

# The Simple Biostat Program

Stanley B. Pounds

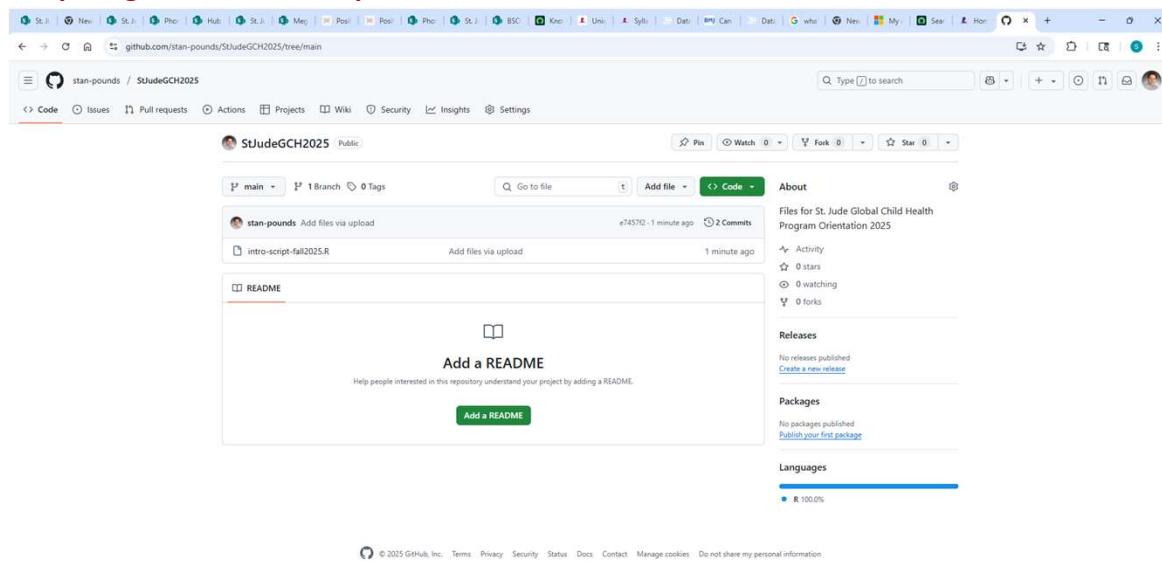
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1

<https://github.com/stan-pounds/StJudeGCH2025/>



2

**Getting Started in Each New R Session**

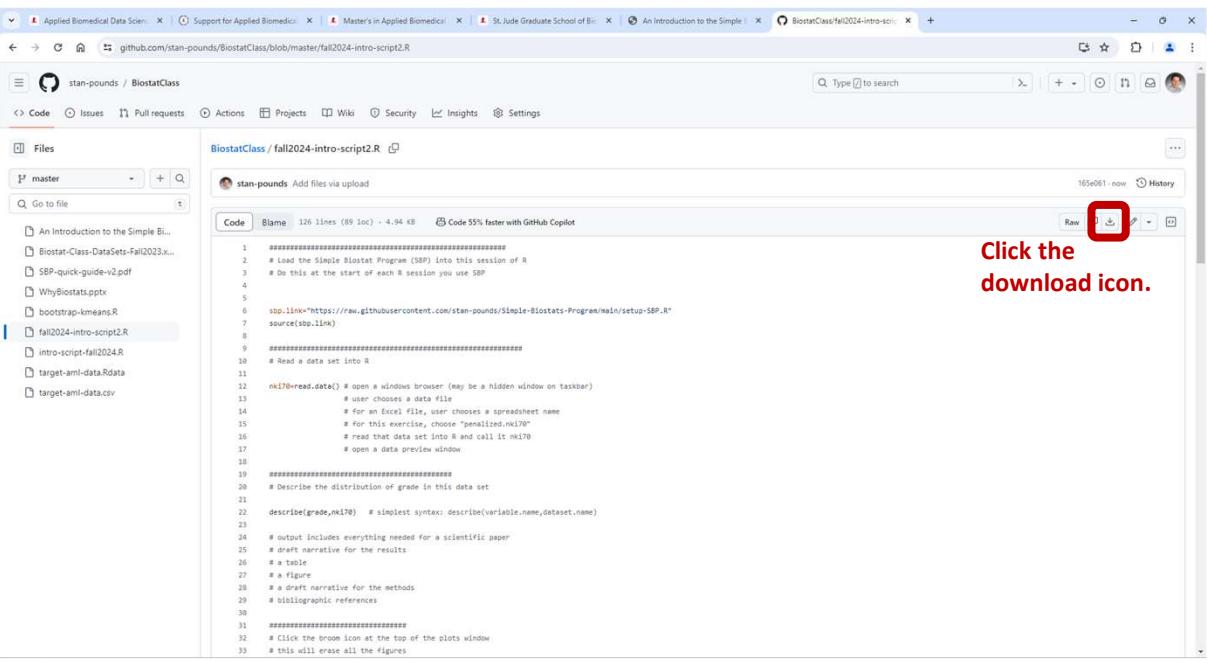
```
sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")
source(sbp.link)
```

| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i> | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)   | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
|---|---|--|--|
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)                   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> .  |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)                | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)       | <b>Common Options</b><br><i>Narrative</i> : txt = 0 (none), 1 (some), 2 ... (more)<br><i>Tables</i> : tbl = 0 (none), 1 (some), 2 ... (more)<br><i>Figures</i> : fig = 0 (none), 1 (some), 2 ... (more)<br><i>Colors</i> : clr = c("color1.name", "color2.name")<br><i>Colors</i> : clr = "palette.name"<br><i>Output Labels</i> : y.name, x.name, or grp.name = "name" |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)                 | <b>Specific Options</b><br><i>estimate</i> : null = number<br><i>correlate</i> : line = NA (no line), 0 (flat line), 1 (fitted line)  |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)                     |   |  |  |

Prepared by Stan Pounds 06/04/2024

3

<https://github.com/stan-pounds/StJudeGCH2025/blob/main/intro-script-fall2025.R>



Click the download icon.

```

#####
# Load the Simple Biostat Program (SBP) into this session of R
#
# Do this at the start of each R session you use SBP
#
# sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R"
# source(sbp.link)

#####
# Read a data set into R
#
# nk170=read.csv() # open a windows browser (may be a hidden window on taskbar)
# user chooses a data file
# for an Excel file, user chooses a spreadsheet name
# For this exercise, choose "penalized.nk170"
# read that data set into R and call it nk170
# open a data preview window

#####
# Describe the distribution of grade in this data set
#
# describe(grade,nk170) # simplest syntax: describe(variable.name,dataset.name)

#####
# output includes everything needed for a scientific paper
# draft narrative for the results
# a table
# a figure
# a draft narrative for the methods
# bibliographic references
#
#####

# Click the broom icon at the top of the plots window
# this will erase all the figures

```

4

## R Studio: intro-script-fall2025.R

The screenshot shows the R Studio interface. On the left, the code editor displays the R script 'intro-script-fall2025.R'. The script contains several comments explaining R's hashtag syntax and how to source external code. It also includes sections for descriptive statistics, population parameter estimation, comparing variables across groups, correlation analysis, and fitting predictive models. On the right, the 'Console' tab shows the output of running the script, which includes loading a dataset named 'my.data' from a local file and performing some basic operations like dev.off() and null device.

```

# The hashtag # in R
# The hashtag tells R "Ignore this comment written for humans."
# If a line starts with a hashtag, R ignores the entire line.
# R also ignores everything to the right of a hashtag in the middle of a line.
# Use hashtags to tell humans (including yourself) what you're trying to do.

# R tries to do everything it is told on lines with no hashtag.
# R also tries to do everything it is told on a line to the left of a hashtag.
# Source the SBP code into R
# In EACH R session, this must be done BEFORE using SBP
sbp.link<-https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R
source(sbp.link)

# Be sure to have the utils package for the download and choose.dir functions
get.package("utils")

# if this doesn't work, it means source(sbp.link) didn't work
# double-check the WiFi connection and try these two sections again

# use R to download the Excel file with example data sets
local.dir<-choose.dir() # choose the directory where you want to save the example data set

```

5

| <b>Getting Started in Each New R Session</b>   |   |  |  |
|--|---|--|--|
| <pre>sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R") source(sbp.link)</pre> |   |  |  |
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i>                                  | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)   | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)  | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> .  |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)   | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)  | <b>Common Options</b><br>Narrative: txt = 0 (none), 1 (some), 2 ... (more)<br>Tables: tbl = 0 (none), 1 (some), 2 ... (more)<br>Figures: fig = 0 (none), 1 (some), 2 ... (more)<br>Colors: clr = c("color1.name", "color2.name")<br>Colors: clr = "palette.name"<br>Output Labels: y.name, x.name, or grp.name = "name" |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)  |   |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)  | <b>Specific Options</b><br>estimate: null = number<br>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)  |  |  |

Prepared by Stan Pounds 06/04/2024

6

**Highlight lines 19-20 and click Run**

The screenshot shows the RStudio interface. The left pane is a script editor containing R code. The right pane is a console window showing the execution of R commands. A red box highlights the 'Run' button in the top toolbar of the script editor, and another red box highlights the command `source(sbp.link)` in the script editor.

```
R intro-script-fall2025.R
intro-script-fall2025.R
Source on Save | Replace | All
Grade Next Prev All Treatment Replace All
In selection Match case Whole word Regular Wrap
1 #####
2 # The hashtag # in R
3 # The hashtag tells R "Ignore this comment written for humans."
4 # If a line starts with a hashtag, R ignores the entire line.
5 # R also ignores everything to the right of a hashtag in the middle of a line.
6 # Use hashtags to tell humans (including yourself) what you're trying to do.
7
8 # R tries to do everything it is told on lines with no hashtag.
9 # R also tries to do everything it is told on a line to the left of a hashtag.
10
11
12
13
14
15 #####
16 # Source the SBP code Into R
17 # To EXECUTE this must be done BEFORE using .com
18 sbp.link<-https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup
19 source(sbp.link)
20
21
22
23
24 #####
25 # Be sure to have the utils packFD0 for the download and choose.dir functions
26
27 get.package("utils")
28
29 # if this doesn't work, it means source(sbp.link) didn't work
30 # double-check the WiFi connection and try these two sections again
31
32
33
34 #####
35 # use R to download the Excel File with example data sets
36
37 local dir<-choose.dir() # choose the directory where you want to save the example data set
38
39
191 [Untitled] R Script
```

```
R-4.4.0 C:\Users\spounds\Box\Biostat-Teaching\Intro-Biostat\fall2025\GCH Orientation>
my.data=read.xlsx("C:/Users/spounds/Box/Biostat-Teaching/Intro-Biostats/Fall2025/GCH
Orientation/coagulation_data_clean.xlsx")
> dev.off()
null device
1
> |
```

Files Plots Packages Help Viewer Presentation

7

**It will produce some messages: SBP is ready.**

The screenshot shows the RStudio interface. The left pane displays an R script named "intro-script-fall2025.R". The right pane shows the R console output.

```
1 #####  
2 # The following line tells R "ignore this comment written for humans."  
3 # If a line starts with a hashtag, R ignores the entire line.  
4 # R also ignores everything to the right of a hashtag in the middle of a line.  
5 # use hashtags to tell humans (including yourself) what you're trying to do.  
6  
7 # R tries to do everything it is told on lines with no hashtag.  
8 # R also tries to do everything it is told on a line to the left of a hashtag.  
9  
10#####  
11  
12  
13  
14  
15#####  
16 # Source the SBP code into R  
17 # In EACH R session, this must be done BEFORE using SBP  
18  
19 sbp.link<-https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup  
20 source(sbp.link)  
21  
22  
23  
24#####  
25 # Be sure to have the utils package for the download and choose.dir functions  
26  
27 get.package("utils")  
28  
29 # if this doesn't work, it means source(sbp.link) didn't work  
30 # double-check the WiFi connection and try these two sections again  
31  
32  
33  
34#####  
35 # use R to download the Excel File with example data sets  
36  
37 local directory # choose the directory where you want to save the example data set  
38  
181 (Untitled) R Script
```

Console output:

```
R 4.4.0 C:/Users/Spounds/Box/Biostat-Teaching/intro-Biostats/Fall2025/GCH Orientation/  
heart  
welcome to penalized. For extended examples, see vignette("penalized").  
data.table 1.15.4 using 18 threads (see ?getDTthreads). Latest news: r-data.table.com  
Attaching package: 'data.table'  
The following object is masked from 'package:DescTools':  
%like%  
riskRegression version 2023.12.21  
Warning message:  
package 'survival' was built under R version 4.4.1
```

8

<https://bmjopen.bmj.com/content/6/12/e012850>

The screenshot shows a web browser displaying a BMJ Open article. The URL in the address bar is <https://bmjopen.bmj.com/content/6/12/e012850>. The page is titled "Intensive care Research" and features the article "Can recombinant human thrombomodulin increase survival among patients with severe septic-induced disseminated intravascular coagulation: a single-centre, open-label, randomised controlled trial". The authors listed are Akiyoshi Hagiwara, Noriko Tanaka, Tatsuki Uemura, Wataru Matsuda, and Akio Kimura. The abstract discusses the objective of determining whether treatment with recombinant human thrombomodulin (rhTM) increases survival among patients with severe septic-induced disseminated intravascular coagulation (DIC). The design is a single-centre, open-label, randomised controlled trial. The setting is a single tertiary hospital. The participant count is 92 patients with severe septic-induced DIC. The intervention involves rhTM treatment. The results show that the treatment group had significantly lower D-dimer levels and faster DIC recovery compared to the control group. The conclusion is that rhTM treatment decreased D-dimer levels and facilitated DIC recovery in severe septic patients with sepsis-induced DIC. However, the treatment did not improve survival in this cohort.

9

<https://zenodo.org/records/5023900>

The screenshot shows a web browser displaying a Zenodo record page for the same study. The URL in the address bar is <https://zenodo.org/records/5023900>. The page includes the title, authors, and abstract from the BMJ Open article. It also provides detailed metadata such as the publication date (November 23, 2016), version (v1), and download statistics (124 views, 6 downloads). The page lists external resources (Indexed in OpenAIRE), communities (Dryad), and keywords (C-reactive protein, recombinant human thrombomodulin).

10

<https://zenodo.org/records/5023900>

The screenshot shows a Zenodo record page. At the top, there's a navigation bar with various links. Below it is a 'Notes' section containing a detailed description of the data. To the right, there are sections for 'Communities' (Dryad), 'Keywords and subjects' (C-reactive protein, recombinant human thrombomodulin, D-dimer, disseminated intravascular coagulation, sepsis), 'Details' (DOI: 10.5061/zenodo.5023900), 'Resource type' (Dataset), 'Publisher' (Zenodo), 'Rights', 'License' (Creative Commons Zero v1.0 Universal), and 'Citation' (Hagawa et al., 2016). The main area shows the file 'coagulation\_data\_clean\_R Open data.xlsx' with a size of 138.8 kB.

11

[coagulation\\_data\\_clean\\_R Open data.xlsx](#)

The screenshot shows an Excel spreadsheet titled 'coagulation\_data\_clean\_R Open data.xlsx'. The data is organized into several columns representing different variables such as Study ID, Treatment, Death at day 28, Nonsurvival within 90 days, Time, Cancer, rINR, FDP0, FDP1, deltaFDP01, deltaFDP02, deltaFDP03, FDP5, FDP7, FDP10, deltaFDP07, deltaFDP00, Ddimer0, Ddimer1, and deltaD01. The data spans from row 1 to row 35, with many cells containing 'NA' or '###'.

12

<https://zenodo.org/records/5023900>

Notes

```
rHTM open data
rHTM, recombinant human thrombomodulin; FDP, fibrin/fibrinogen degradation products; FDP0, FDP value at day 0 delta; Relative change rate from baseline =
fibrin/fibrinogen degradation products at day 0 relative to baseline; data.FDP1, FDP1 value at day 1; PCT, prothrombin clotting time; PCT, partial thromboplastin time; ATIII, antithrombin III; TM, thrombomodulin value; SIRS, Systemic inflammatory response syndrome; SOFA, sequential organ failure assessment score; SOFA PF, SOFA respiratory score; SOFA RL, SOFA coagulation score; SOFA bil, SOFA hepatic dysfunction score; SOFA CV, SOFA cardiovascular system score; SOFA GCS, SOFA Glasgow Coma Scale score; SOFA Cr, SOFA renal dysfunction score
coagulation_data_clean_R_Open data.xlsx
```

Files

| Name                                    | Size     | Action                   |
|---|----------|--------------------------|
| coagulation_data_clean_R_Open data.xlsx | 138.8 kB | <a href="#">Download</a> |

Additional details

Related works Is cited by 10.1136/bmopen-2016-012850 (DOI)

Citations 0

Show only: Literature (0) Dataset (0) Software (0) Unknown (0) Citations To This Version Search for citation Search

No citations found

Communities Dryad

Keywords and subjects C-reactive protein | recombinant human thrombomodulin | D-dimer | disseminated intravascular coagulation | sepsis |

Details

DOI DOI: 10.5061/zenodo.2664

Resource type Dataset

Publisher Zenodo

Rights

License Creative Commons Zero v1.0 Universal

Citation

Hagawa, A., Tanaka, N., Uemura, T., Watanu, M., & Kimura, A. (2016). Data from: Can recombinant human thrombomodulin increase survival among patients with severe septic-induced disseminated intravascular coagulation: a single-centre, open-label, randomised controlled trial [Data set]. Zenodo.

13

### Getting Started in Each New R Session

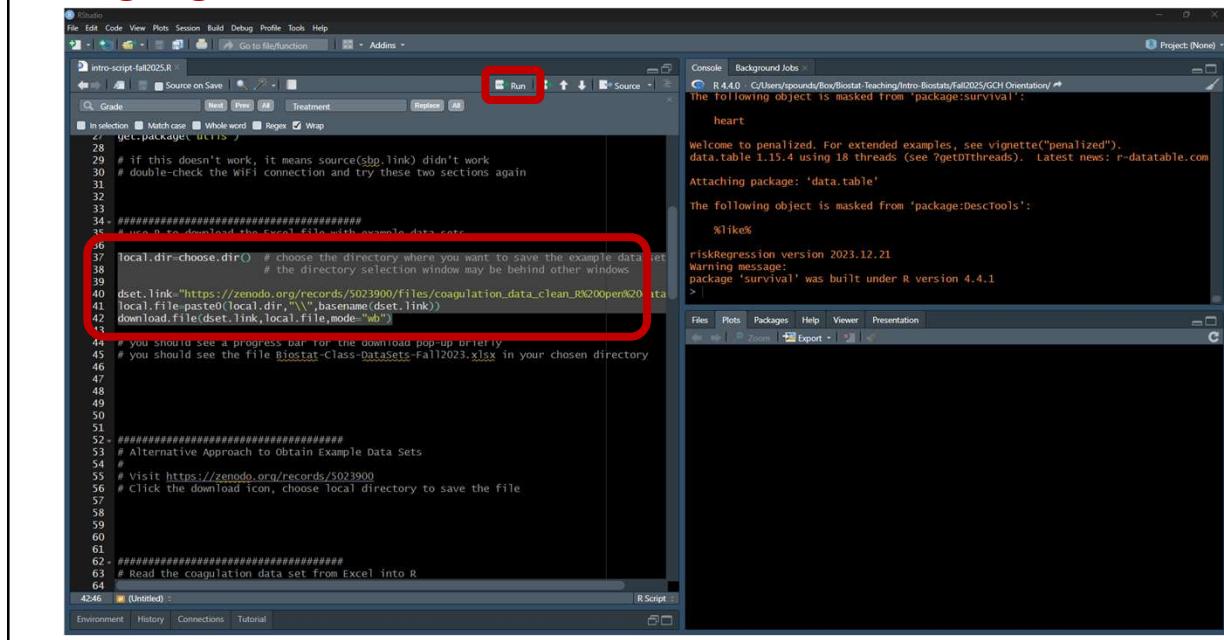
`sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")  
source(sbp.link)`

|  |  |   |   |
|--|--|---|---|
| <b>Read and name data</b><br><code>data.name = read.data()</code><br><i># Choose file in pop-up window</i> | <b>Preview data</b><br><code>View(data.name)</code><br><code>colnames(data.name)</code>                                    | <b>General Syntax</b><br><code>result = function(info1, info2, ...)</code><br><i># user chooses result name</i> | <b>Color Name Legend</b><br><code>show.colors()</code><br><code>show.palettes(number)</code>  |
| <b>Descriptive Stats &amp; Graphs</b><br><code>describe("column.name", data.name)</code>                   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> . | <b>Copy Tabular Result to Word</b><br><code>word.table(result.name)</code>                                      | <b>Common Options</b><br><i>Narrative: txt = 0 (none), 1 (some), 2 ... (more)</i><br><i>Tables: tbl = 0 (none), 1 (some), 2 ... (more)</i><br><i>Figures: fig = 0 (none), 1 (some), 2 ... (more)</i><br><i>Colors: clr = c("color1.name", "color2.name")</i><br><i>Colors: clr = "palette.name"</i><br><i>Output Labels: y.name, x.name, or grp.name = "name"</i> |
| <b>Estimate One Population Parameter</b><br><code>estimate("column.name", data.name)</code>                |  |   | <b>Specific Options</b><br><code>estimate: null = number</code><br><code>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)</code>  |
| <b>Compare a Variable across Groups</b><br><code>compare(variable.name~group.name, data.name)</code>       |  |   |   |
| <b>Correlate Two Numeric Variables</b><br><code>correlate(y.name~x.name, data.name)</code>                 |  |   |   |
| <b>Fit a Predictive Model</b><br><code>model(y.name~x1.name+x2.name, data.name)</code>                     |  |   |   |

Prepared by Stan Pounds 06/04/2024

14

## Highlight lines 37-42 and click run.



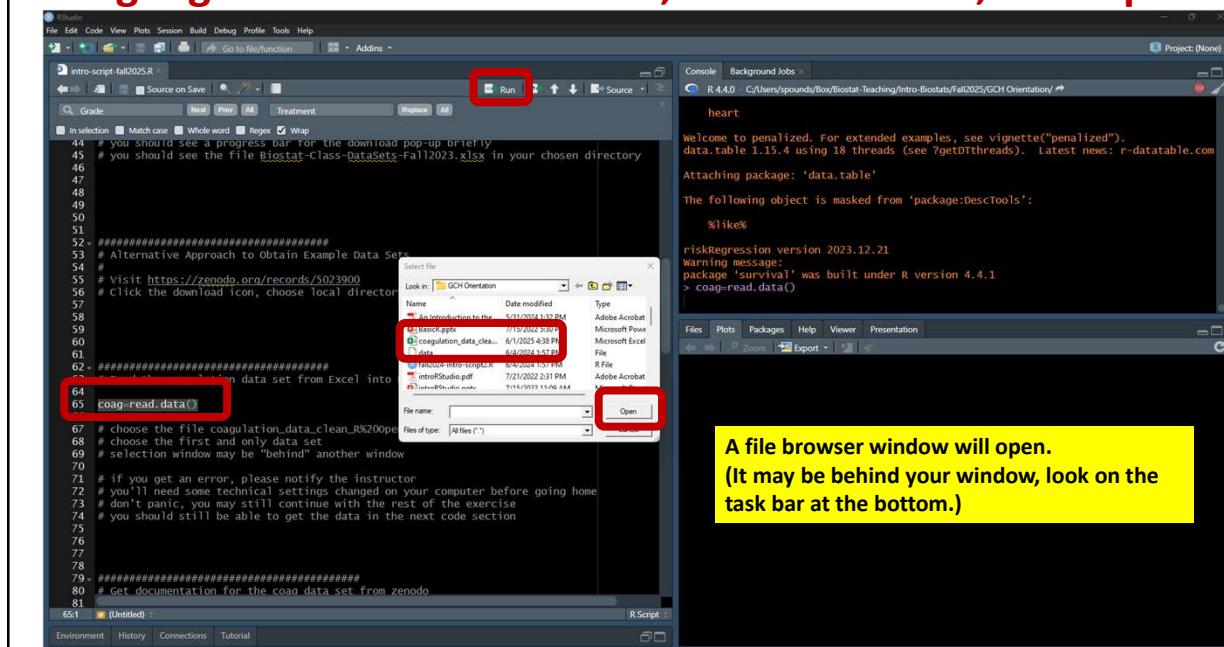
```

File Edit Code View Plots Session Build Debug Profile Tools Help
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function Addins
Grade Next Prev All Treatment Replace All
In selection Match case Whole word Wrap
27 # get package, let's do it
28
29 # if this doesn't work, it means source(sbp.link) didn't work
30 # double-check the WiFi connection and try these two sections again
31
32
33
34 ##### To download the excel file with example data sets
35
36 local.dir<-choose.dir() # choose the directory where you want to save the example data set
37 # the directory selection window may be behind other windows
38
39
40 dset.link<-"https://zenodo.org/records/5023900/files/coagulation_data_clean_R0200open0202.xlsx"
41 local.file<-paste0(local.dir,"\\",basename(dset.link))
42 download.file(dset.link,local.file,mode="wb")
43
44 # you should see a progress bar for the download pop-up briefly
45 # you should see the file Biostat-Class-Datasets-Fall12023.xlsx in your chosen directory
46
47
48
49
50
51
52 #####
53 # Alternative Approach to Obtain Example Data Sets
54
55 # Visit https://zenodo.org/records/5023900
56 # Click the download icon, choose local directory to save the file
57
58
59
60
61
62 #####
63 # Read the coagulation data set from Excel into R
64

```

15

## Highlight line 65 and click run, choose the file, click open.



```

File Edit Code View Plots Session Build Debug Profile Tools Help
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function Addins
Grade Next Prev All Treatment Replace All
In selection Match case Whole word Wrap
44 # you should see a progress bar for the download pop-up briefly
45 # you should see the file Biostat-Class-Datasets-Fall12023.xlsx in your chosen directory
46
47
48
49
50
51
52 #####
53 # Alternative Approach to Obtain Example Data Sets
54
55 # visit https://zenodo.org/records/5023900
56 # click the download icon, choose Local director
57
58
59
60
61
62 #####
63 # Read the coagulation data set from Excel into R
64
65 coag<-read.xlsx()
66
67 # choose the file coagulation_data_clean_R0200open0202.xlsx
68 # choose the first and only data set
69 # selection window may be "behind" another window
70
71 # if you get an error, please notify the instructor
72 # you'll need some technical settings changed on your computer before going home
73 # don't panic, you may still continue with the rest of the exercise
74 # you should still be able to get the data in the next code section
75
76
77
78
79 #####
80 # Get documentation for the coag data set from zenodo
81

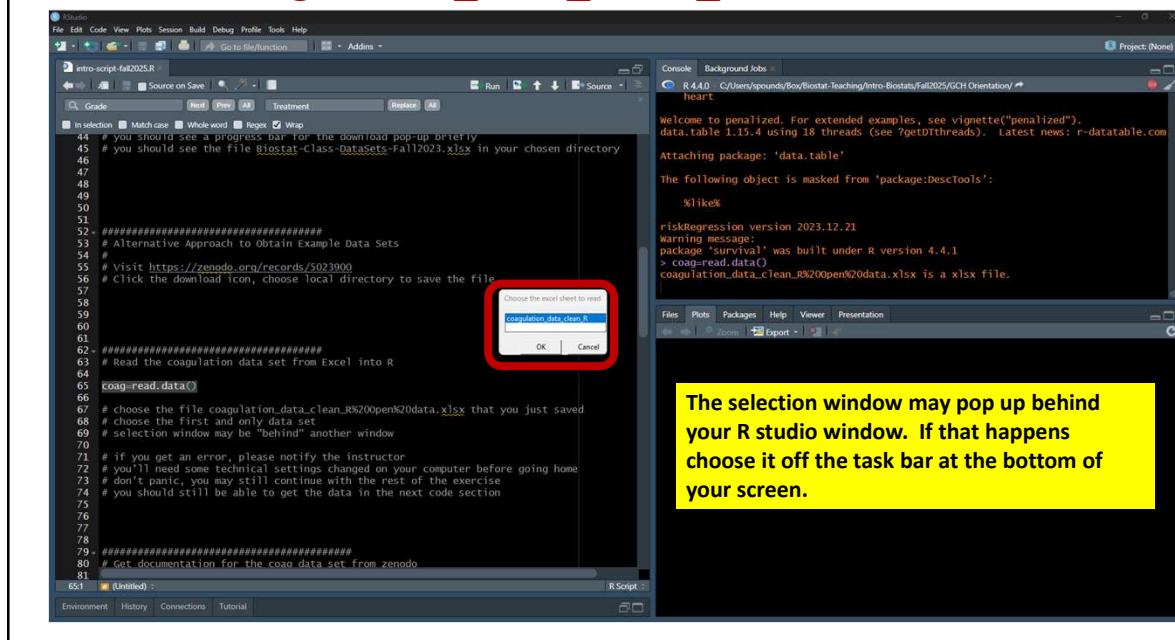
```

A file browser window will open.  
(It may be behind your window, look on the task bar at the bottom.)

16

## Choose coagulation\_data\_clean\_R.

Click OK.



17

The data has been read into R. Check that it matches Excel data.

| Study ID | Treatment rHTM (T) Control ? | Death = 1 Alive = 0 28 day | NonSurvive within 28 Day Time | Death = 1 Alive = 0 90 day C |
|----------|------------------------------|----------------------------|-------------------------------|------------------------------|
| 1        | C                            | 0                          | 28                            |                              |
| 2        | C                            | 0                          | 28                            |                              |
| 3        | C                            | 0                          | 28                            |                              |
| 4        | C                            | 0                          | 28                            |                              |
| 5        | C                            | 0                          | 28                            |                              |
| 6        | C                            | 0                          | 28                            |                              |
| 7        | C                            | 0                          | 28                            |                              |
| 8        | C                            | 0                          | 28                            |                              |
| 9        | C                            | 0                          | 28                            |                              |
| 10       | C                            | 0                          | 28                            |                              |
| 11       | C                            | 0                          | 28                            |                              |
| 12       | C                            | 0                          | 28                            |                              |
| 13       | C                            | 1                          | 1                             |                              |
| 14       | C                            | 0                          | 28                            |                              |
| 15       | C                            | 0                          | 28                            |                              |
| 16       | C                            | 0                          | 28                            |                              |
| 17       | C                            | 0                          | 28                            |                              |
| 18       | C                            | 0                          | 28                            |                              |
| 19       | C                            | 0                          | 28                            |                              |
| 20       | C                            | 1                          | 16                            |                              |
| 21       | C                            | 0                          | 28                            |                              |
| 22       | C                            | 0                          | 28                            |                              |
| 23       | C                            | 0                          | 28                            |                              |
| 24       | C                            | 0                          | 28                            |                              |
| 25       | C                            | 0                          | 28                            |                              |
| 26       | C                            | 1                          | 3                             |                              |

18

The data has been read into R. Check that it matches Excel data.

This screenshot shows two windows side-by-side. The left window is RStudio with the console tab active, displaying R code and its output. The right window is Microsoft Excel showing a large dataset. Both windows show identical data, indicating that the R code successfully read the Excel file.

19

Scroll to the bottom in each view.

This screenshot shows the same setup as the previous one, but both the RStudio console and the Excel spreadsheet are scrolled all the way down to the bottom of the data. This demonstrates that the entire dataset has been read and displayed correctly.

20

10

**Go to the right in each view.**

The screenshot shows the RStudio interface with several windows open:

- Code Editor:** Displays the R script `intro-script-fall2025.R`. A red box highlights the command `library(survival)`.
- Console:** Shows the output of the `library(survival)` command.
- Output:** Displays the results of the `survfit` function, including the survival probability over time for different treatment groups.
- Plots:** Shows a Kaplan-Meier survival plot with time on the x-axis and probability on the y-axis, comparing Treatment (T) and Control (C).
- Packages:** Lists the installed packages: survival, dplyr, ggplot2, and lubridate.
- Help:** Provides information on the `survfit` function.
- File Explorer:** Shows the file structure, including the `coagulation_data_clean.RData` file.

21

**Check that the data matches.**

22

**Getting Started in Each New R Session**

```
sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")
source(sbp.link)
```

| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i>   | <b>Preview data</b><br>View(data.name)<br>colnames(data.name) | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
|---|---|--|--|
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)   |   |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)  |   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)   |   |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)   |   |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)   |   |  |  |
| <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> .  |   |  |  |
| <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |   |  |  |
| <b>Common Options</b><br><i>Narrative</i> : txt = 0 (none), 1 (some), 2 ... (more)<br><i>Tables</i> : tbl = 0 (none), 1 (some), 2 ... (more)<br><i>Figures</i> : fig = 0 (none), 1 (some), 2 ... (more)<br><i>Colors</i> : clr = c("color1.name", "color2.name")<br><i>Colors</i> : clr = "palette.name"<br><i>Output Labels</i> : y.name, x.name, or grp.name = "name" |   |  |  |
| <b>Specific Options</b><br><i>estimate</i> : null = number<br><i>correlate</i> : line = NA (no line), 0 (flat line), 1 (fitted line)  |   |  |  |

Prepared by Stan Pounds 06/04/2024

23

**Click on the script window. Highlight and run line 89.**

The screenshot shows the RStudio interface. The left pane displays an R script named 'intro-script-fall2025.R'. Line 89 is highlighted with a red box and has the word '# default' at its end. The right pane shows the 'Console' tab with the output of the script execution. The 'Run' button in the toolbar above the script window is also highlighted with a red box.

```

67 # choose the file coagulation_data_clean_R%20open%20data.xlsx that you just saved
68 # choose the first and only data set
69 # selection window may be "behind" another window
70
71 # if you get an error, please notify the instructor
72 # you'll need some technical settings changed on your computer before going home.
73 # don't panic, you may still continue with the rest of the exercise
74 # you should still be able to get the data in the next code section
75
76
77
78
79 #####
80 # Get documentation for the coag data set from zenodo
81 # view https://zenodo.org/records/5023900
82
83
84
85
86 #####
87
88 describe(FDPO,coag) # default
89
90 describe(FDPO,coag,fig=3) # even more figures
91 describe(FDPO,coag,fig=2,clr="skyblue") # figures with skyblue color
92
93
94 # requires EXACT spelling and capitalization of data set and column name
95 # data set name: coag; column name: FDPO
96 # must use quotes for column name; must match name in R exactly
97
98
99
100
101
102 #####

```

24

## Error: figure margins too large.

The screenshot shows the RStudio interface with the following details:

- File Menu:** File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help.
- Project:** Project: (None)
- Script Editor:** intro-script-fall2025.R (Untitled) - This file contains R code for data cleaning and visualization. It includes comments explaining the steps, such as choosing the correct file, handling selection windows, and specifying plot colors. The code uses the 'survival' package for survival analysis and 'gridExtra' for figure arrangement.
- Console:** Shows the output of the R code. It includes the following messages:
  - Attaching package: 'robustbase'
  - The following object is masked from 'package:survival': heart
  - Welcome to penalized. For extended examples, see vignette("penalized"). data.table 1.15.4 using 18 threads (see ?getDITHreads). Latest news: r-data.table.com
  - Attaching package: 'data.table'
  - The following object is masked from 'package:DescTools': %like%
  - riskRegression version 2023.12.21
  - warning message: package 'survival' was built under R version 4.4.1
  - > coag<-read.data()
  - coagulation\_data\_clean\_R%20open%20data.xlsx is a xlsx file.
  - Successfully read sheet 1 of coagulation\_data\_clean\_R%20open%20data.xlsx.
  - Next time you may use the following R code:
  - my.data<-read.data("C:/users/spounds/Box/Biostat-Teaching/Intro-Biostats/Fall2025/GH orientation/coagulation\_data\_clean\_ic%20open%20data.xlsx")
- Message Bar:** Error in plot.new() : figure margins too large (highlighted with a red box).
- Bottom Navigation:** Files, Plots, Packages, Help, Viewer, Presentation, Zoom, Export, Publish.

25

**Enlarge the “Plots” window and try again.**

The screenshot shows the RStudio interface with two main panes: a script editor on the left and a console on the right.

**Script Editor (Left):**

```
intro-script-fall2025.R
dset
Grade Next Prev All Treatment Replace All
Source on Save Run Source + Source
in selection Match case Whole word Regex Wrap
66
67 # choose the file coagulation_data_clean_R820open%20data.xlsx that you just saved
68 # choose the first and only data set
69 # selection window may be "behind" another window
70
71 # if you get an error, please notify the instructor
72 # you'll need some technical settings changed on your computer before going home
73 # don't panic, you may still continue with the rest of the exercise
74 # you should still be able to get the data in the next code section
75
76
77
78 #####
80 # Get documentation for the coag data set from zenodo
81 # View https://zenodo.org/records/5023900
82
83
84
85
86 #####
87 # Descriptive stats, Figures, and narrative for baseline FDP
88
89 describe(F900,coag) # default
90 describe(F900,coag,fig=2) # more figures
91 describe(F900,coag,fig=3) # even more Figures
92 describe(F900,coag,fig=2,clr="skyblue") # Figures with skyblue color
93
94 # requires EXACT spelling and capitalization of data set and column name
95 # data set name: coag; column name: FDPO
96 # must use quotes for column name; must match name in R exactly
97
98
99
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108
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172
173
174
175
176
177
178
179 #####
180 # Get documentation for the coag data set from zenodo
181 # View https://zenodo.org/records/5023900
182
183
184
185
186 #####
187 # Descriptive stats, Figures, and narrative for baseline FDP
188
189 describe(F900,coag) # default
190 describe(F900,coag,fig=2) # more figures
191 describe(F900,coag,fig=3) # even more Figures
192 describe(F900,coag,fig=2,clr="skyblue") # Figures with skyblue color
193
194 # requires EXACT spelling and capitalization of data set and column name
195 # data set name: coag; column name: FDPO
196 # must use quotes for column name; must match name in R exactly
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244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
259 (Untitled)
```

**Console (Right):**

```
R 4.4.0 C:\Users\spounds\Box\Biostat-Teaching\Intro-Biostats\Fall2025/GCH Orientation/
```

Output:

```
> sdp.link<-“https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R”
> source(sdp.link)

Attaching package: ‘robustbase’

The following object is masked from ‘package:survival’:

heart

Welcome to penalized. For extended examples, see vignette(“penalized”).
data.table 1.15.4 using 18 threads (see ?getDTthreads). Latest news: r-data.table.com

Attaching package: ‘data.table’

The following object is masked from ‘package:DescTools’:

xlike%
```

Warning message:

```
package ‘survival’ was built under R version 4.4.1
```

```
> coag=read.data()
coagulation_data_clean_R820open%20data.xlsx is a xlsx file.
Success! Your sheet 1 of coagulation_data_clean_R820open%20data.xlsx.
Next time you may use the following R code:
my.data.read.data("C:/users/spounds/Box/Biostat-Teaching/Intro-Biostats/Fall2025/GCH Orientation/coagulation_data_clean_R820open%20data.xlsx")
> describe(FDPO,coag) # default
```

Error in plot.new() : figure margins too large

Red arrows point from the error message "Error in plot.new() : figure margins too large" in the console back to the corresponding code in the script editor.

26

The screenshot shows the RStudio interface. On the left, the code editor displays a script named 'intro-script-fall2025.R' containing R code for data analysis and visualization. On the right, the 'Console' window shows the output of the R session, including statistical results from the Shapiro-Wilk test and a box plot for the 'FDP0' variable.

```

R4.4.0 C:\Users\spounds\Box\Biostat\Teaching\Intro-Biostat\Fall2025/GCH Orientation/
1.088031e+02   3.440000e+01   2.305000e+01   7.080000e+01
minimum          maximum normality.pvalue
2.900000e+00   6.992000e+02   1.029284e-15

Smethod
[1] "The Shapiro-Wilk normality test was used to evaluate the normality of the distribution of FDP0."
[2] "To determine the best statistical procedure to use for estimating the center of the population distribution of FDP0, the Shapiro-Wilk (1965) test was used to evaluate"

Files Plots Packages Help Viewer Presentation

```

**Box Plot for FDP0:**

A box plot titled 'FDP0' is displayed. The x-axis ranges from 0 to 600 with major ticks at 0, 200, 400, and 600. The y-axis has a single tick mark. The box starts at approximately 50 and ends at 150, with a median line at about 100. There are two solid black dots (outliers) located between the box and the whiskers, and three more dots located to the right of the whisker, indicating extreme outliers.

27

## Enlarge the “Console” window.

The screenshot shows the RStudio interface with a red arrow pointing to the 'Console' window and another red arrow pointing to the plot area. This visual cue is likely intended to guide the user on how to interact with or examine the results shown in the right-hand panels.

The code editor on the left shows the same 'intro-script-fall2025.R' script. The 'Console' window on the right displays the same output as the previous screenshot. A box plot for 'FDP0' is also present.

28

## Scroll Up in the “Console” window.

The screenshot shows the RStudio interface with the 'Console' tab selected. The output window has a vertical scrollbar on the right side, indicated by a red box. The console displays several lines of R code and their corresponding results. At the bottom of the output window, there is a reference section titled 'Smethod' and 'Sref' which contains a list of statistical methods and their references. Below the console is a plot window showing a scatter plot of 'FDPO' values.

```

R 4.4.0 C:\Users\spounds\Box\Stat\Teaching\Intro Biostat\Intro Biostat\Fall2025/GCH Orientation
1.088031e+02 3.440000e+01 2.305000e+01 7.080000e+01
minimum maximum normality-pvalue
2.900000e+00 6.992000e+02 1.029284e-15

Smethod
[1] "The Shapiro-Wilk normality test was used to evaluate the normality of the distribution of FDPO."
[2] "To determine the best statistical procedure to use for estimating the center of the population distribution of FDPO, the Shapiro-Wilk (1965) test was used to evaluate the normality of FDPO and the Cabilio-Masaro (1996) test was used to evaluate the symmetry of FDPO."
[3] "Based on these evaluations, the sign test was used to estimate a confidence interval for the population median of FDPO."

Sref
[1] "Peter J. Rousseauw (1984), Least Median of Squares Regression. Journal of the American Statistical Association 79, 871-881."
[2] "Shapiro, S. S.; Wilk, M. B. (1965). "An analysis of variance test for normality (complete samples)". Biometrika. 52 (3-4): 591-611. doi:10.1093/biomet/52.3-4.591. JSTOR 233709. MR 0205384."
[3] "Cabilio P., Masaro J (1996). "A simple test of symmetry about an unknown median." Canadian Journal of Statistics, 24(3), 349-361. doi: 10.2307/3315744."
[4] "Conover, W. J. (1999). "Chapter 3.4: The Sign Test", Practical Nonparametric Statistics, 3rd edn, John Wiley & Sons, New York, pp. 131-140.
```

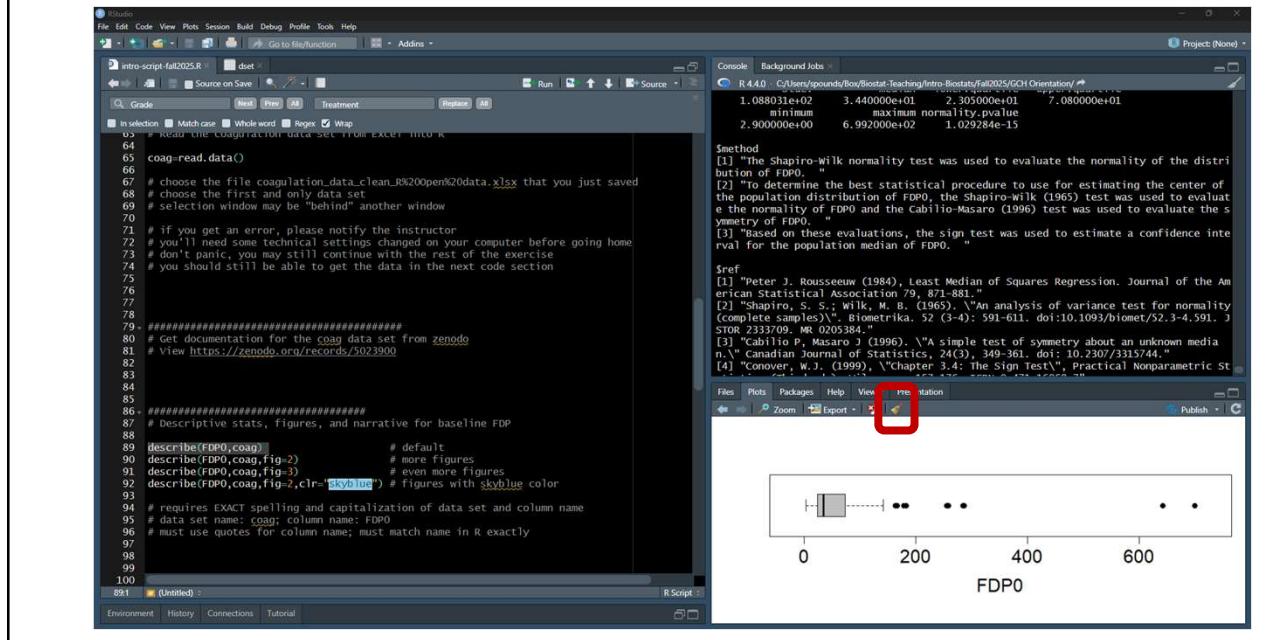
29

## See the text, methods, references. Just what you need!

This screenshot is identical to the one above, showing the RStudio interface with the 'Console' tab selected. A red box highlights the 'Smethod' and 'Sref' sections at the bottom of the console window, which provide statistical details and references. The plot window below shows a scatter plot of 'FDPO' values.

30

## Click the broom icon on the Plots window.



31

**Getting Started in Each New R Session**

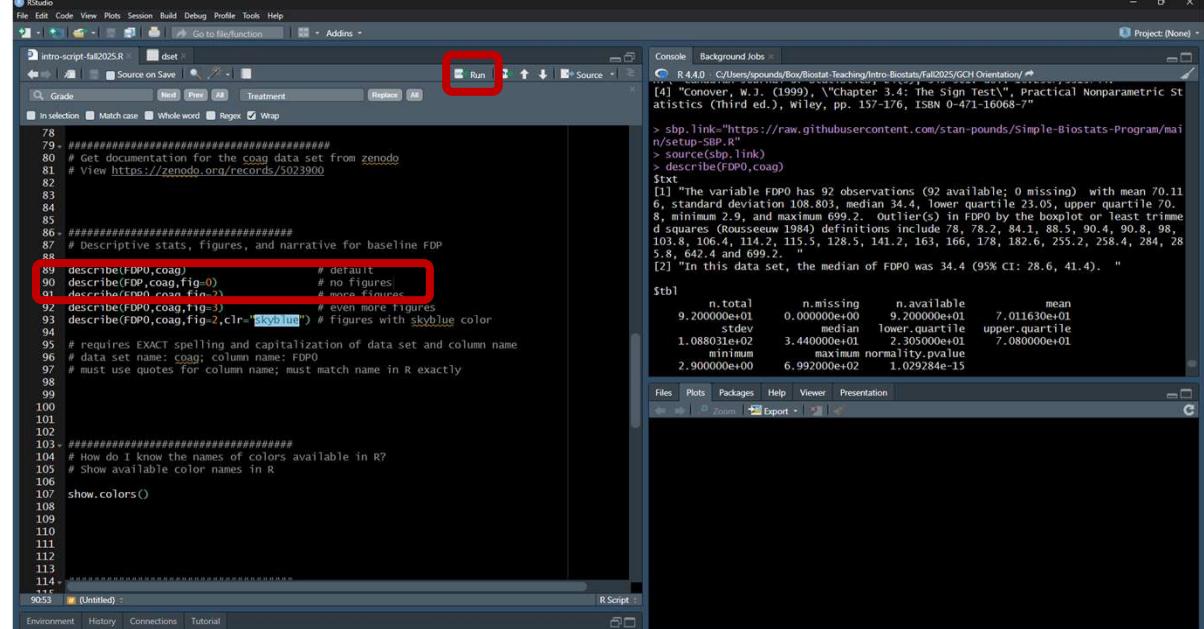
```
sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")
source(sbp.link)
```

|   |  |  |  |
|---|--|--|--|
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i> | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)  | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)                   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> .   |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)                | <b>Copy Tabular Result to Word</b><br>word.table(result.name)  |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)       | <b>Common Options</b>  |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)                 | Narrative: txt = 0 (none), 1 (some), 2 ... (more)<br>Tables: tbl = 0 (none), 1 (some), 2 ... (more)<br><b>Figures: fig = 0 (none), 1 (some), 2 ... (more)</b><br>Colors: clr = c( color1.name , color2.name )<br>Colors: clr = "palette.name"<br>Output Labels: y.name, x.name, or grp.name = "name" |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)                     | <b>Specific Options</b>  |  |  |
|   | estimate: null = number<br>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)  |  |  |

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32

## Highlight and run line 90. We get text & tables but no figure.



```

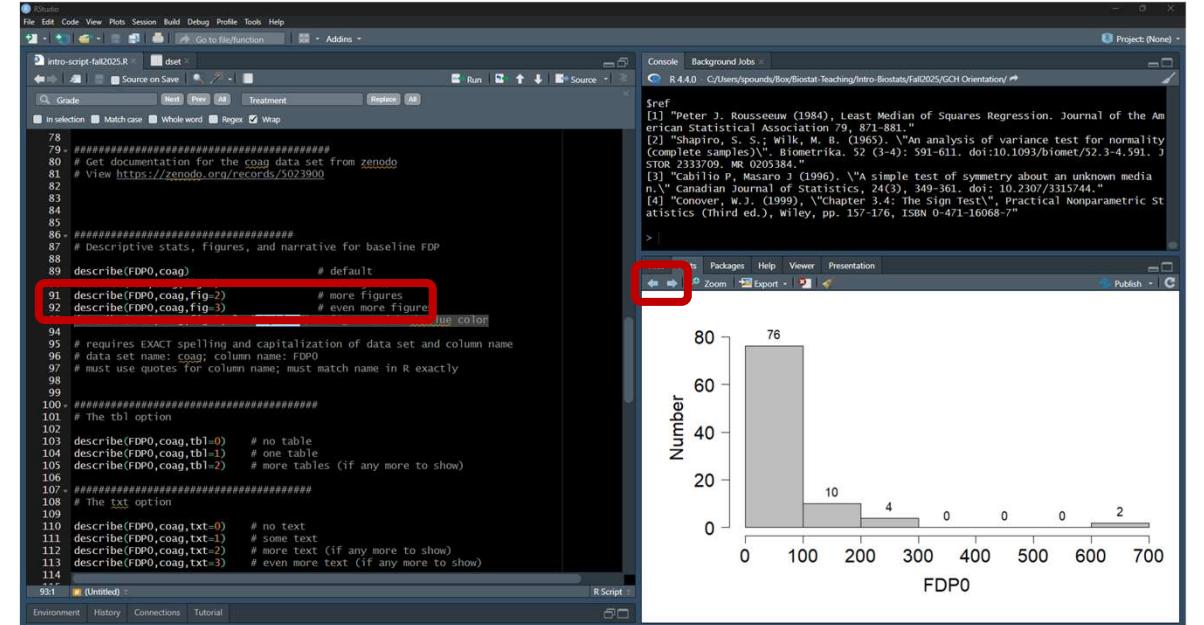
File Edit Code View Plots Session Build Debug Profile Tools Help
intro-script-fall2025.R dset Go to file/function Addins
Grade Next Prev Treatment Replace All
in selection Match case Whole word Regex Wrap
78 #####
79 # Get documentation for the coag data set from zenodo
80 # View https://zenodo.org/records/5023900
81
82
83
84
85
86 #####
87 # Descriptive stats, Figures, and narrative for baseline FDP0
88
89 describe(FDP0,coag) # default
90 describe(FDP0,coag,fig=0) # no figures
91 describe(FDP0,coag,fig=2) # more figures
92 describe(FDP0,coag,fig=3,clr="skyblue") # Figures with skyblue color
93
94
95 # requires EXACT spelling and capitalization of data set and column name
96 # data set name: coag; column name: FDP0
97 # must use quotes for column name; must match name in R exactly
98
99
100
101
102
103 #####
104 # How do I know the names of colors available in R?
105 # Show available color names in R
106 show.colors()
107
108
109
110
111
112
113
114 #####
90:32 (Untitled) R Script
Environment History Connections Tutorial

```

The R script `intro-script-fall2025.R` contains several lines of code for summarizing the `FDP0` variable. Line 90 highlights the command `describe(FDP0,coag)` which generates descriptive statistics. Line 91 highlights the command `describe(FDP0,coag,fig=2)` which generates additional figures. The RStudio interface shows the console output, which includes the summary statistics for `FDP0` and a histogram of the data. The histogram has a light gray background and a dark gray border, with the x-axis labeled 'FDP0' and the y-axis labeled 'Number'. The histogram shows a distribution with a peak at 76 and a long tail extending to the right.

33

## Highlight and run lines 91-92. We get more figures.



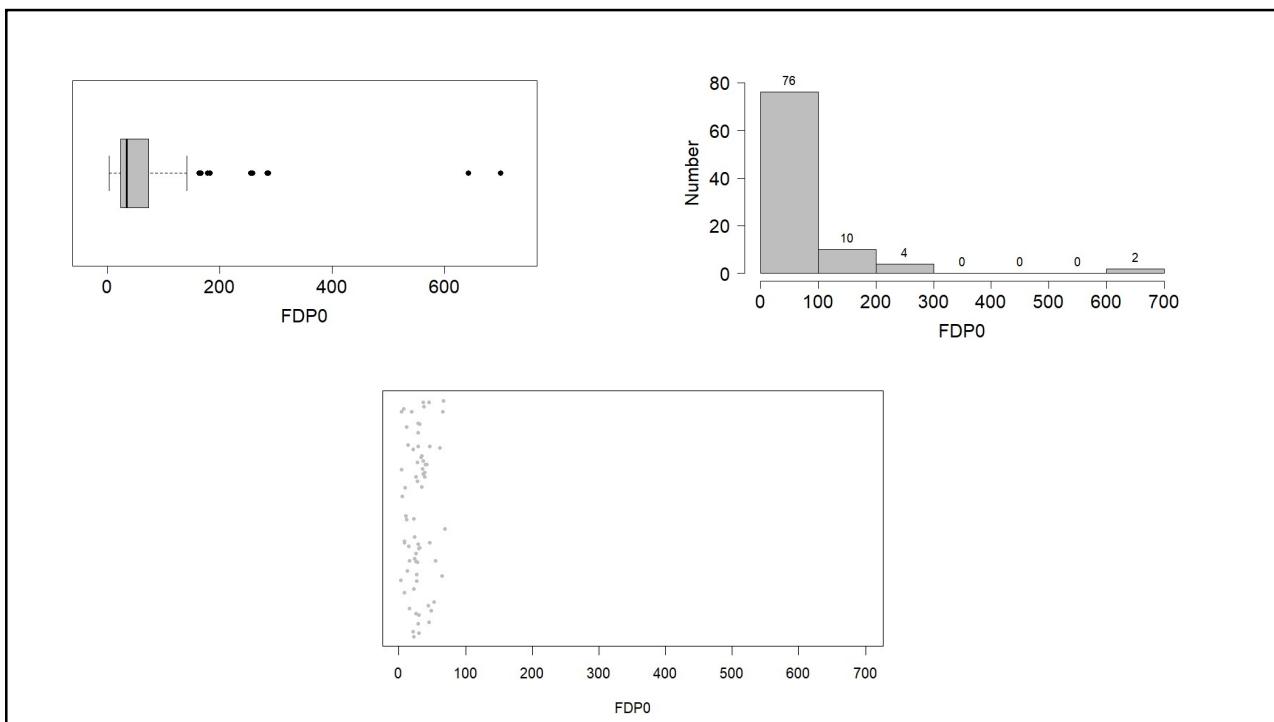
```

File Edit Code View Plots Session Build Debug Profile Tools Help
intro-script-fall2025.R dset Go to file/function Addins
Grade Next Prev Treatment Replace All
in selection Match case Whole word Regex Wrap
78 #####
79 # Get documentation for the coag data set from zenodo
80 # View https://zenodo.org/records/5023900
81
82
83
84
85
86 #####
87 # Descriptive stats, Figures, and narrative for baseline FDP0
88
89 describe(FDP0,coag) # default
90 describe(FDP0,coag,fig=2) # more figures
91 describe(FDP0,coag,fig=3) # even more figure
92
93
94
95 # requires EXACT spelling and capitalization of data set and column name
96 # data set name: coag; column name: FDP0
97 # must use quotes for column name; must match name in R exactly
98
99
100 #####
101 # The tbl option
102
103 describe(FDP0,coag,tbl=0) # no table
104 describe(FDP0,coag,tbl=1) # one table
105 describe(FDP0,coag,tbl=2) # more tables (if any more to show)
106
107 #####
108 # The txt option
109
110 describe(FDP0,coag,txt=0) # no text
111 describe(FDP0,coag,txt=1) # some text
112 describe(FDP0,coag,txt=2) # more text (if any more to show)
113 describe(FDP0,coag,txt=3) # even more text (if any more to show)
93:32 (Untitled) R Script
Environment History Connections Tutorial

```

The R script `intro-script-fall2025.R` continues to generate figures. Lines 91 and 92 highlight the command `describe(FDP0,coag,fig=3)` which generates even more figures. The RStudio interface shows the console output, which includes a reference section with several bibliographic entries and a histogram of the data. The histogram has a light gray background and a dark gray border, with the x-axis labeled 'FDP0' and the y-axis labeled 'Number'. The histogram shows a distribution with a peak at 76 and a long tail extending to the right.

34



35

**Highlight and run line 93. We get figures with skyblue color.**

The screenshot shows the RStudio interface. The left pane contains an R script with several lines highlighted by red boxes. The top right shows a browser window with a reference page. The bottom right displays a histogram of FDP0 values.

Script content (lines 93-94 highlighted):

```
93 describe(FDPO,coag,fig=2,circles="skyblue") # figures with skyblue color
94
```

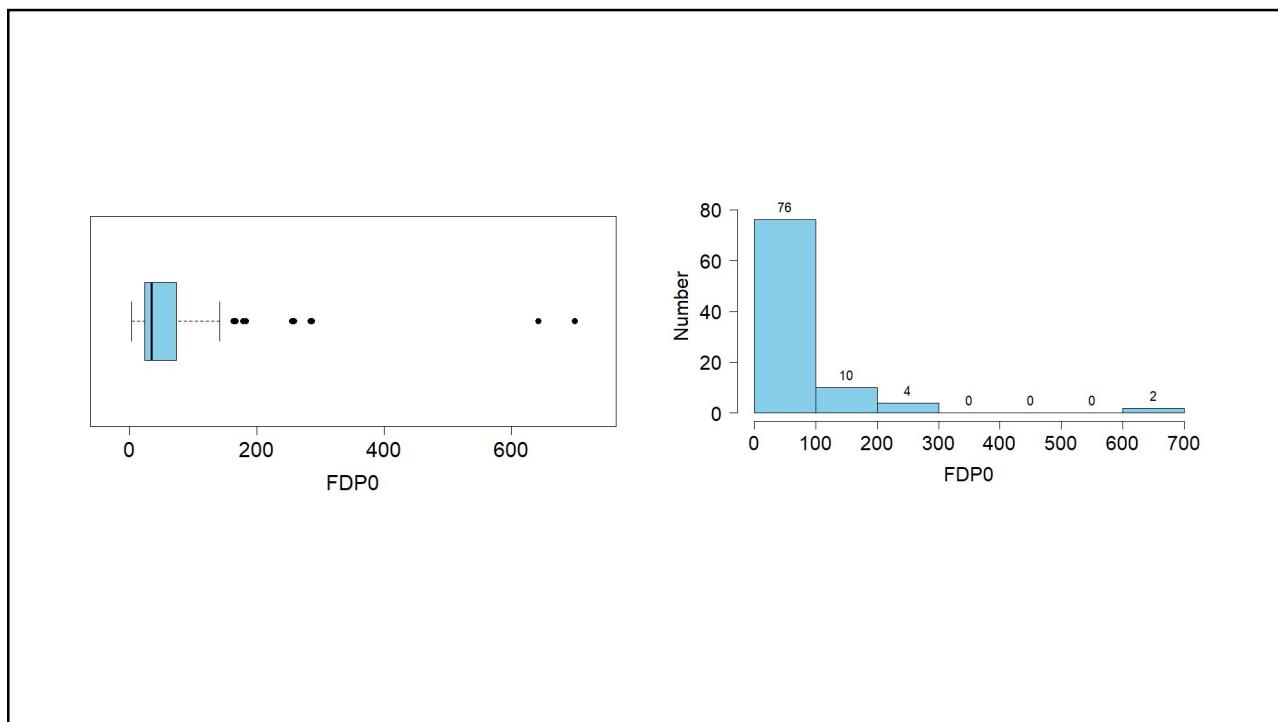
Browser reference (lines 1-14 highlighted):

```
[1] "Peter J. Rousseeuw (1984), Least Median of Squares Regression. Journal of the American Statistical Association 79, 871-881."
[2] "Shapiro, S. S.; Wilk, B. (1965). \"An analysis of variance test for normality (complete samples)\". Biometrika 52 (3-4): 591-611. doi:10.1093/biomet/52.3-4.591. JSTOR 2333709. MR 0205384."
[3] "Conover, W. J.; Massie, R. L. (1996). \"A simple test of symmetry about an unknown median.\" Canadian Journal of Statistics, 24(3), 349-361, doi: 10.2307/3315744."
[4] "Conover, W. J. (1999). \"Chapter 3.4: The Sign Test\". Practical Nonparametric Statistics (Third ed.), Wiley, pp. 157-176, ISBN 0-471-16068-7"
```

Histogram of FDP0 values:

| FDP0 Range | Number |
|------------|--------|
| 0 - 100    | 76     |
| 100 - 200  | 10     |
| 200 - 300  | 4      |
| 300 - 400  | 0      |
| 400 - 500  | 0      |
| 500 - 600  | 0      |
| 600 - 700  | 2      |

36



37

**Getting Started in Each New R Session**

```
sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")
source(sbp.link)
```

|   |   |  |  |
|---|---|--|--|
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i> | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)   | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)                   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export &gt; Copy to Clipboard &gt; Copy Plot</i> .  |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)                | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)       | <b>Common Options</b><br>Narrative: txt = 0 (none), 1 (some), 2 ... (more)<br>Tables: tbl = 0 (none), 1 (some), 2 ... (more) <b>Figures: fig = 0 (none), 1 (some), 2 ... (more)</b><br>Colors: clr = c("color1.name", "color2.name")<br>Colors: clr = "palette.name"<br>Output Labels: y.name, x.name, or grp.name = "name" |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)                 |   |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)                     | <b>Specific Options</b><br>estimate: null = number<br>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)  |  |  |

Prepared by Stan Pounds 06/04/2024

38

**Highlight and run lines 103-105 one at a time.**

The screenshot shows the RStudio interface with the following details:

- Top Bar:** File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help.
- Left Panel:** A code editor window titled "intro-script-fall2025.R". The code contains R script for generating descriptive statistics and histograms for the "FDPO" column of the "coag" dataset. It includes various parameters for `describe` and `hist` functions like `n`, `tbl`, and `txt`.
- Right Panel:** A "Console" tab showing references to statistical tests and their sources. A "Background Jobs" tab is also visible.
- Bottom Panel:** A histogram titled "FDPO" showing the distribution of values. The x-axis ranges from 0 to 700, and the y-axis ranges from 0 to 80. The distribution is highly right-skewed, with the highest frequency (76) occurring at 0.

| FDPO Value | Number of Occurrences |
|------------|-----------------------|
| 0          | 76                    |
| 100        | 10                    |
| 200        | 4                     |
| 300        | 0                     |
| 400        | 0                     |
| 500        | 0                     |
| 600        | 2                     |

39

| Getting Started in Each New R Session  |   |  |  |
|--|---|--|--|
| <a href="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R">sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")</a><br><pre>source(sbp.link)</pre> |   |  |  |
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i>  | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)   | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number)   |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)  |   |  | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export &gt; Copy to Clipboard &gt; Copy Plot</i> . |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)   | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)  | <b>Common Options</b> <p><i>Narrative:</i> txt = 0 (none), 1 (some), 2 ... (more)</p> <p><i>Tables:</i> tbl = 0 (none), 1 (some), 2 ... (more)</p> <p><i>Figures:</i> fig = 0 (none), 1 (some), 2 ... (more)</p> <p><i>Colors:</i> clr = c("color1.name", "color2.name")</p> <p><i>Colors:</i> clr = "palette.name"</p> <p><i>Output Labels:</i> y.name, x.name, or grp.name = "name"</p> |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)  | <b>Specific Options</b> <p><i>estimate:</i> null = number</p> <p><i>correlate:</i> line = NA (no line), 0 (flat line), 1 (fitted line)</p>  |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)  |   |  |  |

## Highlight and run lines 110-113 one at a time.

The screenshot shows the RStudio interface with the 'intro-script-fall2025.R' script open. Lines 110 through 113 are highlighted with a red box. The output pane shows a histogram of FDPO values, with the highest frequency being 76.

```

90 # describe(FDP.coag,fig=0)      # no figures
91 # describe(FDP.coag,fig=2)      # more figures
92 # describe(FDP.coag,fig=3)      # even more figures
93 # describe(FDP.coag,fig=2,clr="skyblue") # Figures with skyblue color
94
95 # requires EXACT spelling and capitalization of data set and column name
96 # data set name: coag; column name: FDP0
97 # must use quotes for column name; must match name in R exactly
98
99
100 ######
101 # The tb option
102
103 # describe(FDP0.coag,tb=0)    # no table
104 # describe(FDP0.coag,tb=1)    # one table
105 # describe(FDP0.coag,tb=2)    # more tables (if any more to show)
106
107 #####
108 # the tx option
109 # describe(FDP0.coag,tx=0)    # no text
110 # describe(FDP0.coag,tx=1)    # some text
111 # describe(FDP0.coag,tx=2)    # more text (if any more to show)
112 # describe(FDP0.coag,tx=3)    # even more text (if any more to show)
113
114
115
116 # How do I know the names of colors available in R?
117 # Show available color names in R
118 show.colors()
119
120
121
122
123
124
125
126
110: (Untitled) : R Script
Environment History Connections Tutorial

```

Console  
Background Jobs  
R 4.4.0 C:/Users/gpounds/BioStat-Teaching/intro-Biostat/Fall2025/GCH Orientation/  
Sref  
[1] "Peter J. Rousseeuw (1984), Least Median of Squares Regression. Journal of the American Statistical Association 79, 871-881."  
[2] "Shapiro, S. S.; Wilk, M. B. (1965). 'An analysis of variance test for normality (complete samples)'. Biometrika. 52 (3-4): 591-611. doi:10.1093/biomet/52.3-4.591."  
[3] "Cabilio P, Macaro J (1996). 'A simple test of symmetry about an unknown median.' Canadian Journal of Statistics. 24(3), 349-361. doi: 10.2307/3315744."  
[4] "Conover, W.J. (1999). 'Chapter 3.4: The Sign Test', Practical Nonparametric Statistics (Third ed.), Wiley, pp. 157-176, ISBN 0-471-16068-7"

Files Plots Packages Help Viewer Presentation  
Zoom Export Publish

Number

FDPO

41

**Getting Started in Each New R Session**

sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")  
source(sbp.link)

|   |  |  |  |
|---|--|--|--|
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i> | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)  | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)                   | <b>Copy Figure to Word</b><br>In the Plots tab, Click Export > Copy to Clipboard > Copy Plot.  |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)                | <b>Copy Tabular Result to Word</b><br>word.table(result.name)  |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)       | <b>Common Options</b><br>Narrative: txt = 0 (none), 1 (some), 2 ... (more)<br>Tables: tb = 0 (none), 1 (some), 2 ... (more)<br>Figures: fig = 0 (none), 1 (some), 2 ... (more)<br>Colors: clr = c("color1.name", "color2.name")<br>Colors: clr = "palette.name"<br>Output Labels: y.name, x.name, or grp.name = "name" |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)                 |  |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)                     | <b>Specific Options</b><br>estimate: null = number<br>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)   |  |  |

Prepared by Stan Pounds 06/04/2024

42

## Highlight and run lines 119-121 one at a time.

The screenshot shows the RStudio interface. On the left is the R Script pane with the following R code:

```

109 describe(FDP0, coag.txt=0) # no text
110 describe(FDP0, coag.txt=1) # some text
111 describe(FDP0, coag.txt=2) # more text (if any more to show)
112 describe(FDP0, coag.txt=3) # even more text (if any more to show)
113
114
115
116 ##### Descriptives for treatment (an unordered category variable)
117
118 describe(Treatment, coag) # default
119 describe(Treatment, coag, clr=c("red", "blue")) # red and blue for the figure
120 describe(Treatment, coag, clr=c("gold", "green")) # gold and green
121
122
123 ##### How do I know the names of colors available in R?
124 # Show available color names in R
125
126 show.colors()
127
128
129
130
131
132 ##### Show available color palettes in R
133 # show available color palettes in R
134
135 show.palettes(2) # palettes of 2 colors
136 show.palettes(4) # palettes of 4 colors
137 show.palettes(10) # palettes of 10 colors
138
139
140 ##### Use color palettes for figures
141
142
143
144 describe(Treatment, coag, clr="Tropic") # use the "Tropic" color palette
145

```

A red box highlights lines 119 through 121. On the right is the R Console pane showing output and the Plots pane displaying a bar chart titled "Treatment (n)". The chart compares two treatments: T (blue bar) and C (red bar). The x-axis ranges from 0 to 60. Treatment T has a value of 47 (51.09%) and Treatment C has a value of 45 (48.91%).

43

**Getting Started in Each New R Session**

```

sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")
source(sbp.link)

```

|   |   |  |  |
|---|---|--|--|
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i> | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)   | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)                   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> .  |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)                | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)       | <b>Common Options</b><br>Narrative: txt = 0 (none), 1 (some), 2 ... (more)<br>Tables: tbl = 0 (none), 1 (some), 2 ... (more)<br>Figures: fig = 0 (none), 1 (some), 2 ... (more)<br>Colors: clr = c("color1.name", "color2.name")<br>Colors: clr = "palette.name"<br>Output Labels: y.name, x.name, or grp.name = "name" |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)                 |   |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)                     | <b>Specific Options</b><br>estimate: null = number<br>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)  |  |  |

Prepared by Stan Pounds 06/04/2024

44

**Highlight and run line 128. Get a color legend.**

The screenshot shows an RStudio interface with a script editor containing R code and a 'Named Colors in R' palette.

**Script Content:**

```
File Edit Code View Plots Session Build Debug Profile Tools Help
File Go to file/function Addins -
intro-script-fa2025.R dset Source
Grade Next Prev AB Treatment
In selection Match case Whole word RegEx Wrap
109
110 describe(FDP0.coag,txt=0) # no text
111 describe(FDP0.coag,txt=1) # some text
112 describe(FDP0.coag,txt=2) # more text
113 describe(FDP0.coag,txt=3) # even more t
114
115
116 ##### Descriptives for treatment (an unorderc
117 # Descriptives for treatment (an unorderc
118 describe(Treatment.coag)
119 describe(Treatment.coag,clr=c("red","blue",
120 describe(Treatment.coag,clr=c("yellow","green",
121
122
123 #####
124 #####
125 How do I know the names of colors availa
126 Show available color names in R
127
128 show.colors()
129
130
131
132 #####
133 # Show available color palettes in R
134
135 show.palettes(2) # palettes of 2 colors
136 show.palettes(4) # palettes of 4 colors
137 show.palettes(10) # palettes of 10 colors
138
139
140 #####
141 # Use color palettes for figures
142
143
144 describe(Treatment.coag,clr="Tropic1")
145
146
```

**Named Colors in R Palette:**

| Color Name           | Color Swatch         |
|----------------------|----------------------|
| white                | White                |
| darkgreen            | Dark Green           |
| ghostwhite           | Ghost White          |
| lightpink            | Light Pink           |
| mistyrose            | Misty Rose           |
| saddlebrown          | Saddle Brown         |
| slategray            | Slate Gray           |
| darkgrey             | Dark Grey            |
| gold                 | Gold                 |
| lightsalmon          | Light Salmon         |
| tan                  | Tan                  |
| darkkhaki            | Dark Khaki           |
| goldenrod            | Goldenrod            |
| navy                 | Navy                 |
| seashell             | Seashell             |
| antiquewhite         | Antique White        |
| darlmagenta          | Darlmagenta          |
| gray                 | Gray                 |
| lightslateblue       | Lightslateblue       |
| navajowhite          | Navajowhite          |
| seasHELL             | SeasHELL             |
| aquamarine           | Aquamarine           |
| darkolivegreen       | Darkolivegreen       |
| green                | Green                |
| lightslategray       | Lightslategray       |
| olivedrab            | Olivedrab            |
| sienna               | Sienna               |
| azure                | Azure                |
| darkorange           | Darkorange           |
| yellow               | Yellow               |
| lightslategray       | Lightslategray       |
| skyblue              | Skyblue              |
| beige                | Beige                |
| darkred              | Darkred              |
| honeydew             | Honeydew             |
| orange               | Orange               |
| bisque               | Bisque               |
| darkviolet           | Darkviolet           |
| hotpink              | Hotpink              |
| orangered            | Orangered            |
| black                | Black                |
| darksalmon           | Darksalmon           |
| indianred            | Indianred            |
| slategray            | Slategray            |
| blanchedalmond       | Blanchedalmond       |
| darkseagreen         | Darkseagreen         |
| limegreen            | Limegreen            |
| steelblue            | Steelblue            |
| blue                 | Blue                 |
| darkslateblue        | Darkslateblue        |
| ivory                | Ivory                |
| palegreen            | Palegreen            |
| wheat                | Wheat                |
| blueviolet           | Blueviolet           |
| darkslategray        | Darkslategray        |
| khaki                | Khaki                |
| magenta              | Magenta              |
| springgreen          | Springgreen          |
| brown                | Brown                |
| darkslategray        | Darkslategray        |
| lavender             | Lavender             |
| maroon               | Maroon               |
| tan                  | Tan                  |
| bunywood             | Bunywood             |
| darkturquoise        | Darkturquoise        |
| lavenderblush        | Lavenderblush        |
| paleturquoise        | Paleturquoise        |
| cadetblue            | Cadetblue            |
| darkviolet           | Darkviolet           |
| lawngreen            | Lawngreen            |
| mediumaquamarine     | Mediumaquamarine     |
| thistle              | Thistle              |
| chartreuse           | Chartreuse           |
| deeppink             | Deeppink             |
| lemonchiffon         | Lemonchiffon         |
| papayaWhip           | PapayaWhip           |
| chocolate            | Chocolate            |
| deeppink             | Deeppink             |
| lightblue            | Lightblue            |
| mediumorchid         | Mediumorchid         |
| peachPUff            | PeachPUff            |
| coral                | Coral                |
| deepskyblue          | Deepskyblue          |
| lightcyan            | Lightcyan            |
| mediumpurple         | Mediumpurple         |
| peru                 | Peru                 |
| confettiblue         | Confettiblue         |
| dimgray              | Dimgray              |
| lightgreen           | Lightgreen           |
| mediumseagreen       | Mediumseagreen       |
| turquoise            | Turquoise            |
| comsilk              | Comsilk              |
| dodgerblue           | Dodgerblue           |
| lightgoldenrod       | Lightgoldenrod       |
| mediumspringgreen    | Mediumspringgreen    |
| violet               | Violet               |
| cyan                 | Cyan                 |
| firebrick            | Firebrick            |
| lightgoldenrodyellow | Lightgoldenrodyellow |
| powderblue           | Powderblue           |
| darkblue             | Darkblue             |
| floralwhite          | Floralwhite          |
| lightgray            | Lightgray            |
| purple               | Purple               |
| darkcyan             | Darkcyan             |
| forestgreen          | Forestgreen          |
| mediumvioletred      | Mediumvioletred      |
| red                  | Red                  |
| darkgoldenrod        | Darkgoldenrod        |
| gainsboro            | Gainsboro            |
| midnightblue         | Midnightblue         |
| rosybrown            | Rosybrown            |
| lightgray            | Lightgray            |
| mintcream            | Mintcream            |
| royalblue            | Royalblue            |

45

| Getting Started in Each New R Session  |   |  |  |
|--|---|--|--|
| <a href="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R">sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")</a><br><code>source(sbp.link)</code> |   |  |  |
| <b>Read and name data</b><br><code>data.name = read.data()</code><br># Choose file in pop-up window  | <b>Preview data</b><br><code>View(data.name)</code><br><code>colnames(data.name)</code>   | <b>General Syntax</b><br><code>result = function(info1, info2, ...)</code><br># user chooses result name | <b>Color Name Legend</b><br><code>show.colors()</code><br><code>show.palettes(number)</code>                               |
| <b>Descriptive Stats &amp; Graphs</b><br><code>describe("column.name", data.name)</code>   |   |  | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> . |
| <b>Estimate One Population Parameter</b><br><code>estimate("column.name", data.name)</code>  |   | <b>Copy Tabular Result to Word</b><br><code>word.table(result.name)</code>                               |  |
| <b>Compare a Variable across Groups</b><br><code>compare(variable.name~group.name, data.name)</code>   | <b>Common Options</b><br><i>Narrative</i> : <code>txt = 0</code> (none), <code>1</code> (some), <code>2</code> ... (more)<br><i>Tables</i> : <code>tbl = 0</code> (none), <code>1</code> (some), <code>2</code> ... (more)<br><i>Figures</i> : <code>fig = 0</code> (none), <code>1</code> (some), <code>2</code> ... (more)<br><b>Colors</b> : <code>clr = c("color1.name", "color2.name")</code><br><b>Colors</b> : <code>clr = "palette.name"</code><br><b>Output Labels</b> : <code>y.name, x.name, or grp.name = "name"</code> |  |  |
| <b>Correlate Two Numeric Variables</b><br><code>correlate(y.name~x.name, data.name)</code>   |   |  |  |
| <b>Fit a Predictive Model</b><br><code>model(y.name~x1.name+x2.name, data.name)</code>   | <b>Specific Options</b><br><code>estimate</code> : <code>null = number</code><br><code>correlate</code> : <code>line = NA</code> (no line), <code>0</code> (flat line), <code>1</code> (fitted line)  |  |  |

**Highlight and Run line 135, get palettes of two colors.**

47

**Run lines 136-137. See palettes of more colors.**

The screenshot shows the RStudio interface with the following details:

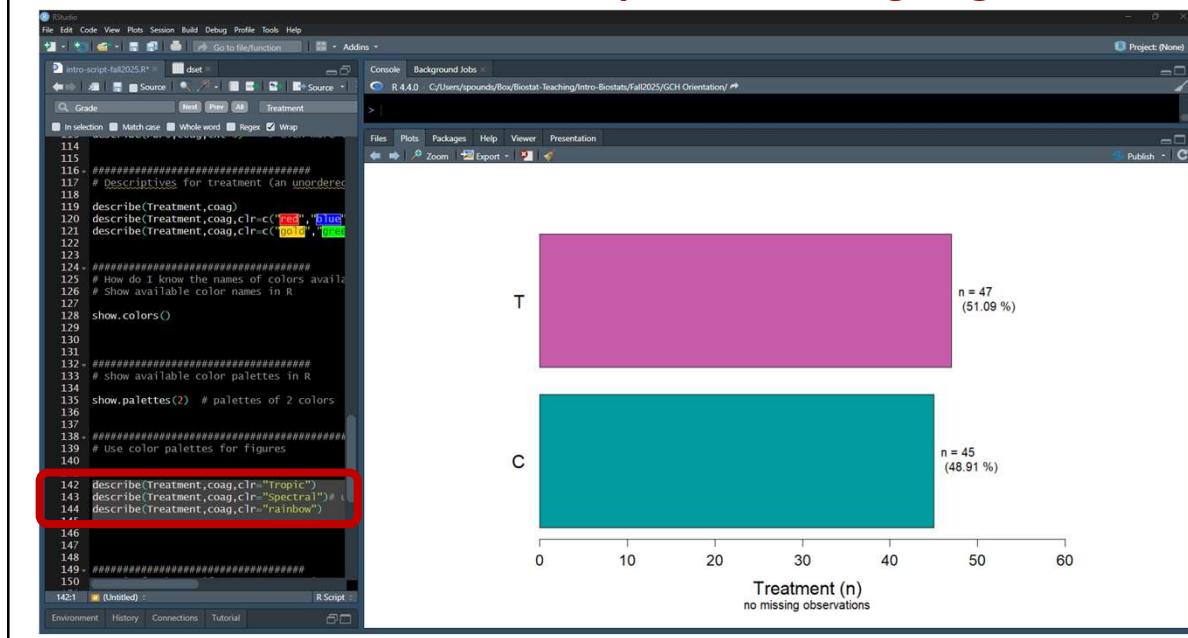
- File**, **Edit**, **Code**, **View**, **Plots**, **Session**, **Build**, **Debug**, **Profile**, **Tools**, **Help** menu.
- Addins** tab selected.
- Console** tab active, showing R code and output:

```
R 4.4.0  C:\Users\grouds\Box\Biostat\Teaching\Intro_Biostats\Fall2025\GCH Orientation/ > show.palettes(10) # palettes of 10 colors
```
- Background Jobs** tab.
- Source** tab selected.
- Grade**, **Next**, **Prev**, **All**, **Treatment** buttons.
- Search** bar.
- Match case**, **Whole word**, **Regex**, **Wrap** checkboxes.
- Files**, **Plots**, **Packages**, **Help**, **Viewer**, **Presentation** tabs.
- Zoom**, **Export** buttons.
- Project**: None
- Color Palettes in R** section with two columns of color palettes:

| rainbow        | BluM          | Purples    | Brc          |
|----------------|---------------|------------|--------------|
| heat.colors    | Purple-Blue   | ag_gmRt    | Cork         |
| terrain.colors | Red-Purple    | PuBuGn     | Vik          |
| topo.colors    | Red-Blue      | PnkYl      | Berlin       |
| cm.colors      | Purple-Orange | Burg       | Lisbon       |
| Pastel 1       | Purple-Yellow | BurgYl     | Tofino       |
| Dark 2         | Blue-Yellow   | RedOr      | ArmyRose     |
| Dark 3         | Green-Yellow  | OrYel      | Earth        |
| Dark 4         | Yellow        | OrBr       | TealRose     |
| Set 1          | Heat          | PurpOr     | Temp         |
| Set 2          | Heat          | Sunset     | Balwo        |
| Set 3          | Heat 2        | Magenta    | Hawaii       |
| Warm           | Terrain       | SunsetDark | Blue-Red     |
| Cold           | Terrain 2     | ag_Sunse   | Blue-Red 2   |
| Harmonic       | Dynamic       | BrownR     | RdBlu        |
| Dynamic        | Grayscale     | BlueR      | RdGn         |
| Grayscale      | Grays         | BlueGn     | Blue-Green   |
| Blues 1        | Blues         | YlOrRd     | Purple-Green |
| Blues 2        | Blues 2       | YlOrBr     | PRGn         |
| Blues 3        | Blues 3       | OrRd       | Purple-Brown |
| Purples 2      | Purples 2     | Oranges    | BBG          |
| Purples 3      | Purples 3     | YlGn       | Green-Brown  |
| Reds 2         | Reds 2        | YlGnBu     | RdYlBu       |
| Reds 3         | Reds 3        | Reds       | RdYlGn       |
| Greens 2       | Greens 2      | TealGn     | Spectral     |
| Greens 3       | Greens 3      | Emrd       | Zissou 1     |
- 109**, **110**, **111**, **112**, **113**, **114**, **115**, **116**, **117**, **118**, **119**, **120**, **121**, **122**, **123**, **124**, **125**, **126**, **127**, **128**, **129**, **130**, **131**, **132**, **133**, **134**, **135**, **136**, **137**, **138**, **139**, **140**, **141**, **142**, **143**, **144**, **145** lines of R code.
- 136**, **137**, **138** lines highlighted with a red box.
- 136:1** line number.
- R Script** tab.
- Environment**, **History**, **Connections**, **Tutorial** buttons.

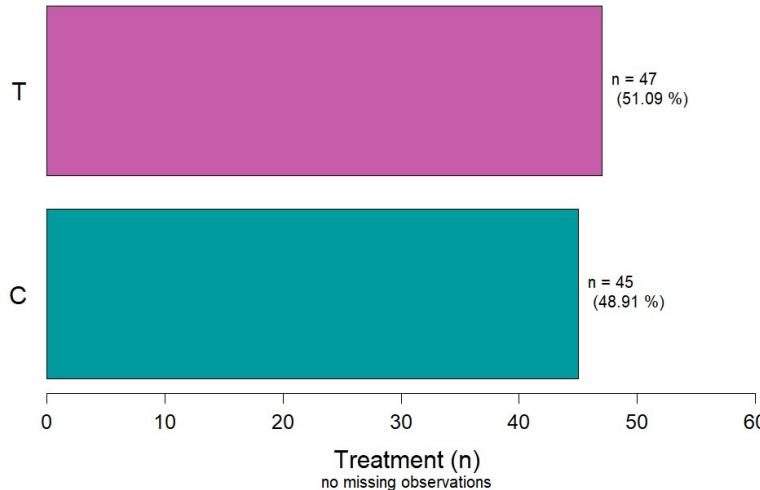
48

Run lines 142-144. See how palettes change figures.



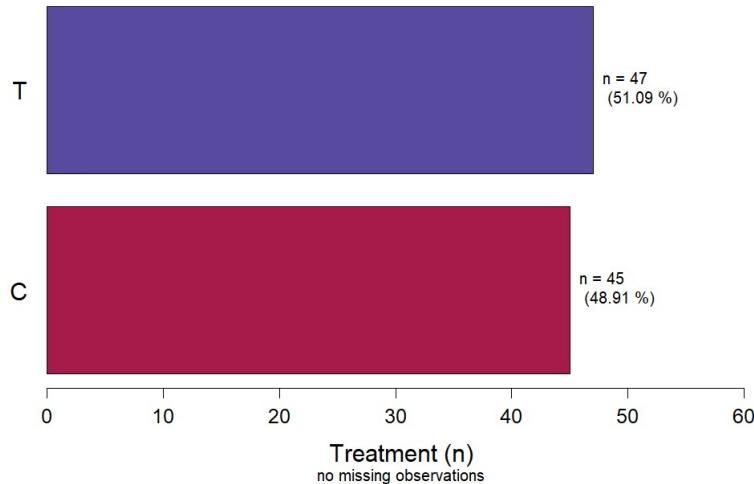
49

## Option `clr="Tropic"`



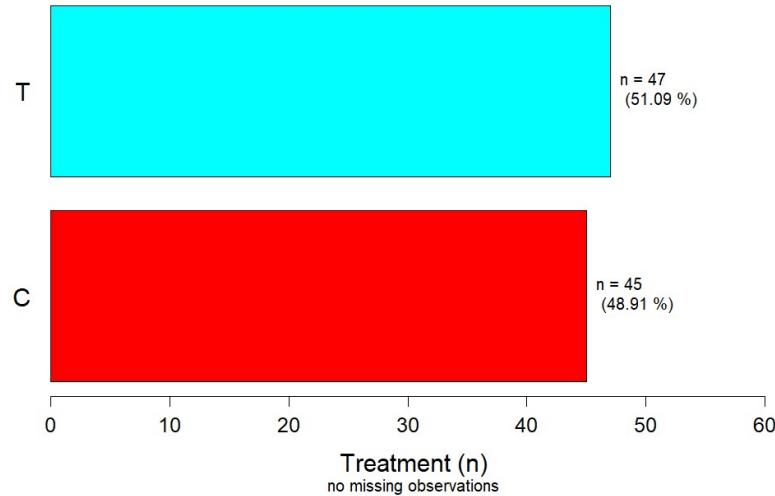
50

## Option `clr="Spectral"`



51

## Option `clr="rainbow"`



52

**Try multiple options ... highlight and run sections.**

The screenshot shows an RStudio interface with two panes. The left pane contains R code from a script named 'intro-script-fall2025.R'. The right pane shows the R console output and a binomial distribution plot.

**R Code (intro-script-fall2025.R):**

```
1 # intro-script-fall2025.R
2 # Go to my function
3 # Addins
4
5 # In selection Match case Whole word Regex Wrap
6
7 # Grade Next Prev All Treatment Replace All
8
9 142 describe(Treatment,coag,clr="Tropic") # use the "Tropic" color palette
10 143 describe(Treatment,coag,clr="Spectral")# use the "Spectral" color palette
11 144 describe(Treatment,coag,clr="Rainbow")
12 145
13 146 #####
14 147 # Try multiple options
148 149
150 149 describe(Treatment,coag,
151   clr="Spectral",fig=2,txt=0)
152
153 153 describe(Treatment,coag,
154   clr="Lisbon",fig=1,tbl=0)
155
156 156 describe(Treatment,coag,
157   fig=0,txt=1,tbl=0)
158
159
160 # Don't freak out if you get errors in R.
161 # Everyone who uses R gets errors.
162 # Dr. Pounds has been using R for over two decades.
163 # He still gets many errors, just not as many as he did in the first few extensions of R.
164 # He still gets many errors every time he uses R.
165 # Errors are usually just typos.
166 # So for practice, Run these lines with errors, fix the typos, run them again.
167
168 describe(Fdp0) # capitalize Fdp0
169 # Fdp0,coag,fig=2) # should be Fdp0,coag,fig=2 instead of Fig2
170 describe(Fdp0,coag) # should be comma instead of semi-colon
171 describe(Fdp0,coag,clr=red) # color name "red" must be in quotes
172
173
174
175
176
177
178
179 -
180
181 15625 [Untitled] : R Script
182 Environment History Connections Tutorial
```

**Console Output:**

```
R 4.4.0 C:\Users\Box\Biostat-teaching\Intro-Biostat\fall2025\GCH Orientations\ -->
1 y.
2
3 stbl
4 [1] "The binomial distribution was used to estimate confidence intervals for the proportions o
f Treatment C and T in the population."
5
6 Sref
7 NULL
8
9 > |
```

**Plots:**

A binomial distribution plot showing the proportion of Treatment T and C. The x-axis represents the number of treatments (n), ranging from 0 to 60. The y-axis represents the proportion of each treatment.

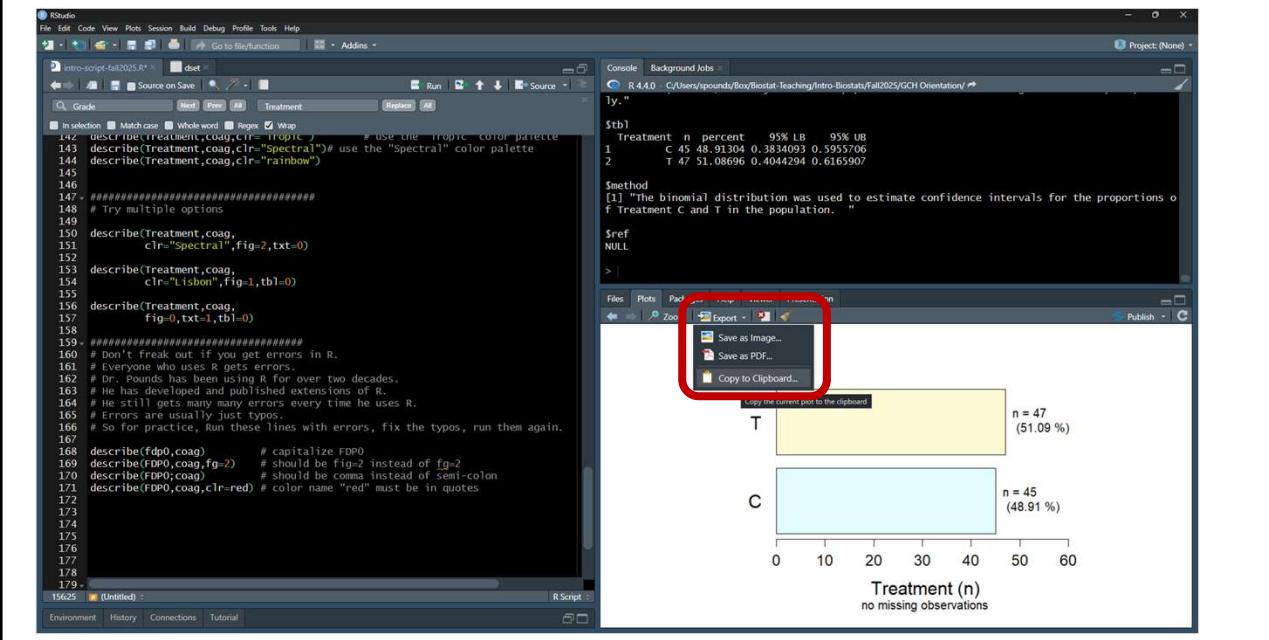
| Treatment | n  | proportion |
|-----------|----|------------|
| T         | 47 | (51.09%)   |
| C         | 45 | (48.91%)   |

Treatment (n)  
no missing observations

53

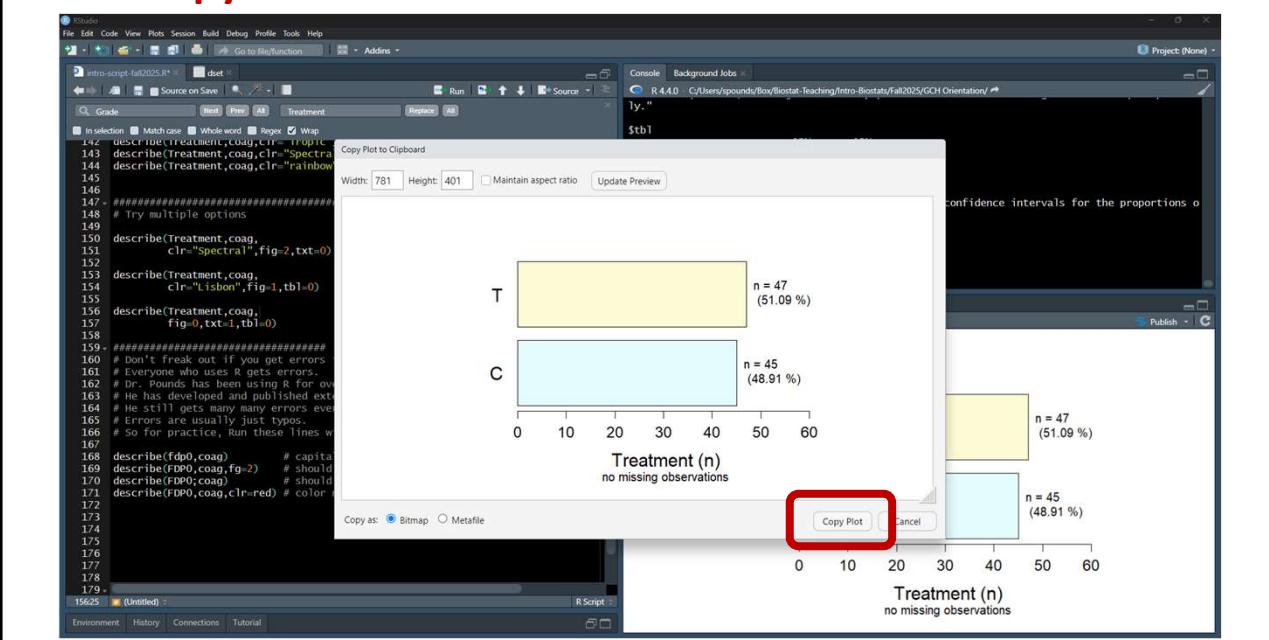
| Getting Started in Each New R Session  |   |   |  |
|--|---|---|--|
| <a href="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R">sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")</a><br><pre>source(sbp.link)</pre> |   |   |  |
| <b>Read and name data</b><br><code>data.name = read.data()<br/># Choose file in pop-up window</code>   | <b>Preview data</b><br><code>View(data.name)<br/>colnames(data.name)</code>   | <b>General Syntax</b><br><code>result = function(info1, info2, ...)<br/># user chooses result name</code> | <b>Color Name Legend</b><br><code>show.colors()<br/>show.palettes(number)</code>   |
| <b>Descriptive Stats &amp; Graphs</b><br><code>describe("column.name", data.name)</code>   |   |   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export</i> > <i>Copy to Clipboard</i> > <i>Copy Plot</i> . |
| <b>Estimate One Population Parameter</b><br><code>estimate("column.name", data.name)</code>  | <b>Copy Tabular Result to Word</b><br><code>word.table(result.name)</code>  |   |  |
| <b>Compare a Variable across Groups</b><br><code>compare(variable.name~group.name, data.name)</code>   | <b>Common Options</b><br><i>Narrative</i> : <code>txt = 0 (none), 1 (some), 2 ... (more)</code><br><i>Tables</i> : <code>tbl = 0 (none), 1 (some), 2 ... (more)</code><br><i>Figures</i> : <code>fig = 0 (none), 1 (some), 2 ... (more)</code><br><i>Colors</i> : <code>clr = c("color1.name", "color2.name")</code><br><i>Colors</i> : <code>clr = "palette.name"</code><br><i>Output Labels</i> : <code>y.name, x.name, or grp.name = "name"</code> |   |  |
| <b>Correlate Two Numeric Variables</b><br><code>correlate(y.name~x.name, data.name)</code>   | <b>Specific Options</b><br><i>estimate</i> : <code>null = number</code><br><i>correlate</i> : <code>line = NA (no line), 0 (flat line), 1 (fitted line)</code>  |   |  |
| <b>Fit a Predictive Model</b><br><code>model(y.name~x1.name+x2.name, data.name)</code>   |   |   |  |

## Go to Export ... Copy to Clipboard.

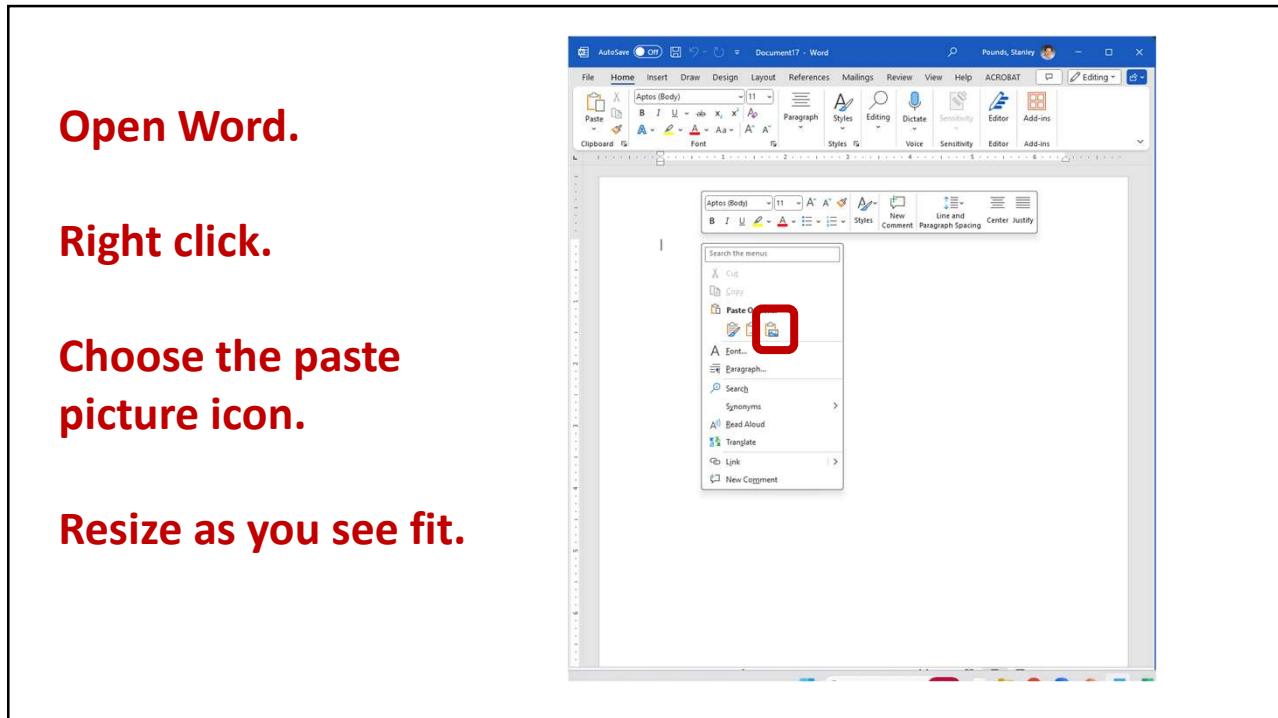


55

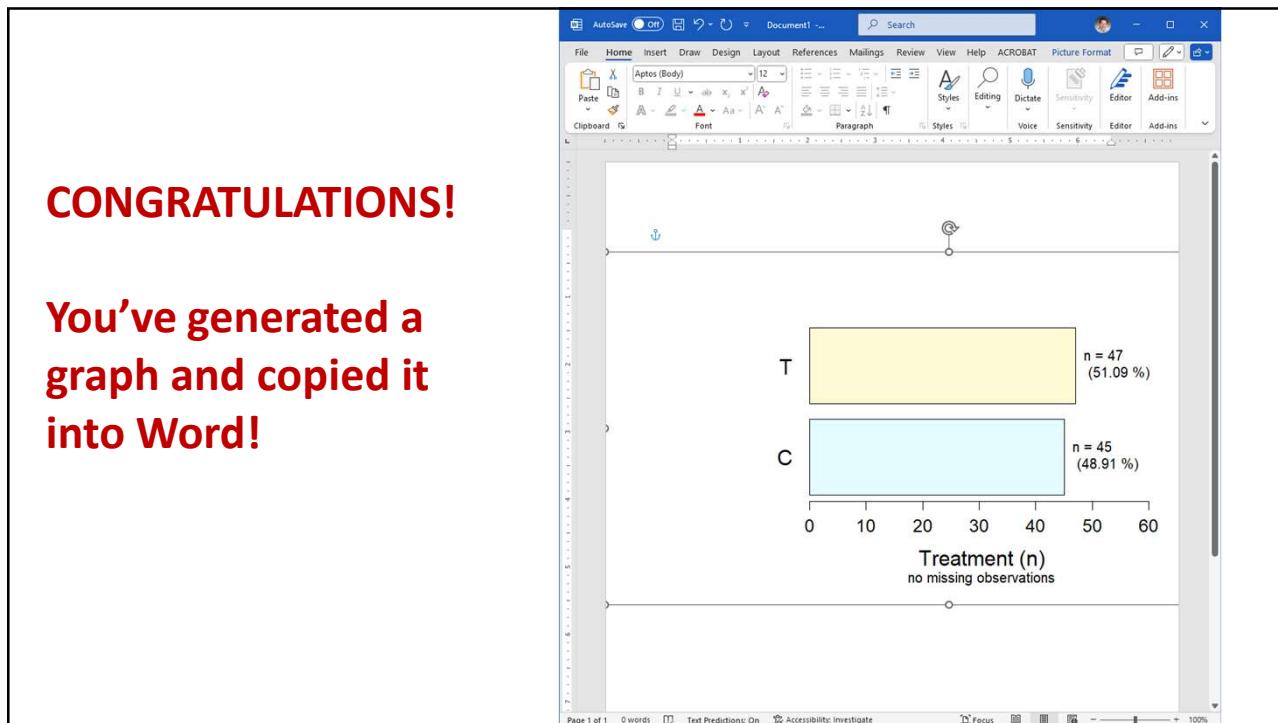
## Click Copy Plot.



56



57



58

| <b>Getting Started in Each New R Session</b>   |   |   |  |
|--|---|---|--|
| <pre>sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R") source(sbp.link)</pre> |   |   |  |
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i>                                  | <b>Preview data</b><br>View(data.name)<br>colnames(data.name) | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i>  | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)  |   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export &gt; Copy to Clipboard &gt; Copy Plot</i> .  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)   |   | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)  |   | <b>Common Options</b><br><i>Narrative</i> : txt = 0 (none), 1 (some), 2 ... (more)<br><i>Tables</i> : tbl = 0 (none), 1 (some), 2 ... (more)<br><i>Figures</i> : fig = 0 (none), 1 (some), 2 ... (more)<br><i>Colors</i> : clr = c("color1.name", "color2.name")<br><i>Colors</i> : clr = "palette.name"<br><i>Output Labels</i> : y.name, x.name, or grp.name = "name" |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)  |   | <b>Specific Options</b><br><i>estimate</i> : null = number<br><i>correlate</i> : line = NA (no line), 0 (flat line), 1 (fitted line)  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)  |   |   |  |

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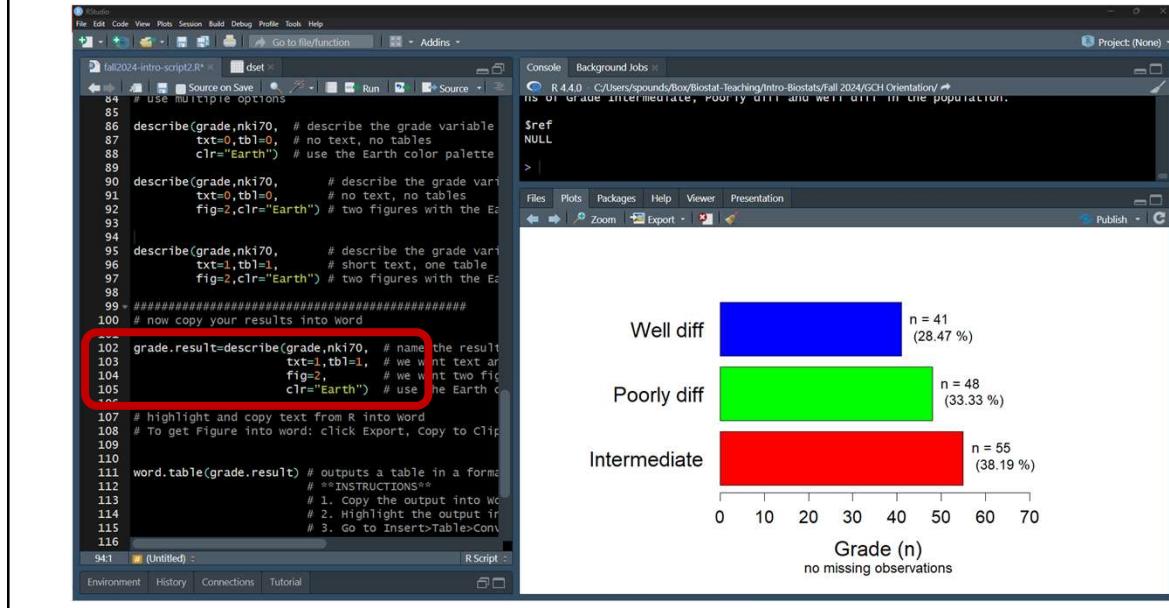
59

| <b>Getting Started in Each New R Session</b>   |   |   |  |
|--|---|---|--|
| <pre>sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R") source(sbp.link)</pre> |   |   |  |
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i>                                  | <b>Preview data</b><br>View(data.name)<br>colnames(data.name) | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i>  | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number)   |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)  |   |   | <b>Copy Figure to Word</b><br>In the <i>Plots</i> tab, Click <i>Export &gt; Copy to Clipboard &gt; Copy Plot</i> . |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)   |   | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)  |   | <b>Common Options</b><br><i>Narrative</i> : txt = 0 (none), 1 (some), 2 ... (more)<br><i>Tables</i> : tbl = 0 (none), 1 (some), 2 ... (more)<br><i>Figures</i> : fig = 0 (none), 1 (some), 2 ... (more)<br><i>Colors</i> : clr = c("color1.name", "color2.name")<br><i>Colors</i> : clr = "palette.name"<br><i>Output Labels</i> : y.name, x.name, or grp.name = "name" |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)  |   | <b>Specific Options</b><br><i>estimate</i> : null = number<br><i>correlate</i> : line = NA (no line), 0 (flat line), 1 (fitted line)  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)  |   |   |  |

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60

## Highlight and run lines 102-105.



61

**Getting Started in Each New R Session**

```
sbp.link="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R")
source(sbp.link)
```

|   |   |  |  |
|---|---|--|--|
| <b>Read and name data</b><br>data.name = read.data()<br><i># Choose file in pop-up window</i> | <b>Preview data</b><br>View(data.name)<br>colnames(data.name)   | <b>General Syntax</b><br>result = function(info1, info2, ...)<br><i># user chooses result name</i> | <b>Color Name Legend</b><br>show.colors()<br>show.palettes(number) |
| <b>Descriptive Stats &amp; Graphs</b><br>describe("column.name", data.name)                   | <b>Copy Figure to Word</b><br>In the Plots tab, Click Export > Copy to Clipboard > Copy Plot.   |  |  |
| <b>Estimate One Population Parameter</b><br>estimate("column.name", data.name)                | <b>Copy Tabular Result to Word</b><br>word.table(result.name)   |  |  |
| <b>Compare a Variable across Groups</b><br>compare(variable.name~group.name, data.name)       | <b>Common Options</b><br>Narrative: txt = 0 (none), 1 (some), 2 ... (more)<br>Tables: tbl = 0 (none), 1 (some), 2 ... (more)<br>Figures: fig = 0 (none), 1 (some), 2 ... (more)<br>Colors: clr = c("color1.name", "color2.name")<br>Colors: clr = "palette.name"<br>Output Labels: y.name, x.name, or grp.name = "name" |  |  |
| <b>Correlate Two Numeric Variables</b><br>correlate(y.name~x.name, data.name)                 |   |  |  |
| <b>Fit a Predictive Model</b><br>model(y.name~x1.name+x2.name, data.name)                     | <b>Specific Options</b><br>estimate: null = number<br>correlate: line = NA (no line), 0 (flat line), 1 (fitted line)  |  |  |

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62

**Run line 111. See the output in the Console.**

The figure shows two panels of the RStudio interface. The left panel displays an R script with several lines of code highlighted in red, indicating they have been run. The right panel shows the R console output and a scatter plot.

**R Script Content:**

```
File Edit Code View Plots Session Build Debug Profile Tools Help
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function Addins - Project (None) -
dset Run Source On Save Grade Next Prev All Treatment Replace All
In selection Match case Whole word RegEx Wrap
145
146
147 ##### Try multiple options
148 # Try multiple options
149
150 describe(Treatment.coag,
151   clr="Spectral",fig=2,txt=0)
152
153 describe(Treatment.coag,
154   clr="Lisbon",fig=1,tbl=0)
155
156 describe(Treatment.coag,
157   fig=0,txt=1,tbl=0)
158
159
160 #####
161 # Copy a table into word
162
163 FDP0.result<-describe(FDP0,coag) # save results as "FDP0.result" in R
164 word.table(FDP0.result) # ask R to produce a table to copy into word
165
166 #####
167 # Don't freak out if you get errors in R.
168 # Everyone who uses R gets errors.
169 # Dr. Pounds has been using R for over two decades.
170 # He still uses the original, unmodified extensions of R.
171 # He still gets many many errors every time he uses R.
172 # Errors are usually just typos.
173 # So for practice, Run these lines with errors, fix the typos, run them again.
174
175 describe(fdp0,coag) # capitalizes FDP0
176 describe(FDP0,coag,fg=2) # should be fig=2 instead of fg=2
177 describe(FDP0,coag) # should be comma instead of semi-colon
178 describe(FDP0,coag,clr=red) # color name "red" must be in quotes
179
180
181
```

**R Console Output:**

```
R 4.0.0 -- Copyright (C) 2019 The R Foundation for Statistical Computing
R> FDP0.result<-describe(FDP0,coag) # save results as "FDP0.result" in R
R> word.table(FDP0.result) # ask R to produce a table to copy into word
,x
n.total,92
n.missing,0
n.available,92
mean,63.043478261
stddev,10.8313836494
median,34.4
lower quartile,23.05
upper quartile,70.8
minimum,2.9
maximum,699.2
normality.pvalue,1.02928373724457e-15

**INSTRUCTIONS**
1. Copy the output into Word.
2. Highlight the output in Word.
3. Go to Insert>Table>Convert Text to Table.
>
```

**Scatter Plot:**

A scatter plot titled "FDP0" showing a positive correlation between two variables. The x-axis ranges from 0 to 700 with major ticks at 0, 100, 200, 300, 400, 500, 600, and 700. The y-axis has three tick marks labeled "...". The data points are represented by small black dots.

63

# Note the instructions in the output.

The screenshot shows the RStudio interface with several windows open:

- Code Editor:** The main window displays an R script named `fall2024-intro-script2.R`. The code includes instructions for copying R output into Microsoft Word, specifically for the `grade` dataset. It uses the `gridExtra` package to create a two-figure plot where the second figure is labeled "Earth".
- Console:** Shows the R session environment. The command `gridExtra::grid.arrange(grade,n,percent,95 LB,95% UB)` was run, resulting in the following output:

```
Grade,n,percent,95% LB,95% UB
1,Intermediate,55,38.19444444444444,0.302309313300611,0.46654277355128
2,Poorly diff,48,33.333333333333,0.257045442150201,0.416639127502788
3,Well diff,41,28.472222222222,0.212695898217411,0.36583462849322
```
- Background Jobs:** Shows the R session ID R 4.4.0 and its current working directory.
- Output:** A Microsoft Word document titled "Grade" is shown. It contains a table with three rows: "Poorly diff", "Intermediate", and "Well diff". Each row has four columns: the category name, the count (n), the percentage (percent), and two numerical values representing LB and UB.
- File Explorer:** Shows the project structure with files like `fall2024-intro-script2.R`, `fall2024-intro-script2.Rproj`, and `fall2024-intro-script2.Rmd`.
- Help:** A help window for the `gridExtra` package is visible.
- Environment:** Shows the current workspace.
- History:** Shows the history of R commands run.
- Connections:** Shows available databases.
- Tutorial:** Shows the R documentation.

64

## Note and follow the instructions in the output.

The screenshot shows the RStudio interface. On the left is the R Script editor with code for generating a grade report. On the right is the R Console window displaying the generated report. A red box highlights the 'INSTRUCTIONS' section in the console output, which contains three steps: 1. Copy the output into Word, 2. Highlight the output in word, and 3. Go to Insert>Table>Convert Text to Table.

```

96   txt=1, tb1=1, # short text, one table
97   fig=2,clr="Earth") # two figures with the Earth
98
99 #####
100 # now copy your results into Word
101
102 grade.result=describe(grade,nki70, # name the results
103   txt=1,tb1=1, # we want text and tables
104   fig=2, # we want two figures
105   clr="Earth") # use the Earth color
106
107 # highlight and copy text from R into word
108 # To get Figure into word: click Export, Copy to ClipBoard
109
110
111 word.table(grade.result) # outputs a table in a format
112   # ***INSTRUCTIONS***
113   # 1. Copy the output into Word.
114   # 2. Highlight the output in Word.
115   # 3. Go to Insert>Table>Convert Text to Table.
116
117 #####
118 # Practice: describe age and get your results into Word
119 # Here's a start
120
121 describe(age,nki70,clr="skyblue")
122 describe(age,nki70,clr="skyblue",fig=2)
123
124
125
126
127
118:11 (Untitled) : R Script
Environment History Connections Tutorial

```

**Grade**

|                  | Poorly diff | Intermediate | Well diff        |
|------------------|-------------|--------------|------------------|
| (n = 48; 33.33%) | 38.19%      | 55; 38.19%   | (n = 41; 28.47%) |

no missing observations

65

## Highlight the output. Right Click. Choose Copy.

The screenshot shows the RStudio interface. On the left is the R Script editor with code for generating a report. On the right is the R Console window displaying the report. A context menu is open over the text in the console, with 'Copy' selected. A red box highlights the 'INSTRUCTIONS' section in the console output, which contains three steps: 1. Copy the output into Word, 2. Highlight the output in word, and 3. Go to Insert>Table>Convert Text to Table.

```

145
146 #####
147 # Try multiple options
148
149 FDP0.describe(Treatment,coag,
150   clr="Spectral",fig=2,txt=0)
151 describe(Treatment,coag,
152   clr="Lisbon",fig=1,tb1=0)
153
154 describe(Treatment,coag,
155   fig=0,txt=1,tb1=0)
156
157 #####
158 # Copy a table into Word
159
160 FDP0.result=describe(FDP0,coag) # save results as "FDP.result" in R
161 word.table(FDP0.result) # ask R to produce a table to copy into word
162
163 #####
164 # Don't freak out if you get errors in R.
165 # Everyone who uses R gets errors.
166 # Dr. Pounds has been using R for over two decades.
167 # He has developed and published extensions of R.
168 # He still gets many many errors every time he uses R.
169 # Errors are usually just typos.
170 # So for practice, Run these lines with errors, fix the typos, run them again.
171
172 describe(FDP0,coag) # capitalize FDP0
173 describe(FDP0,coag,fg=2) # should be fig=2 instead of fg=2
174 describe(FDP0,coag) # should be comma instead of semi-colon
175 describe(FDP0,coag,clr="red") # color name "red" must be in quotes
176
177
178
179
180
181
163:1 (Untitled) : R Script
Environment History Connections Tutorial

```

FDPO

66

In Word,

Right click

Choose paste (text only)

Table with commas is inserted.

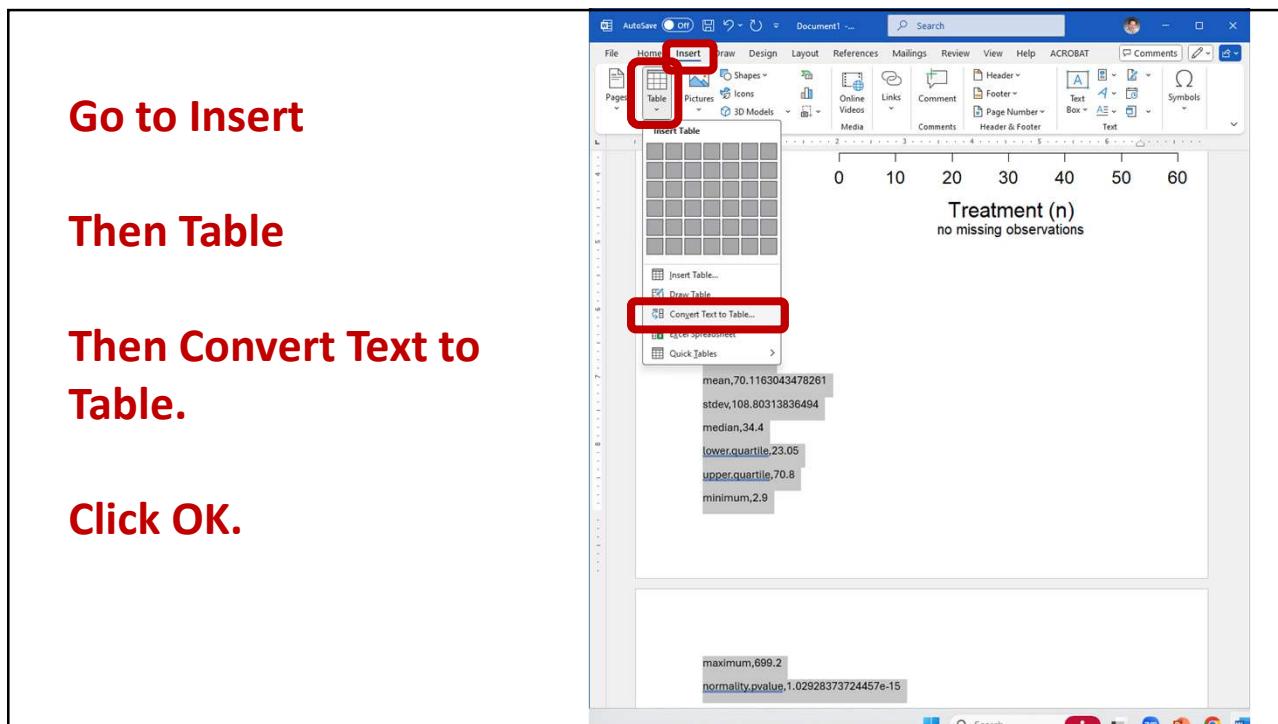
A screenshot of a Microsoft Word document titled 'Document1'. A context menu is open over a chart, with the 'Paste Options' item highlighted by a red box. The chart shows two categories: 'T' with n = 47 (51.09 %) and 'C' with n = 45 (48.91 %). The chart has a title 'Treatment (n)' and a subtitle 'no missing observations'.

67

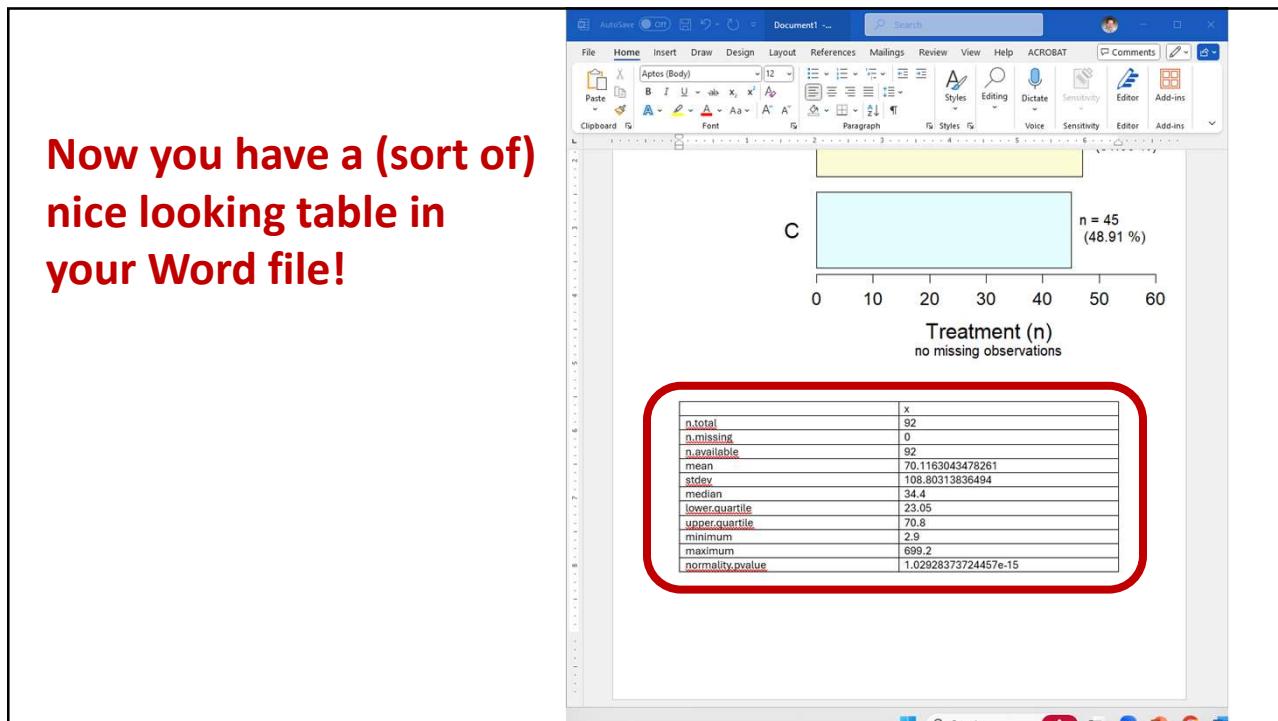
Highlight the table with commas.

A screenshot of a Microsoft Word document showing a clipboard containing a list of statistical values. A red box highlights this list. The values include: n.total,92; n.missing,0; n.available,92; mean,70.1163043478261; stdev,108.80313836494; median,34.4; lower.quartile,23.05; upper.quartile,70.8; minimum,2.9; maximum,699.2; normality.pvalue,1.02928373724457e-15.

68



69



70

**Highlight, right click, copy in R.**

In Word, right click and paste.  
Edit to make it look and read nice.

71

## For Practice

- Try making your own descriptive report for another variable in this data set.

72