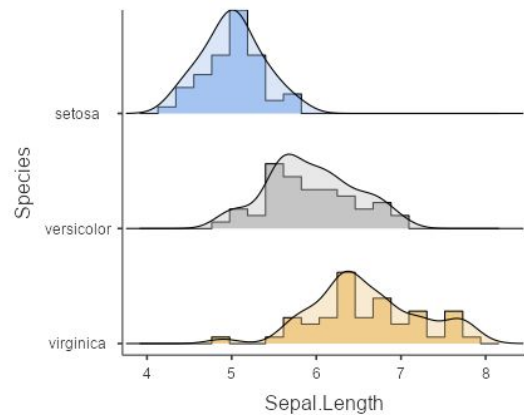
```
jmv::descriptives(
  formula = Sepal.Length + Sepal.Width + Petal.Length + Petal.Width ~ Species,
  data = data,
  hist = TRUE,
  dens = TRUE,
  box = TRUE,
  violin = TRUE,
  dot = TRUE,
  boxMean = TRUE,
  skew = TRUE,
  kurt = TRUE)
```

	Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
N	setosa	50	50	50	50
	versicolor	50	50	50	50
	virginica	50	50	50	50
Missing	setosa	0	0	0	0
	versicolor	0	0	0	0
	virginica	0	0	0	0
Mean	setosa	5.006	3.428	1.462	0.2460
	versicolor	5.936	2.770	4.260	1.326
	virginica	6.588	2.974	5.552	2.026
Median	setosa	5.000	3.400	1.500	0.2000
	versicolor	5.900	2.800	4.350	1.300
	virginica	6.500	3.000	5.550	2.000
Standard deviation	setosa	0.3525	0.3791	0.1737	0.1054
	versicolor	0.5162	0.3138	0.4699	0.1978
	virginica	0.6359	0.3225	0.5519	0.2747
Minimum	setosa	4.300	2.300	1.000	0.1000
	versicolor	4.900	2.000	3.000	1.000
	virginica	4.900	2.200	4.500	1.400
Maximum	setosa	5.800	4.400	1.900	0.6000
	versicolor	7.000	3.400	5.100	1.800
	virginica	7.900	3.800	6.900	2.500
Skewness	setosa	0.1201	0.04117	0.1064	1.254
	versicolor	0.1054	-0.3628	-0.6065	-0.03118
	virginica	0.1180	0.3659	0.5494	-0.1295
Std. error skewness	setosa	0.3366	0.3366	0.3366	0.3366

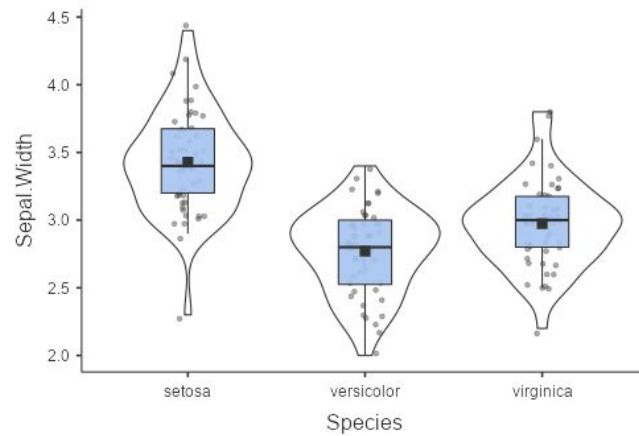
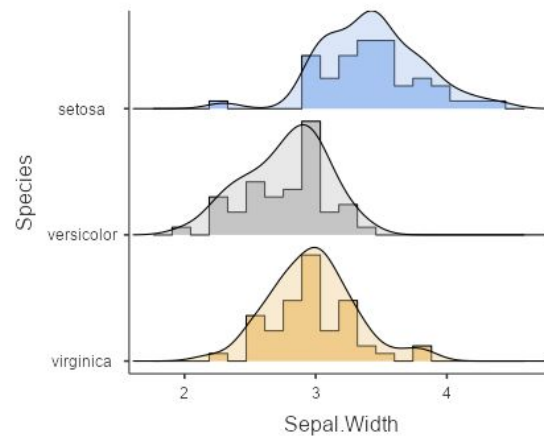
I now split the descriptives by flower species.

Plots

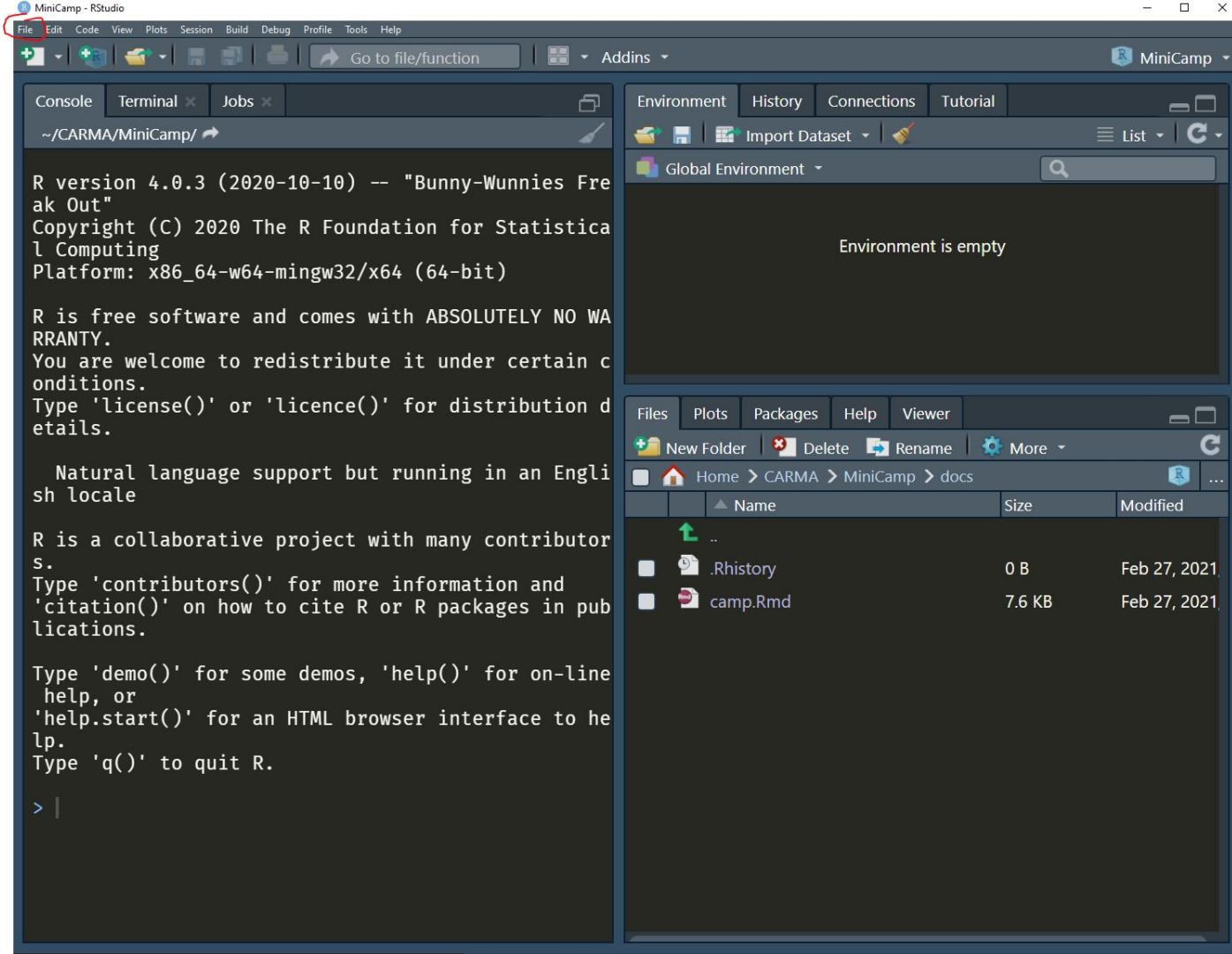
Sepal.Length



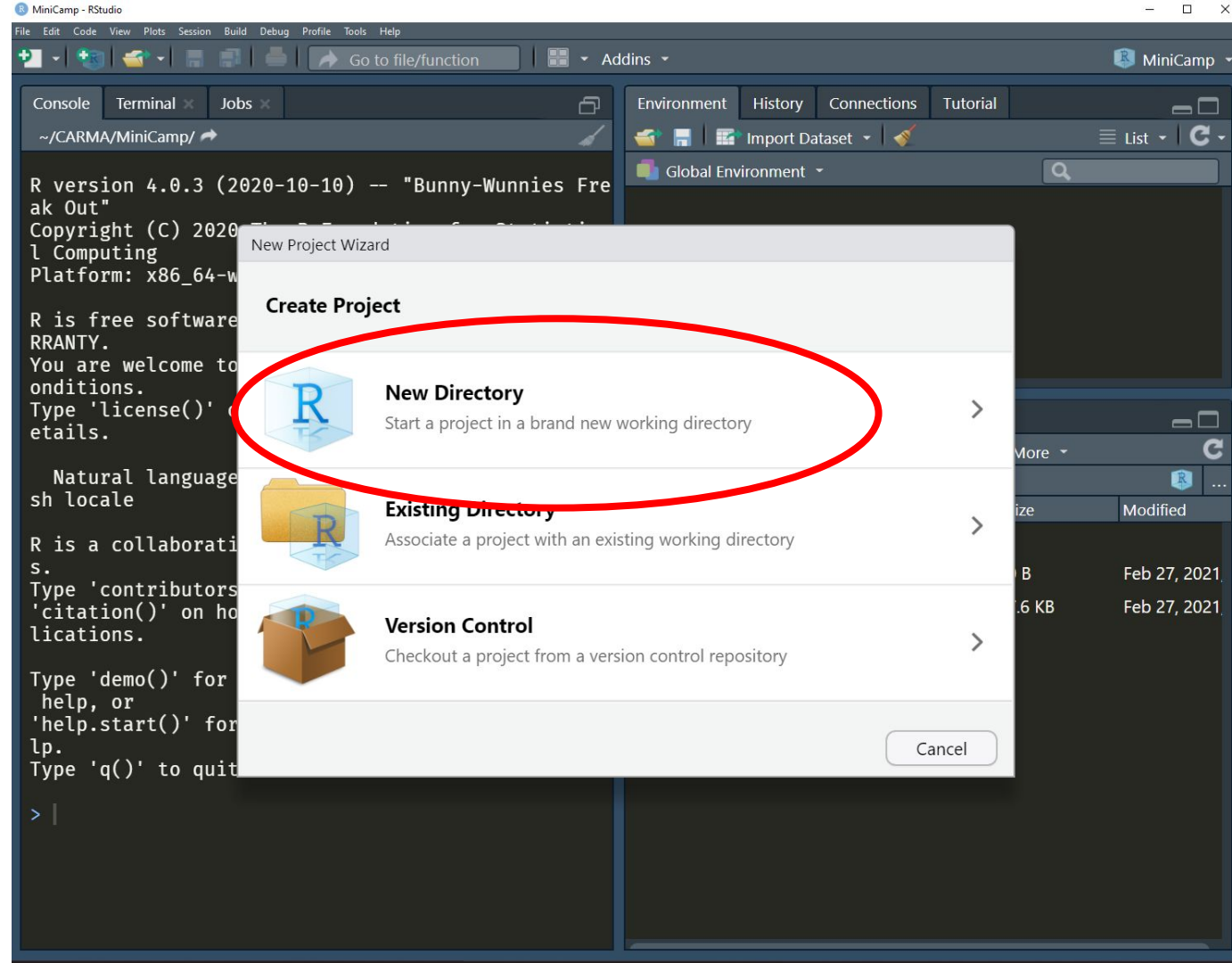
Sepal.Width



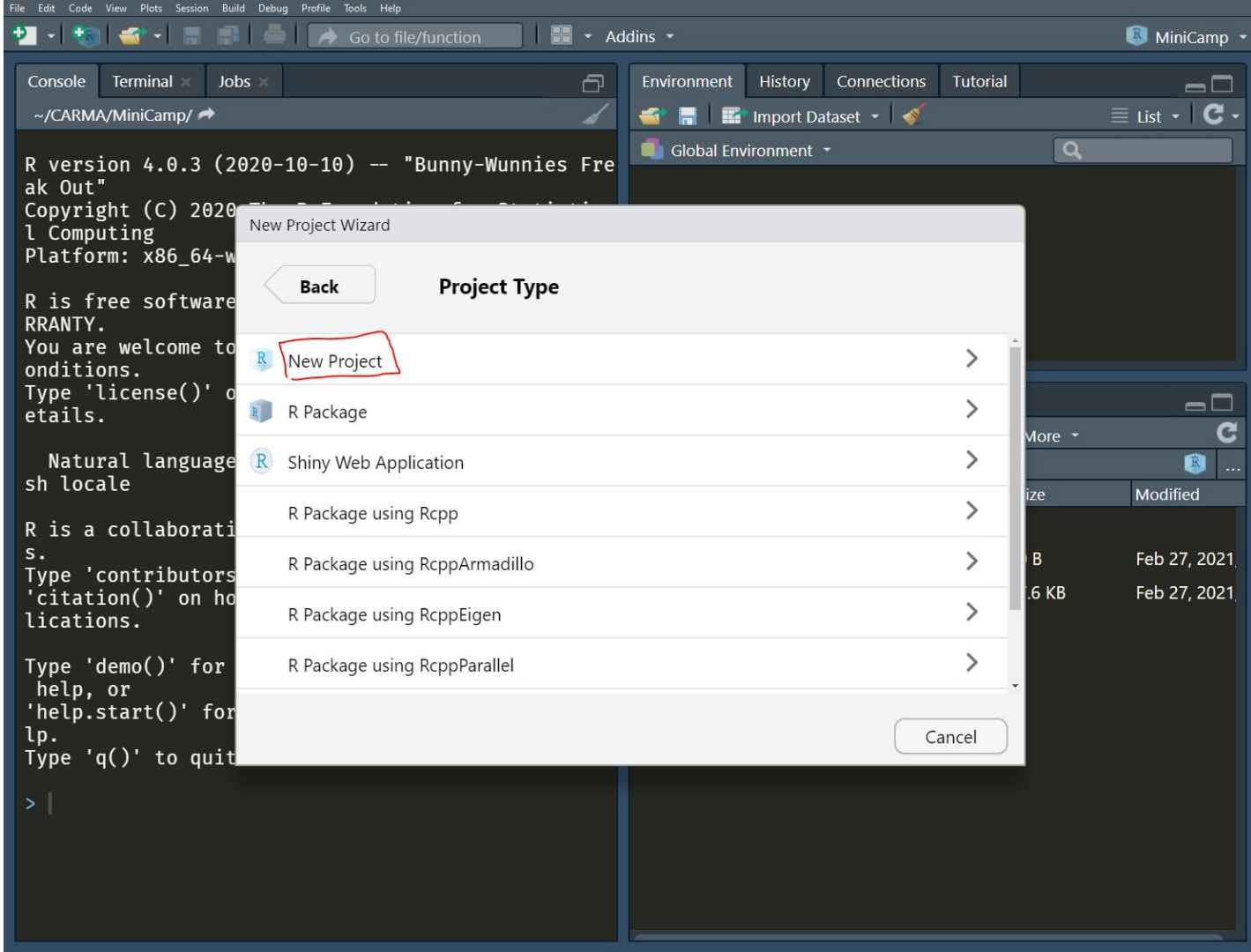
Open R Studio and Press File then New Project



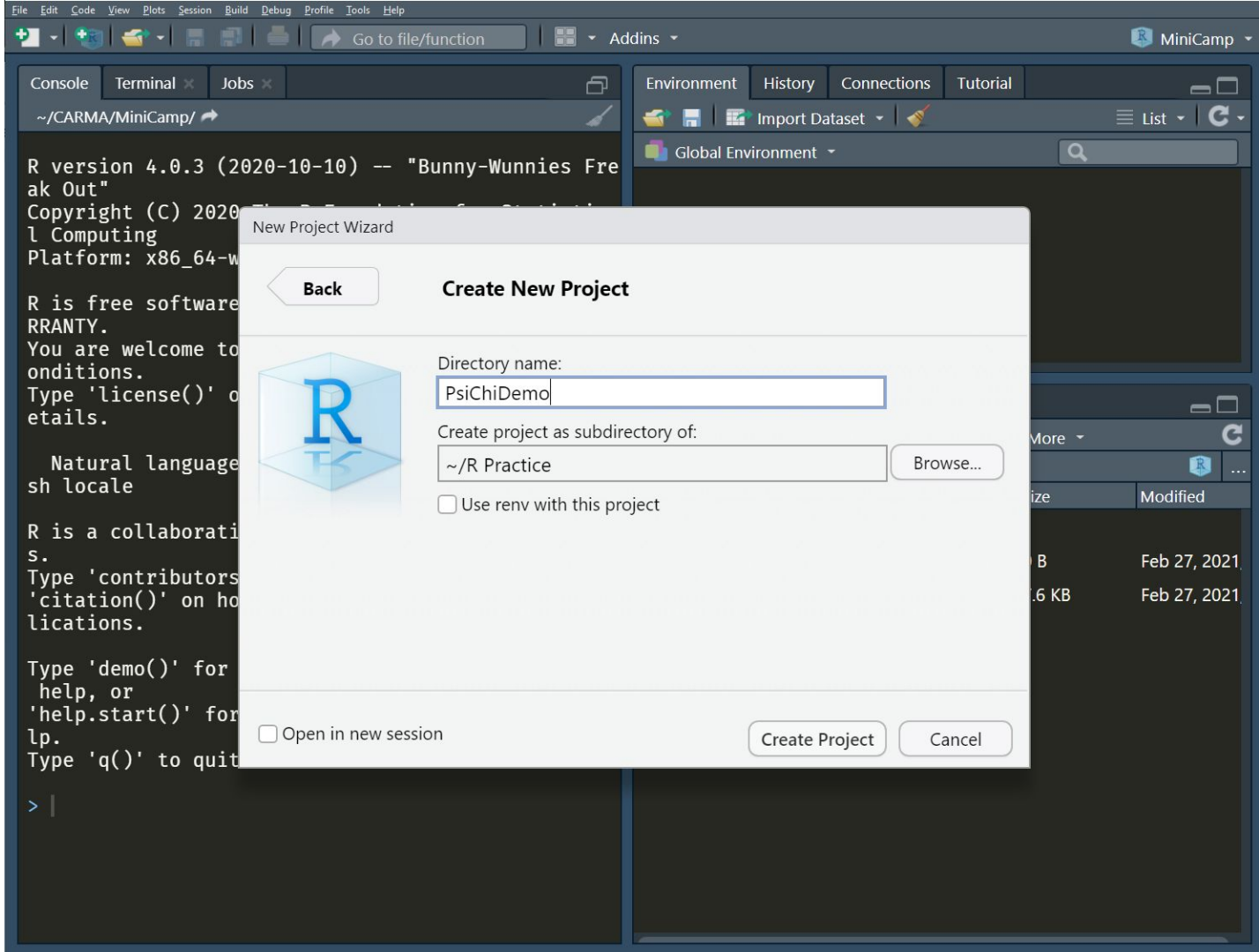
Select New Directory



Select New Project

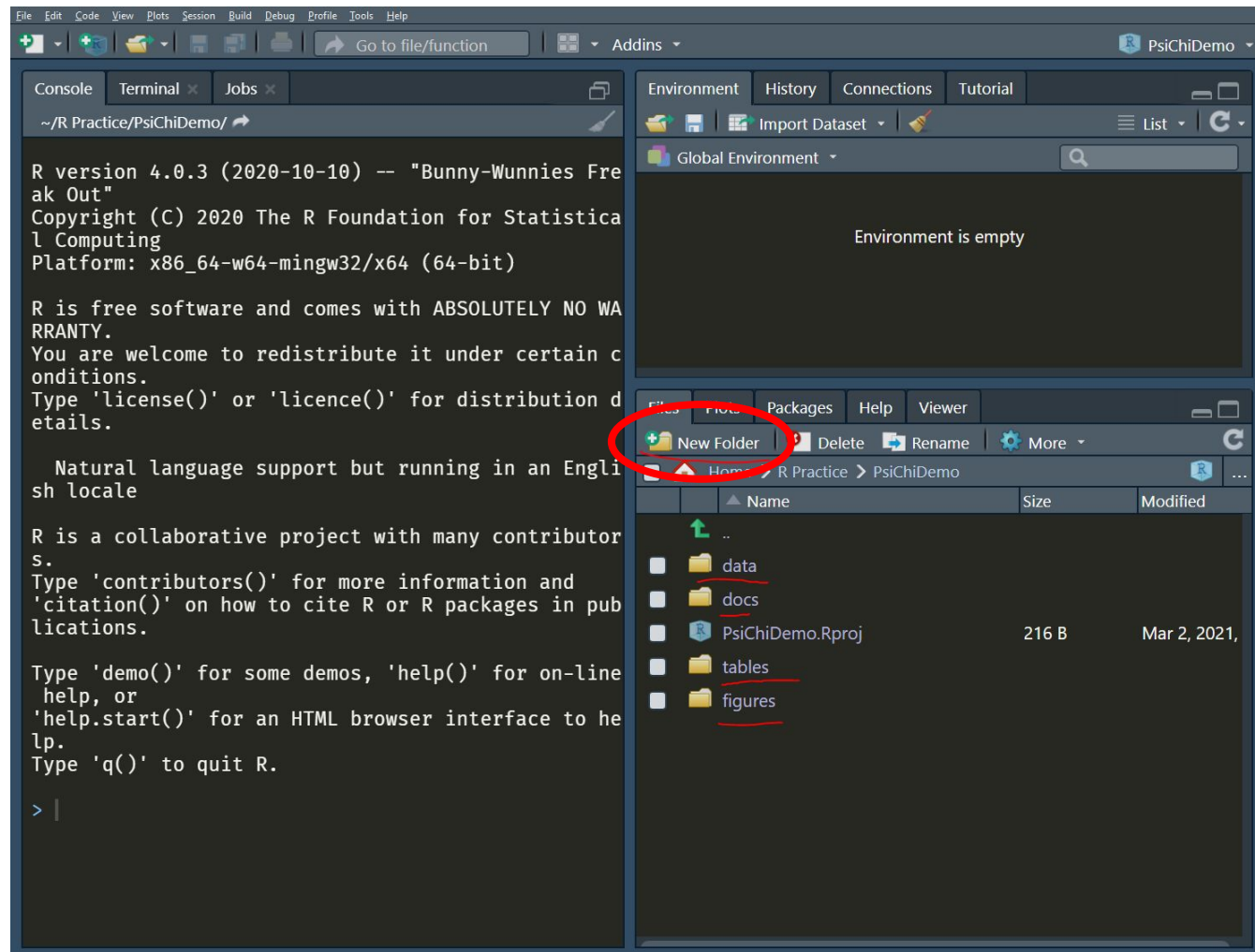


Name the Directory (the new project folder) and choose the location.

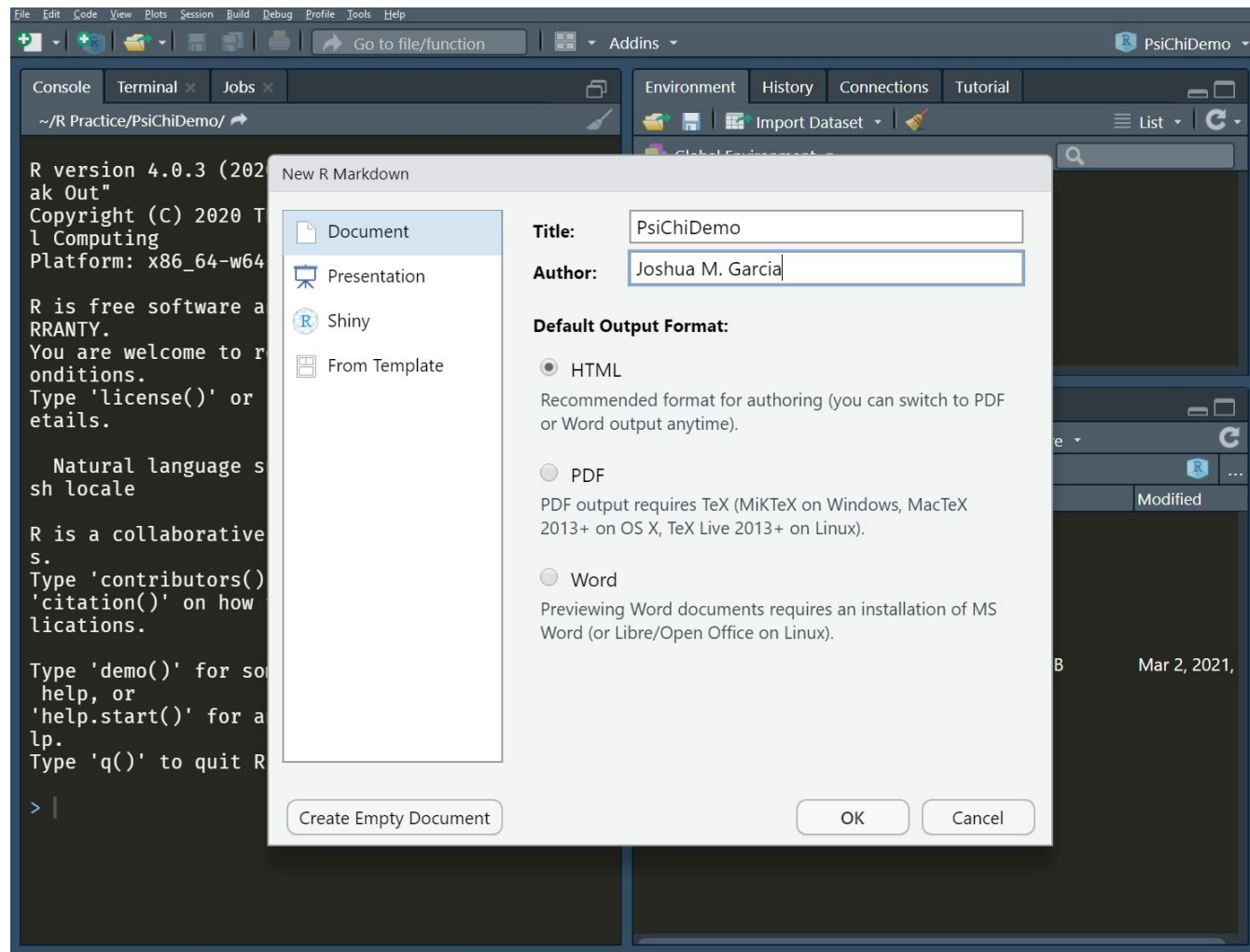


It's typically
good practice to
make folders for:

- data
- docs
- tables
- figures

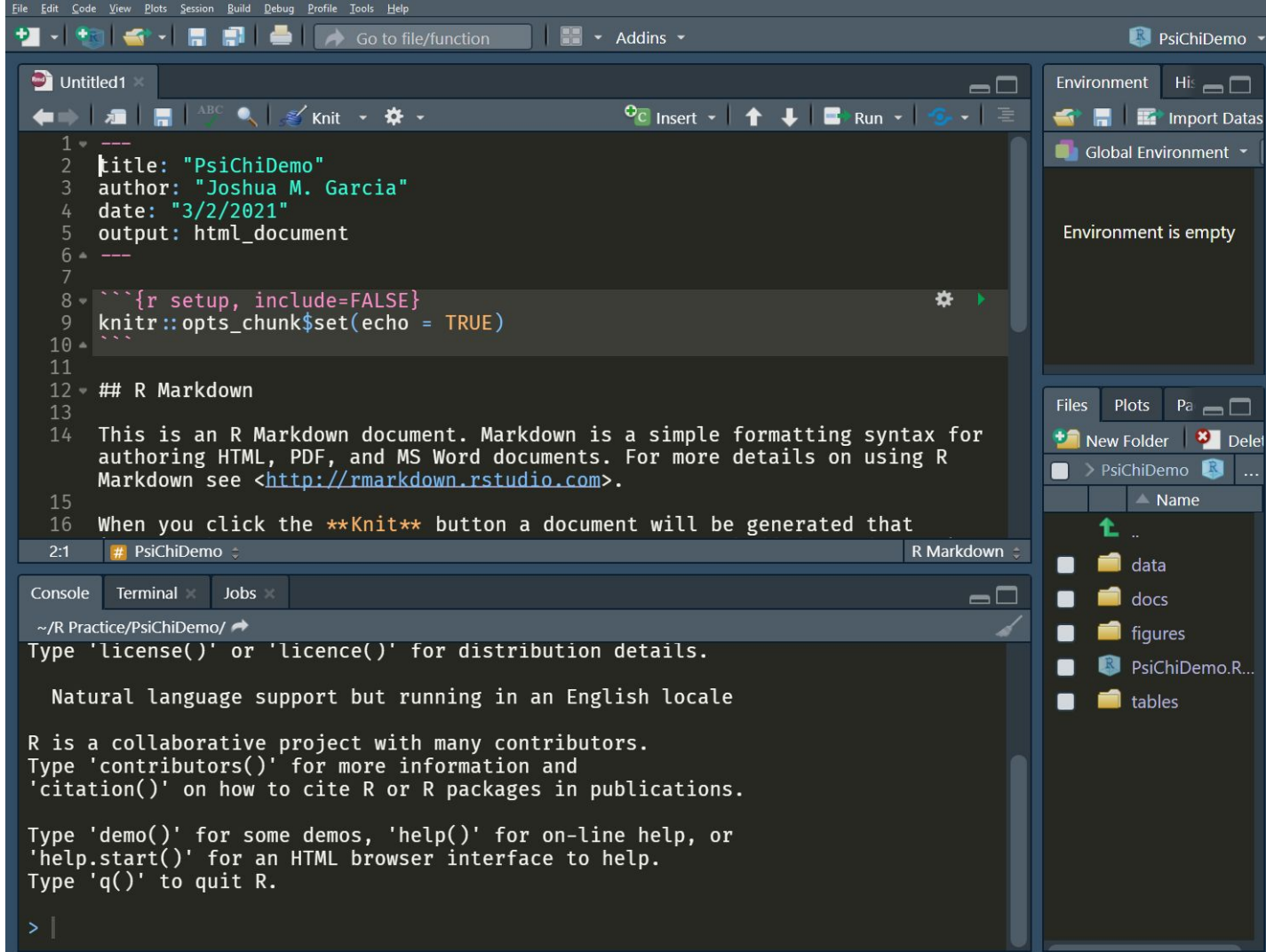


Select File →
New File →
R Markdown



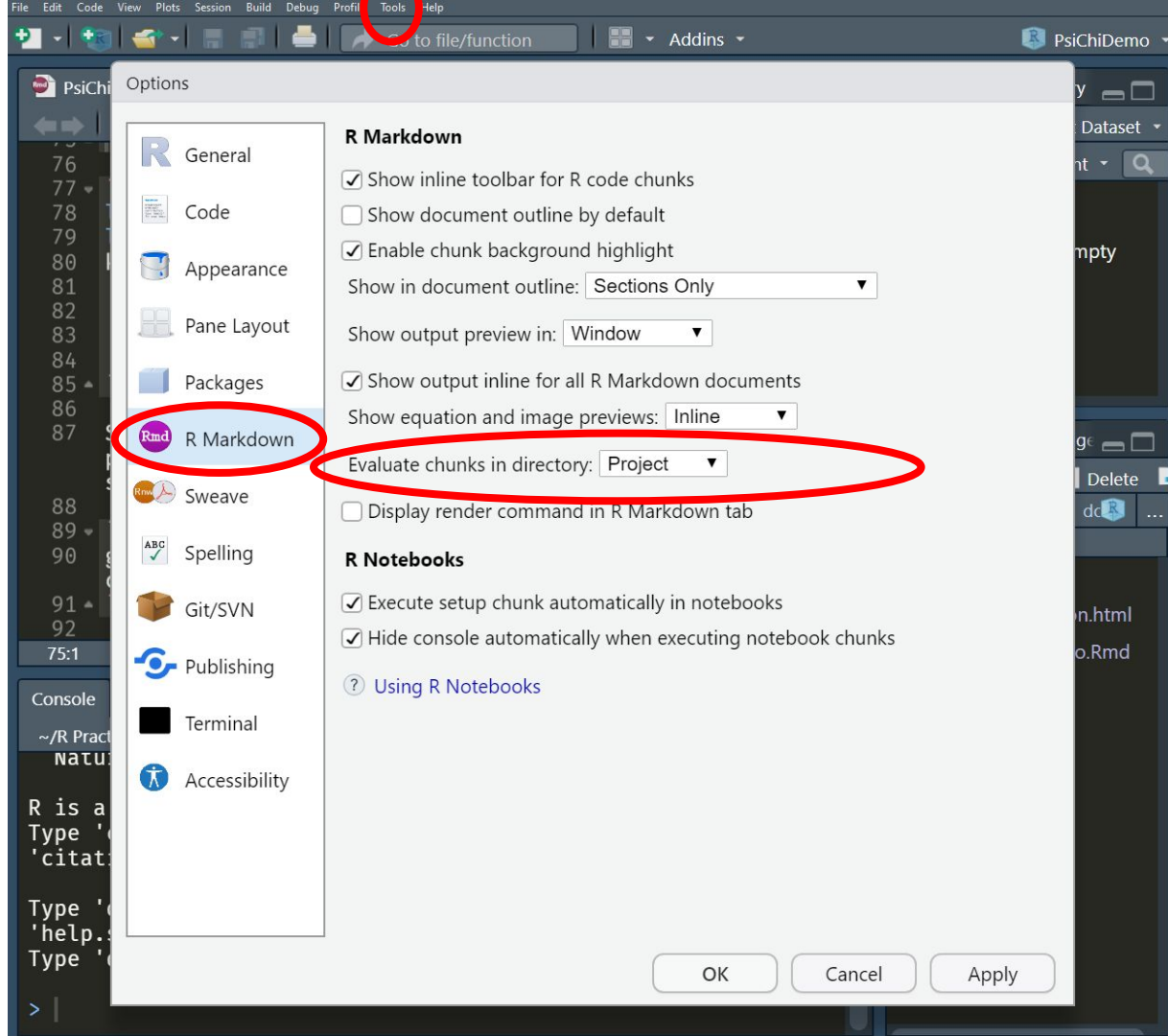
R Studio presents with a description of the R Markdown document. Read this for clarification.

Save the file to your docs folder.



1. Select Tools
2. Global Options
3. R Markdown
4. Set your R Markdown document to evaluate chunks in directory to “Project”

Note that Global Settings are saved between sessions and R projects.



The screenshot shows the RStudio application window. The title bar reads "PsiChiDemo - RStudio". The menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. The toolbar contains icons for adding files, saving, printing, and a search bar labeled "Go to file/function". The Addins pane is open on the right. The active file is "PsiChiDemo.Rmd". The editor shows a YAML header for a presentation slide with the following content:

```
1 ---
2 title: "Descriptive Statistics Demo"
3 author: "Joshua M. Garcia"
4 date: "3/2/2021"
5 output:
6   html_document:
7     theme: readable
8     highlight: tango
9 ---
10
11 ```{r setup, include=FALSE}
12 knitr::opts_chunk$set(echo = TRUE, warning=FALSE, message=FALSE)
13 ```
```

I updated the header to have preferable settings. I also added warning and message to FALSE.

This line of code is to install the "jmv" package that is integrated with jamovi. "eval=FALSE" means that this line will not run unless you manually tell it to. This is to avoid reinstalling each time this code is ran.

I also install the tableone, tidyverse, and kableExtra packages for later on.

```
```{r, eval=FALSE}  
install.packages('jmv')
install.packages('tableone')
install.packages('tidyverse')
install.packages('kableExtra')
```
```



PsiChiDemo.Rmd x

24
25
26 # Import Data
27
28 In this data chunk, I assign the iris data set to a data frame titled "data". This will be stored in the Global Environment.
29
30 ````\{r\}`
31 `data <- iris`
32
33

Environment History Connections Tutorial

Import Dataset

Global Environment

Data

| | |
|------|-------------------------|
| data | 150 obs. of 5 variables |
|------|-------------------------|

This command is to view the top of the data.

```
head(data)
```

| | Sepal.Length
<dbl> | Sepal.Width
<dbl> | Petal.Length
<dbl> | Petal.Width
<dbl> |
|---|-----------------------|----------------------|-----------------------|----------------------|
| 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 |

6 rows | 1-5 of 5 columns

These next lines are copy and pasted from jamovi. Figure width and figure height are set to 50% to improve readability.

```
```{r, out.height= "50%", out.width="50%"}
jmv::descriptives(
 data = data,
 vars = vars(Sepal.Length, Sepal.Width, Petal.Length,
Petal.Width),
 hist = TRUE,
 dens = TRUE,
 box = TRUE,
 violin = TRUE,
 dot = TRUE,
 skew = TRUE,
 kurt = TRUE)
```
```

```
```{r, out.height= "50%", out.width="50%"}
jmv::descriptives(
 formula = Sepal.Length + Sepal.Width + Petal.Length +
Petal.Width ~ Species,
 data = data,
 hist = TRUE,
 dens = TRUE,
 box = TRUE,
 violin = TRUE,
 dot = TRUE,
 skew = TRUE,
 kurt = TRUE)
```
```


Comparison to Other Packages

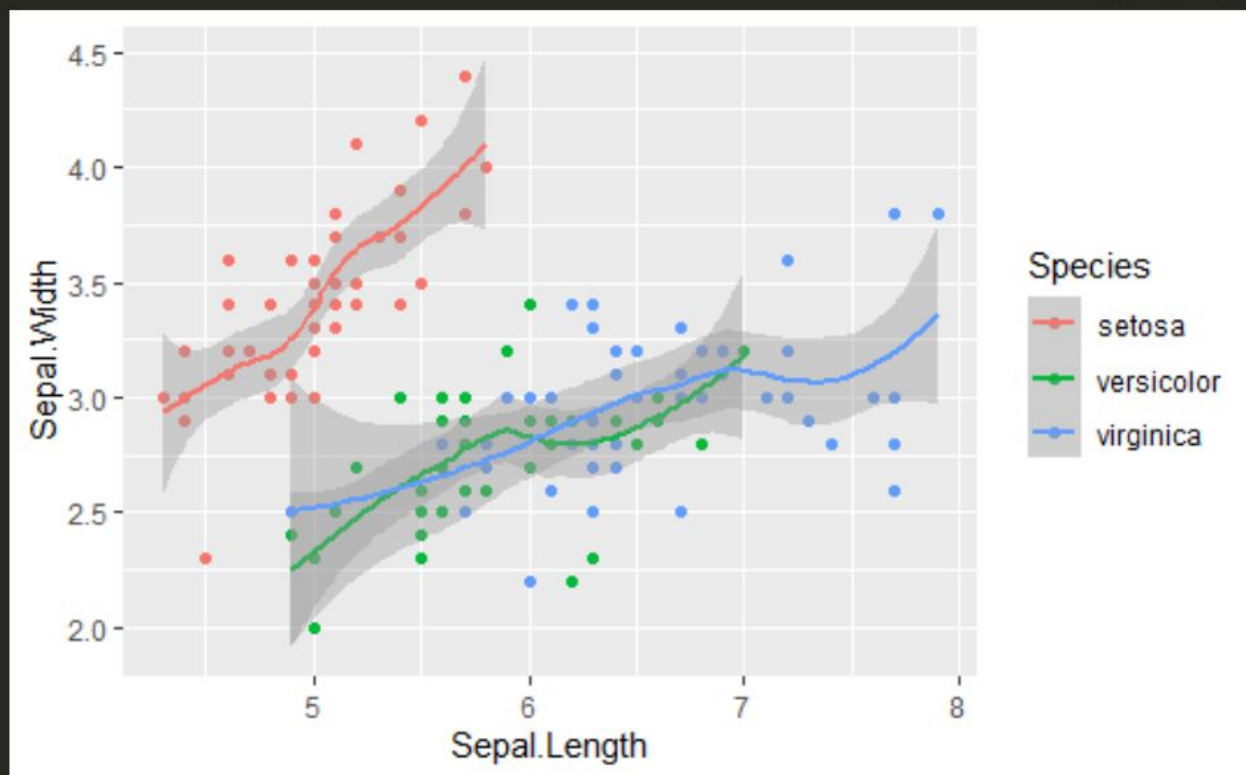
Here, I demonstrate the package called "tableone" that helps make descriptive statistics tables.

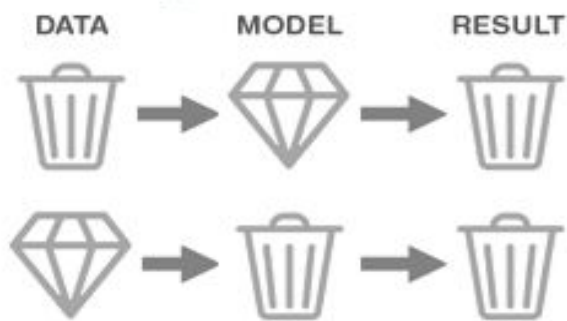
```
```{r}
t1 <- tableone::CreateTableOne(data = data)
table <- print(t1)
```
```

```
```{r}
library(tidyverse)
library(kableExtra)
kable(table, caption = "Iris Data") %>%
 kable_styling(c("bordered", "condensed"),
 latex_options = c("HOLD_position"),
 font_size = 10,
 full_width = F)
```
```

Sneak peak for next time. Ggplot is a very flexible plotting program. Here I plot sepal length by sepal width split by species.

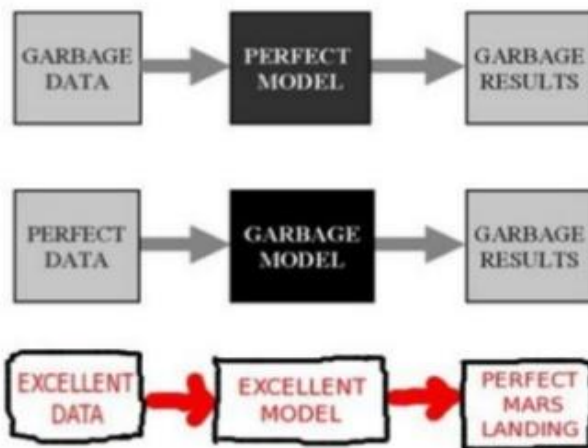
```
library(ggplot2)
ggplot(data, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) +
  geom_point() + geom_smooth()
```





MODEL CALCULATIONS

"Garbage In-garbage Out" Paradigm



*"The old
concept
of*

***Garbage in,
Garbage out
(GIGO)***

still reigns"

R Resources

- [New to R? Kickstart your learning and career with these 6 steps!](#)
- [R resources \(free courses, books, tutorials, & cheat sheets\)](#)
- [swirl teaches you R programming and data science interactively, at your own pace, and right in the R console!](#)
- [R for Psychological Science by Danielle Navarro](#)
- [R for Data Science](#)
- [Andy Field - Youtube](#)
- [Statistics of DOOM - Youtube](#)
- [StatQuest with Josh Starmer - Youtube](#)
- [3Blue1Brown - Youtube](#)
- [An Introduction to Psychological Statistics - Textbook](#)
- [Get R Done | R Tutorials - Youtube](#)
- [R for the Rest of Us](#)