A Progressive Introduction to Linear Models

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2023-06-20

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Preliminaries

I designed this book to progressively introduce you to the analysis of data using linear models. My goal is to provide you with the skills needed to perform a linear regression analysis sooner rather than later. Most of the detailed derivations have been placed in **Going Deeper** sections or in their own chapter, which can be skipped over to more quickly progress through the material if you do not want to focus as much on theory.

Acknowledgments

The writing of the book was partially supported by the Colorado Department of Higher Education as part of the proposal "OER for the Creation of Interactive Computational Notebooks and a Computational Pathway in Mathematics and Statistics".

The computational examples utilize the R programming language and environment (R Core Team 2023).

We will also make use of the following packages:

- api2lm (French 2023).
- dplyr (Wickham, François, et al. 2023).
- tidyverse (Wickham 2023b).

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1 R Foundations

Meaningful data analysis requires the use of computer software.

R statistical software is one of the most popular tools for data analysis in academia, industry, and government. In what follows, we will attempt to build a foundation of basic knowledge and skills with R that we will need for data analysis. Our discussion will not be exhaustive, and many other important aspects of data analysis using R (like plotting) will be discussed later, as needed.

1.1 Setting up R and RStudio Desktop

What is R?

R is a programming language and environment designed for statistical computing. It was introduced by Robert Gentleman and Robert Ihaka in 1993 as a free implementation of the S programming language developed at Bell Laboratories (https://www.r-project.org/about.html)

Some important facts about R are that:

- R is free, open source, and runs on many different types of computers (Windows, Mac, Linux, and others).
- R is an interactive programming language.
 - We can type and run a command in the Console for immediate feedback, in contrast to a compiled programming language, which compiles a program that is then executed.
- R is highly extendable.
 - Many user-created packages are available to extend the functionality beyond what is installed by default.
 - Users can write their own functions and easily add software libraries to R.

Installing R

To install R on our personal computer, we will need to download an installer program from the R Project's website (https://www.r-project.org/). Links to download the installer program for a specific operating system are found at https://cloud.r-project.org/.

We should click on the download link appropriate for our computer's operating system and then go through the process of installing R. A stable link for the most current installer program for the Windows operating system is available at https://cloud.r-project.org/bin/windows/base/release.html. (Similar links are not currently available for Mac and Linux computers.)

Installing RStudio

RStudio Desktop is a free "front end" for R provided by Posit Software (https://posit.co/). RStudio Desktop makes doing data analysis with R much easier by adding an Integrated Development Environment (IDE) and providing many other features. Currently, we can download RStudio at https://posit.co/download/rstudio-desktop/. We should download the Free version of RStudio Desktop appropriate for our computer and install it.

Having installed both R and RStudio Desktop, we will want to open RStudio Desktop as we continue to learn about R.

RStudio Layout

RStudio Desktop has four panes:

- 1. Console: the pane where commands are run.
- 2. Source: the pane where we prepare commands to be run.
- 3. Environment/History: the pane where we can see all the objects in our workspace, our command history, and other information.
- 4. The Files/Plot/Packages/Help: the pane where we can navigate between directories, view plots, see available packages, and view help documentation.

To see all RStudio panes, press the keys Ctrl + Alt + Shift + O on a PC or Cmd + Option + Shift + O on a Mac.

Figure 1.1 displays a labeled graphic of the panes. The position of the panes can change depending on how the display preferences are specified, but the look of each pain will be similar.

Customizing the RStudio workspace

At this point, we should make a small workspace customization that will likely save us from experiencing future frustration. R provides a "feature" that allows us to "save a workspace". This allows us to easily pick up our analysis where we last left off. The issue with this is that over time we accumulate a lot of environmental artifacts that can conflict with each other. This can lead to errors and incorrect results that we will need to deal with. Additionally, this "feature" hinders the ability of others to reproduce our analysis because other users are unlikely to have the same workspace.

To turn off this feature, in the RStudio menu bar we click Tools \rightarrow Global Options and then make sure the "General" option is selected. Then we make the following changes (if necessary):

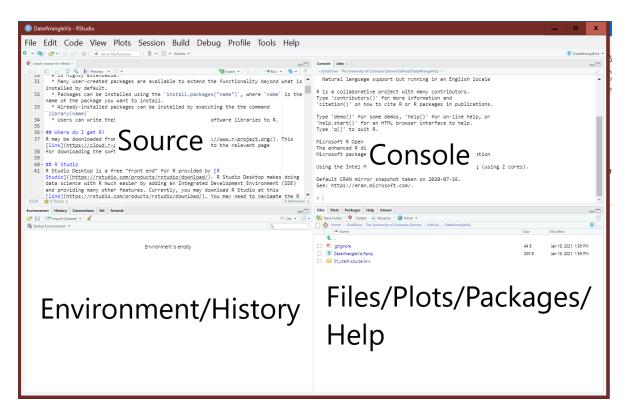


Figure 1.1: The RStudio panes labeled for convenience.

- 1. Uncheck the box for "Restore .RData into workspace at startup".
- 2. Change the toggle box for "Save workspace to .RData on exit" to "Never".
- 3. Click Apply then OK to save the changes.

Figure 1.2 displays what these options should look like.

1.2 Running code, scripts, and comments

We can run code in R by typing it in the Console next to the > symbol and pressing the Enter key.

If we need to successively run multiple commands, it's better to write our commands in a "script" file and then save the file. The commands in a Script file are often generically referred to as "code".

Script files make it easy to:

- Reproduce our data analysis without retyping all our commands.
- Share our code with others.

A new Script file can be obtained by:

- Clicking File \rightarrow New File \rightarrow R Script in the RStudio menu bar.
- Pressing Ctrl + Shift + n on a PC or Cmd + Shift + n on a Mac.

There are various ways to run code from a Script file. The most common ones are:

- 1. Highlight the code we want to run and click the Run button at the top of the Script pane. The Run button icon is shown in Figure 1.3.
- 2. Highlight the code we want to run and press "Ctrl + Enter" on our keyboard. If we don't highlight anything, by default, RStudio runs the command the cursor currently lies on.

To save a Script file:

- Click File \rightarrow Save in the RS tudio menu bar.
- Press Ctrl + s on a PC or Cmd + s on a Mac.

A comment is a set of text ignored by R when submitted to the Console.

A comment is indicated by the # symbol. Nothing to the right of the # is executed by the Console.

To comment (or uncomment) multiple lines of code in the Source pane of RStudio, we highlight the code we want to comment and press Ctrl + Shift + c on a PC or Cmd + Shift + c on a Mac.

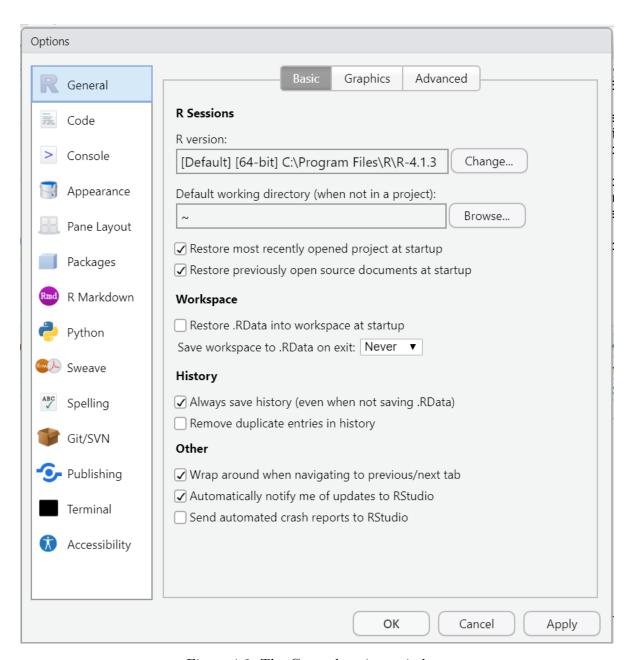


Figure 1.2: The General options window.



Figure 1.3: The Run icon can be clicked to run a selection of commands.

Perform the following tasks:

- 1. Type 1+1 in the Console and press Enter.
- 2. Open a new Script in RStudio.
- 3. Type mean(1:3) in the Script file.
- 4. Type # mean(1:3) in the Script file.
- 5. Run the commands from the Script using an approach mentioned above.
- 6. Save the Script file.
- 7. Use the keyboard shortcut to "comment out" some of the lines of the Script file.

1.3 Assignment

R works on various types of objects that we'll learn more about later.

To store an object in the computer's memory we must assign it a name using the assignment operator <- or the equal sign =.

Some comments:

- In general, both <- and = can be used for assignment.
- Pressing Alt + on a PC or Option + on a Mac will insert <- into the R Console and Script files.
 - If we are creating an R Markdown (rmd) or Quarto Markdown (qmd) file, then this shortcut will only insert <- if we are in an R code block.
- <- and = are NOT synonyms, but can be used identically most of the time.

It is best to use <- for assigning a name to an object and reserving = for specifying function arguments. See Section Section 1.14.1 for a deeper explanation.

Once an object has been assigned a name, it can be printed by running the name of the object in the Console or using the print function.

Run the following commands in the Console:

```
m \leftarrow mean(1:10)
```

In the code above, we compute the sample mean of the values 1, 2, ..., 10, then assign it the name m. However, nothing is printed by the R Console.

m

When we type the name of an object in the R Console and run the command, R will print at least some of the information in the object. In this case, the value stored in m, the value 5.5 will be returned.

```
print(m)
```

The command above is a formal way of printing an object in R and can be especially useful when an object has a defined **print** method with additional arguments. We will discuss this later when it is relevant.

1.4 Functions

A function is an object that performs a certain action or set of actions based on objects it receives from its arguments. We use a sequence of function calls to perform data analysis.

To use a function, we type the function's name in the Console (or Script) and then supply the function's "arguments" between parentheses, ().

The arguments of a function are pieces of data or information the function needs to perform the requested task (i.e., the function "inputs"). Each argument we supply is separated by a comma, ,. Some functions have default values for certain arguments and do not need to specified unless something besides the default behavior is desired.

The mean function computes the sample mean of an R object x. (We can look at the documentation for the function by running ?mean in the Console. We'll talk more about getting help with R shortly.) The mean function also has a trim argument that indicates the, "... fraction ... of observations to be trimmed from each end of x before the mean is computed" (R Core Team 2023, ?mean).

Consider the command below, in which we compute the mean of the set of values 1, 5, 3, 2, 10.

```
mean(c(1, 5, 3, 4, 10))
```

[1] 4.6

In the next command, we compute a trimmed mean of the numeric vector. Since the trim argument is 0.2, we "trim" the smallest 20% of values and the largest 20% of values from the numeric vector prior to computing the mean.

```
mean(c(1, 5, 3, 4, 10), trim = 0.2)
```

[1] 4

The output differs for the two function calls because in the first we compute (1 + 5 + 3 + 4 + 10)/5 = 23/5 = 4.6 while in the second we remove the smallest 20% and largest 20% of the values (i.e., dropping 1 and 10) and compute (5 + 3 + 4)/3 = 12/3 = 4.

1.5 Packages

Packages are collections of functions, data, and other objects that extend the functionality available in R by default.

R packages can be installed using the install.packages function and loaded using the library function.

Hands-on Practice

The **tidyverse** (Wickham 2023b) is a popular ecosystem of R packages used for manipulating, tidying, and plotting data. Currently, the **tidyverse** is comprised of the following packages:

- **ggplot2**: A package for plotting based on the "Grammar of Graphics" (Wickham, Chang, et al. 2023).
- purrr: A package for functional programming (Wickham and Henry 2023).
- tibble: A package providing a more advanced data frame (Müller and Wickham 2023).
- **dplyr**: A package for manipulating data (Wickham, François, et al. 2023). . More specifically, it provides "a grammar of data manipulation".
- tidyr: A package to help create "tidy" data (Wickham, Vaughan, and Girlich 2023). Tidy data is an data organization style often convenient for data analysis.

- stringr: A package for working with character/string data (Wickham 2022).
- readr: A package for importing data (Wickham, Hester, and Bryan 2023).
- forcats: A package for working with categorical data (Wickham 2023a).

Install the set of tidyverse R packages by running the command below in the Console.

```
install.packages("tidyverse")
```

After we install the **tidyverse**, we load the collection of packages by running the command below.

```
library(tidyverse)
```

We should see something like the output below.

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr
           1.1.2
                     v readr
                                  2.1.4
v forcats
           1.0.0
                     v stringr
                                  1.5.0
          3.4.2
                     v tibble
                                  3.2.1
v ggplot2
v lubridate 1.9.2
                     v tidyr
                                  1.3.0
           1.0.1
v purrr
-- Conflicts -----
                                     -----cidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()
                 masks stats::lag()
i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become
```

Notice that when we loaded the **tidyverse** packages above that dplyr::lag() masks stats::lag(). What this means is that both the dplyr and stats packages have a function called lag. Different packages may use the same function name to provide certain functionality. The functions will likely be used for different tasks or require different arguments.

To refer to a function in a specific package, we should add the syntax package:: prior to the function name. In the code below, we run stats::lag and dplyr::lag on two different objects using the :: syntax.

```
# run stats::lag on a numeric vector
stats::lag(1:10, 2)

[1] 1 2 3 4 5 6 7 8 9 10
attr(,"tsp")
```

```
[1] -1 8 1
```

```
# run dplyr::lag on a numeric vector
dplyr::lag(1:10, 2)
[1] NA NA 1 2 3 4 5 6 7 8
```

The output returned by the two functions is different because the functions are intended to do different things. The stats::lag function call shifts the time base of the provided time series object back 2 units, while the call to dplyr::lag provides the values 2 positions earlier in the object.

Note: this example is not intended to help us understand the lag function. This example highlights how to use the :: syntax to call a function in a specific package when the function name is used in multiple packages.

1.6 Getting help

There are many ways to get help in R.

If we know the command for which we want help, then we run ?command in the Console to access the documentation for the object (where command is replaced by the name of the relevant command). This approach will also work with data sets, package names, object classes, etc. If we need to refer to a function in a specific package, we can use ?package::function to get help on a specific function, e.g., ?dplyr::filter.

The documentation will provide:

- A **Description** section with general information about the function or object.
- A Usage section with a generic template for using the function or object.
- An **Arguments** section summarizing the function inputs the function needs.
- A Details section may be provided with additional information about the function or object.
- A Value section that describes what is returned by the function.
- An **Examples** section providing examples of how to use the function. Usually, these can be copied and pasted into the Console to better understand the function arguments and what it produces.

If we need to find a command related to a certain *topic*, then ??topic will search for the topic through all installed documentation and bring up any vignettes, code demonstrations, or help pages that include the topic for which we searched.

If we are trying to figure out why an error is being produced, what packages can be used to perform a certain analysis, how to perform a complex task that we can't seem to figure out, etc., then we can simply do a web search for what we're trying to figure out! Because R is such a popular programming language, it is likely we will find a stackoverflow response, a helpful blog post, an R users forum response, etc., that addresses our question.

Hands-on Practice

Do the following:

- 1. Run?lm in the Console to get help on the lm function, which is one of the main functions used for fitting linear models.
- 2. Run ??logarithms in the Console to search the R documentation for information about logarithms. It is likely that we will see multiple help pages that mention "logarithm", so we may end up needing to find the desired entry via trial and error.
- 3. Run a web search for something along the lines of "How do I change the size of the axis labels in an R plot?".

1.7 Data types and structures

1.7.1 Basic data types

R has 6 basic ("atomic") vector types (https://cran.r-project.org/doc/manuals/r-release/R-lang.html#Basic-types) (R Core Team 2023):

- 1. character: collections of characters. E.g., "a", "hello world!".
- 2. double: decimal numbers. e.g., 1.2, 1.0.
- 3. integer: whole numbers. In R, we must add L to the end of a number to specify it as an integer. E.g., 1L is an integer but 1 is a double.
- 4. logical: Boolean values, TRUE and FALSE.
- 5. complex: complex numbers. E.g., 1+3i.
- 6. raw: a type to hold raw bytes.

Both double and integer values are specific types of numeric values.

The type of function returns the R internal type or storage mode of any object.

Consider the output of the commands below. What are some of the difference in the output?

```
typeof(1)

[1] "double"

typeof(1L)

[1] "integer"

typeof("hello world!")

[1] "character"
```

1.7.2 Other important object types

There are other important types of objects in R that are not basic. We will discuss a few. The R Project manual provides additional information about available types (https://cran.r-project.org/doc/manuals/r-release/R-lang.html#Basic-types).

1.7.2.1 Numeric

An object is numeric if it is of type integer or double. In that case, it's mode is said to be numeric.

The is.numeric function tests whether an object can be interpreted as numbers. We can use it to determine whether an object is numeric. We do some examples of this in the code chunks run below. Are any of the results surprising?

```
is.numeric("hello world!")
[1] FALSE
is.numeric(1)
```

[1] TRUE

```
is.numeric(1L)
```

[1] TRUE

1.7.2.2 NULL

NULL is a special object to indicate an object is absent. An object having a length of zero is not the same thing as an object being absent.

1.7.2.3 NA

A "missing value" occurs when the value of something isn't known. R uses the special object NA to represent a missing value.

If we have a missing value, we should represent that value as NA. "NA" is not the same object as NA.

1.7.2.4 Functions

From R's perspective, a function is simply another data type.

1.7.2.5 A comment about classes

Every R object has a class that may be distinct from its type. Many functions will operate differently depending on an object's class.

1.7.3 Data structures

R operates on data structures. A data structure is a "container" that holds certain kinds of information.

R has 5 basic data structures:

- 1. vector.
- 2. matrix.
- 3. array.
- 4. data frame.

5. list.

Vectors, matrices, and arrays are homogeneous objects that can only store a single data type at a time. Data frames and lists can store multiple data types.

Vectors and lists are considered one-dimensional objects. A list is technically a vector. Vectors of a single type are atomic vectors (https://cran.r-project.org/doc/manuals/r-release/R-lang.html#List-objects). Matrices and data frames are considered two-dimensional objects. Arrays can have 1 or more dimensions.

The relationship between dimensionality and data type for the basic data structures is summarized in Table 1.1, which is based on a table in the first edition of Hadley Wickham's Advanced R (Wickham 2019).

Table 1.1: A table summarizing the relationship between dimensionality and data type homogeneity for the 5 basic data structures.

number of dimensions	homogeneous data type	heterogeneous data types
1	atomic vector	list
2	matrix	data frame
1 or more	array	

1.8 Vectors

A *vector* is a one-dimensional set of data of the same type.

1.8.1 Direct creation

The most basic way to create a vector is the c (combine) function. The c function combines values into an atomic vector or list.

The following commands create vectors of type numeric, character, and logical, respectively.

- c(1, 2, 5.3, 6, -2, 4)
- c("one", "two", "three")
- c(TRUE, TRUE, FALSE, TRUE)

R provides two main functions for creating vectors with specific patterns: seq and rep.

1.8.2 The seq function

The seq (sequence) function is used to create an equidistant series of numeric values. Some examples:

- seq(1, 10) creates a sequence of numbers from 1 to 10 in increments of 1.
- 1:10 creates a sequence of numbers from 1 to 10 in increments of 1.
- seq(1, 20, by = 2) creates a sequence of numbers from 1 to 20 in increments of 2.
- seq(10, 20, len = 100) creates a sequence of numbers from 10 to 20 of length 100.

Hands-on Practice

Run the commands below in the Console and try to answer the questions below.

What does the by argument of the seq function control?

What does the len argument of the seq function control?

```
seq(1, 10)

1:10

seq(1, 20, by = 2)

seq(10, 20, len = 100)
```

1.8.3 The rep function

The rep (replicate) function can be used to create a vector by replicating values. Some examples:

- rep(1:3, times = 3) replicates the sequence 1, 2, 3 three times in a row.
- rep(c("trt1", "trt2", "trt3"), times = 1:3) replicates "trt1" once, "trt2" twice, and "trt3" three times.
- rep(1:3, each = 3) replicates each element of the sequence 1, 2, 3 three times.

Run the commands below in the Console and try to answer the questions below.

What does the times argument of the rep function control?

What does the each argument of the rep function control?

```
rep(1:3, times = 3)
rep(c("trt1", "trt2", "trt3"), times = 1:3)
rep(1:3, each = 3)
```

1.8.4 Combining vectors

Multiple vectors can be combined into a new vector object using the c function. E.g., c(v1, v2, v3) will combine vectors v1, v2, and v3.

Hands-on Practice

Run the commands below in the Console. Determine what action each command performs.

```
v1 <- 1:5

v2 <- c(1, 10, 11)

v3 <- rep(1:2, each = 3)

new <- c(v1, v2, v3)

new
```

1.8.5 Categorical vectors

Categorical data should be stored as a factor in R. Even though our code related to categorical data may work when stored as character or numeric data because a cautious developer planned for that possibility, it is best to use good coding practices that minimize potential issues.

1.8.5.1 Creating a factor object

The factor function takes a vector of values that can be coerced to type character and converts them to an object of class factor. In the code chunks below, we create two factor objects from vectors.

```
f1 <- factor(rep(1:6, times = 3))
f1

[1] 1 2 3 4 5 6 1 2 3 4 5 6 1 2 3 4 5 6
Levels: 1 2 3 4 5 6

f2 <- factor(c("a", 7, "blue", "blue", FALSE))
f2

[1] a 7 blue blue FALSE
Levels: 7 a blue FALSE</pre>
```

A printed factor object lists the Levels (i.e., unique categories) of the object.

The is.factor function can be used to determine whether an object is a factor.

factor objects aren't technically vectors (e.g., running is.factor(f2) based on the above code will return FALSE) though they essentially behave like vectors, which is why they are included here.

Complete the following tasks:

- 1. Create a vector named grp that has two levels: a and b, where the first 7 values are a and the second 4 values are b.
- 2. Run is.factor(grp) in the Console.
- 3. Run is.vector(grp) in the Console.
- 4. Run typeof(grp) in the Console.

Related to the last task, a factor object is *technically* a collection of integers that have labels associated with each unique integer value.

1.8.5.2 Creating an ordered factor object

Let's create an ordered factor object.

Suppose we have categorical data with the categories small, medium, and large. We create a size vector with hypothetical data below.

```
size <- c("small", "medium", "small", "large", "medium", "medium", "large")</pre>
```

If we convert size to a factor object, R will automatically order the levels of size alphabetically, as seen from the code chunk below.

```
factor(size)
```

[1] small medium small large medium medium large Levels: large medium small

This is not technically a problem, but can result in undesirable side effects such as plots with levels in an undesirable order.

To create an ordered factor object, we specify the desired order of the levels using the levels argument and set the ordered argument to TRUE, as in the code below.

```
factor(size, levels = c("small", "medium", "large"), ordered = TRUE)
```

[1] small medium small large medium medium large Levels: small < medium < large

1.8.6 Extracting parts of a vector

Parts a vector can be extracted by appending an index vector in square brackets [] to the name of the vector, where the index vector indicates which parts of the vector to retain or exclude. We can include either numbers or logical values in our index vector. We discuss both approaches below.

1.8.6.1 Selection using a numeric index vector

Let's create a numeric vector a with the values 2, 4, 6, 8, 10, 12, 14, 16.

```
a <- seq(2, 16, by = 2)
a
```

```
[1] 2 4 6 8 10 12 14 16
```

To extract the 2nd, 4th, and 6th elements of a, we can use the code below. The code indicates that the 2nd, 4th, and 6th elements of a should be extracted.

```
a[c(2, 4, 6)]
```

[1] 4 8 12

We can also use "negative" indexing to indicate the elements of the vector we want to exclude. Specifically, supplying a negative index vector indicates the values we want to exclude from our selection.

In the example below, we use the minus (-) sign in front of the index vector c(2, 4, 6) to indicate we want all elements of a EXCEPT the 2nd, 4th, and 6th.

```
a[-c(2, 4, 6)]
```

Running the code chunk below excludes the 3rd through 6th elements of a.

```
a[-(3:6)]
```

[1] 2 4 14 16

1.8.6.2 Logical expressions

A logical expression uses one or more logical operators to determine which elements of an object satisfy the specified statement. The basic logical operators are:

- <, <=: less than, less than or equal to.
- >, >=: greater than, greater than or equal to.
- ==: equal to.
- !=: not equal to.

Creating a logical expression with a vector will result in a logical vector indicating whether each element satisfies the logical expression.

Hands-on Practice

Run the following commands in R and see what is printed. What task is each statement performing?

a > 10

a <= 4

a == 10

a != 10

1.8.6.3 The "and", "or", and "not" operators

We can create more complicated logical expressions using the "and", "or", and "not" operators.

- &: and.
- |: or.
- !: not, i.e., not true.

The & operator returns TRUE if all logical values connected by the & are TRUE, otherwise it returns FALSE.

The | operator returns TRUE if any logical values connected by the | are TRUE, otherwise it returns FALSE.

The ! operator returns the complement of a logical value or expression.

Hands-on Practice

Run the following commands below in the Console.

What action is each command performing?

What role does & serve in a sequence of logical values?

Similarly, what roles do | and ! serve in a sequence of logical values?

```
TRUE & TRUE & TRUE

TRUE & TRUE & FALSE

FALSE | TRUE | FALSE

FALSE | FALSE | FALSE

!TRUE

!FALSE
```

1.8.6.4 Connecting logical expressions

Logical expressions can be connected via & and | (and impacted via !), in which case the operators are applied elementwise (i.e., to all of the first elements in the expressions, then all the second elements in the expressions, etc).

Run the following commands in R and see what is printed. What task is each statement performing?

Note that the parentheses () are used to group logical expressions to more easily understand what is being done. This is a good coding style to follow.

```
(a > 6) & (a <= 10)

(a <= 4) | (a >= 12)

!((a <= 4) | (a >= 12))
```

1.8.6.5 Selection using logical expressions

Logical expressions can be used to return parts of an object satisfying the appropriate criteria. Specifically, we pass logical expressions within the square brackets to access part of a data structure. This syntax will return each element of the object for which the expression is TRUE.

Hands-on Practice

Run the following commands in R and see what is printed. What task is each statement performing?

```
a[a < 6]

a[a == 10]

a[(a < 6) | (a == 10)]
```

1.9 Helpful functions

We provide a brief overview of R functions we often use in our data analysis.

1.9.1 General functions

For brevity, Table 1.2 provides a table of functions commonly useful for basic data analysis along with a description of their purpose.

Table 1.2: Functions frequently useful for data analysis.

function. purpose		
length	Determines the length/number of elements in an object.	
sum	Sums the elements in the object.	
mean	Computes the sample mean of the elements in an object.	
var	Computes the sample variance of the elements in an object.	
sd	Computes the sample standard deviation the elements of an object.	
range	Determines the range (minimum and maximum) of the elements of an object.	
log	Computes the (natural) logarithm of elements in an object.	
summary	Returns a summary of an object. The output changes depending on the class type	
	of the object.	
str	Provides information about the structure of an object. Usually, the class of the	
	object and some information about its size.	

Hands-on Practice

Run the following commands in the Console. Determine what task each command is performing.

```
x <- rexp(100) # sample 100 iid values from an Exponential(1) distribution
length(x)
sum(x)
mean(x)</pre>
```

```
var(x)
sd(x)
range(x)
log(x)
summary(x)
str(x) # structure of x
```

1.9.2 Functions related to statistical distributions

R is designed specifically for statistical analysis, so it natively includes functionality for determining properties of statistical distributions. R makes it easy to evaluate the cumulative distribution function (CDF) of a distribution, the quantiles of a distribution, the density or mass of a distribution, and to sample random values from a distribution.

Suppose that a random variable X has the dist distribution. The function templates in the list below describe how to obtain certain properties of X.

- p[dist](q, ...): returns the cdf of X evaluated at q, i.e., $p = P(X \le q)$.
- q[dist] (p, ...): returns the inverse cdf (or quantile function) of X evaluated at p, i.e., $q = \inf\{x : P(X \le x) \ge p\}$.
- d[dist](x, ...): returns the mass or density of X evaluated at x (depending on whether it's discrete or continuous).
- r[dist](n, ...): returns an independent and identically distributed random sample of size n having the same distribution as X.
- The ... indicates that additional arguments describing the parameters of the distribution may be required.

To determine the distributions available by default in R, run ?Distributions in the R Console. We demonstrate some of this functionality in the practice below.

Note: If we are using functions related to statistical distributions in R, then it is imperative that we look at the associated documentation to determine the parameterization of the distribution, as this dramatically impacts the results. Some distributions have multiple common parameterizations.

Run the following commands in R to see the output. Before each command is a description of the action performed by the command.

pnorm(1.96, mean = 0, sd = 1) returns the probability that a standard normal random variable is less than or equal to 1.96, i.e., $P(X \le 1.96)$.

```
pnorm(1.96, mean = 0, sd = 1)
```

qunif(0.6, min = 0, max = 1) returns the value x such that $P(X \le x) = 0.6$ for a uniform random variable on the interval [0,1].

```
qunif(0.6, min = 0, max = 1)
```

dbinom(2, size = 20, prob = .2) returns the probability that X equals 2 when X has a Binomial distribution with n = 20 trials and the probability of a successful trial is 0.2.

```
dbinom(2, size = 20, prob = .2)
```

dexp(1, rate = 2) evaluates the density of an exponential random variable with mean = 1/2 (i.e., the reciprocal of the rate) at x = 1.

```
dexp(1, rate = 2)
```

rchisq(100, df = 5) draws a sample of 100 observations from a chi-squared random variable with 5 degrees of freedom.

```
rchisq(100, df = 5)
```

1.10 Data Frames

Data frames are two-dimensional data objects. Each column of a data frame is a vector (or variable) of possibly different data types. This is a *fundamental* data structure used by most of R's modeling software. The class of a **base** R data frame is **data.frame**, which is technically a specially structured list.

In general, I recommend *tidy data*, which means that each variable forms a column of the data frame, and each observation forms a row.

1.10.1 Direct creation

Data frames are directly created by passing vectors into the data.frame function.

The names of the columns in the data frame are the names of the vectors we give the data.frame function. Consider the following simple example.

```
# simple data frame creation
  d \leftarrow c(1, 2, 3, 4)
  e <- c("red", "white", "blue", NA)
  f <- c(TRUE, TRUE, TRUE, FALSE)
  df <- data.frame(d,e,f)</pre>
  df
  d
               f
1 1
           TRUE
      red
2 2 white
           TRUE
3 3 blue
           TRUE
    <NA> FALSE
```

The columns of a data frame can be renamed using the names function on the data frame and assigning a vector of names to the data frame.

```
# name columns of data frame
names(df) <- c("ID", "Color", "Passed")
df

ID Color Passed
1 1 red TRUE
2 2 white TRUE
3 3 blue TRUE
4 4 <NA> FALSE
```

The columns of a data frame can be named when we create the data frame by using the syntax name = for each vector of data.

```
# create data frame with better column names
df2 <- data.frame(ID = d, Color = e, Passed = f)
df2

ID Color Passed
1 1 red TRUE
2 2 white TRUE
3 3 blue TRUE
4 4 <NA> FALSE
```

1.10.2 Importing Data

Direct creation of data frames is only appropriate for very small data sets. In practice, we likely want to import data from a file into R.

The read.table function imports data in table format from file into R as a data frame.

The basic usage of this function is: read.table(file, header = TRUE, sep = ",").

- file is the file path and name of the file we want to import into R.
 - If we don't know the file path, setting file = file.choose() will bring up a dialog box asking us to locate the file we want to import.
- header specifies whether the data file has a header (variable labels for each column of data in the first row of the data file).
 - If we don't specify this option in R or use header = FALSE, then R will assume the file doesn't have any headings.
 - header = TRUE tells R to read in the data as a data frame with column names taken from the first row of the data file.
- sep specifies the delimiter separating elements in the file.
 - If each column of data in the file is separated by a space, then use sep = " ".
 - If each column of data in the file is separated by a comma, then use sep = ",".
 - If each column of data in the file is separated by a tab, then use $sep = "\t"$.

Consider reading in a csv (comma separated file) with a header.

The file in question is available in the **api2lm package** (French 2023) and contains crime-related information for U.S. states for the year 2009. However, we will import the data directly from a location where it is stored on GitHub.

In the code below, we specify the path of the file prior to specifying the file name (crime2009.csv). Since the file has a header, we specify header = TRUE. Since the data values are separated by commas, we specify sep = ",".

```
# specify file path
 path <- "https://raw.githubusercontent.com/jfrench/api2lm/main/inst/extdata/crime2009.csv"</pre>
  # import data as data frame
  crime2009 <- read.table(file = path, header = TRUE, sep = ",")</pre>
  # view data structure
  str(crime2009)
'data.frame':
               51 obs. of 8 variables:
$ state : chr "Alabama" "Alaska" "Arizona" "Arkansas" ...
$ violent: num 460 633 423 530 473 ...
$ murder : num 7.1 3.2 5.5 6.3 5.4 3.2 3 4.6 24.2 5.5 ...
$ hs grad: num 82.1 91.4 84.2 82.4 80.6 89.3 88.6 87.4 87.1 85.3 ...
$ poverty: num
               17.5 9 16.5 18.8 14.2 12.9 9.4 10.8 18.4 14.9 ...
$ single : num
               29 25.5 25.7 26.3 27.8 21.4 25 27.6 48 26.6 ...
                70 68.3 80 78.4 62.7 84.6 79.1 71.9 38.7 76.9 ...
$ white : num
               48.6 44.5 80.1 39.5 89.7 ...
$ urban : num
```

Running str on the data frame gives us a general picture of the values stored in the data frame.

The read_table function in the readr package (Wickham, Hester, and Bryan 2023) is arguably a better way of importing tabular data from file and uses similar syntax. To import data contained in Microsoft Excel files, we can use functions available in the readxl package (Wickham and Bryan 2023).

1.10.3 Extracting parts of a data frame

R provides many ways to extract parts of a data frame. We will provide several examples using the mtcars data frame in the datasets package.

The mtcars data frame has 32 observations for 11 variables. The variables are:

- mpg: miles per gallon.
- cyl: number of cylinders.
- disp: engine displacement (cubic inches).
- hp: horsepower.
- drat: rear axle ratio.
- wt: weight in 1000s of pounds.
- qsec: time in seconds to travel 0.25 of a mile.
- vs: engine shape (0 = V-shaped, 1 = straight).
- am: transmission type (0 = automatic, 1 = manual).
- gear: number of forward gears.
- carb: number of carburetors.

We load the data set and examine the basic structure by running the commands below.

```
data(mtcars) # load data set
  str(mtcars) # examine data structure
'data.frame':
               32 obs. of 11 variables:
$ mpg : num 21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
$ cyl : num 6 6 4 6 8 6 8 4 4 6 ...
$ disp: num
             160 160 108 258 360 ...
$ hp : num
             110 110 93 110 175 105 245 62 95 123 ...
$ drat: num
             3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
$ wt : num
             2.62 2.88 2.32 3.21 3.44 ...
             16.5 17 18.6 19.4 17 ...
$ qsec: num
$ vs : num
             0 0 1 1 0 1 0 1 1 1 ...
$ am : num 1 1 1 0 0 0 0 0 0 0 ...
$ gear: num 4 4 4 3 3 3 3 4 4 4 ...
$ carb: num 4 4 1 1 2 1 4 2 2 4 ...
```

We should do some data cleaning on this data set (see Chapter 2), but we will refrain from this for simplicity.

1.10.3.1 Direct extraction

The column variables of a data frame may be extracted from a data frame by specifying the data frame's name, then \$, and then specifying the name of the desired variable. This pulls the actual variable vector out of the data frame, so the thing extracted is a vector, not a data frame

Below, we extract the mpg variable from the mtcars data frame.

```
mtcars$mpg
```

```
[1] 21.0 21.0 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2 10.4 [16] 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26.0 30.4 15.8 19.7 [31] 15.0 21.4
```

Another way to extract a variable from a data frame as a vector is df[, "var"], where df is the name of our data frame and var is the desired variable name. We extract the mpg vector from mtcars below.

```
mtcars[,"mpg"]
```

```
[1] 21.0 21.0 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2 10.4 [16] 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26.0 30.4 15.8 19.7 [31] 15.0 21.4
```

The syntax above is a special case of extracting information from a data frame using df [rows, columns] style syntax, where rows and columns indicate the desired rows or columns to extract. If either the rows or columns are left blank, then all rows or columns, respectively, are extracted.

The df [rows, columns] syntax has confusing behavior when you only specify a single column. Specifically, the [operator has a drop argument that is set to TRUE by default. The drop argument controls whether the result is coerced to the lowest possible dimension. If we we only specify a single column of our data frame, then R will coerce the result to a vector by default

To get around the default **drop** behavior we can change the **drop** argument to FALSE, as shown below.

```
# extract mpg variable, keep as data frame
mtcars[,"mpg", drop = FALSE]
```

mpg
21.0
21.0
22.8
21.4
18.7
18.1
14.3
24.4
22.8
19.2
17.8
16.4
17.3
15.2
10.4
10.4
14.7
32.4
30.4
33.9
21.5
15.5
15.2
13.3
19.2
27.3
26.0
30.4
15.8
19.7
15.0
21.4

An easier approach to avoiding the default drop behavior is to use the slightly different syntax df["var"] (notice we no longer have the comma to separate rows and columns). We use this syntax below for the mpg variable in mtcars.

```
# extract mpg variable, keep as data frame
mtcars["mpg"]
```

 ${\tt mpg}$

Mazda RX4	21.0
Mazda RX4 Wag	21.0
Datsun 710	22.8
Hornet 4 Drive	21.4
Hornet Sportabout	18.7
Valiant	18.1
Duster 360	14.3
Merc 240D	24.4
Merc 230	22.8
Merc 280	19.2
Merc 280C	17.8
Merc 450SE	16.4
Merc 450SL	17.3
Merc 450SLC	15.2
Cadillac Fleetwood	10.4
Lincoln Continental	10.4
Chrysler Imperial	14.7
Fiat 128	32.4
Honda Civic	30.4
Toyota Corolla	33.9
Toyota Corona	21.5
Dodge Challenger	15.5
AMC Javelin	15.2
Camaro Z28	13.3
Pontiac Firebird	19.2
Fiat X1-9	27.3
Porsche 914-2	26.0
Lotus Europa	30.4
Ford Pantera L	15.8
Ferrari Dino	19.7
Maserati Bora	15.0
Volvo 142E	21.4

To select multiple variables in a data frame, we can provide a character vector with multiple variable names between []. In the example below, we extract both the mpg and cyl variables from mtcars.

```
mtcars[c("mpg", "cyl")]
```

			mpg	cyl
${\tt Mazda}$	RX4		21.0	6
Mazda	RX4	Wag	21.0	6

Datsun 710	22.8	4
Hornet 4 Drive	21.4	6
Hornet Sportabout	18.7	8
Valiant	18.1	6
Duster 360	14.3	8
Merc 240D	24.4	4
Merc 230	22.8	4
Merc 280	19.2	6
Merc 280C	17.8	6
Merc 450SE	16.4	8
Merc 450SL	17.3	8
Merc 450SLC	15.2	8
Cadillac Fleetwood	10.4	8
Lincoln Continental	10.4	8
Chrysler Imperial	14.7	8
Fiat 128	32.4	4
Honda Civic	30.4	4
Toyota Corolla	33.9	4
Toyota Corona	21.5	4
Dodge Challenger	15.5	8
AMC Javelin	15.2	8
Camaro Z28	13.3	8
Pontiac Firebird	19.2	8
Fiat X1-9	27.3	4
Porsche 914-2	26.0	4
Lotus Europa	30.4	4
Ford Pantera L	15.8	8
Ferrari Dino	19.7	6
Maserati Bora	15.0	8
Volvo 142E	21.4	4

We can also use numeric indices to directly indicate the rows or columns of the data frame that we would like to extract. We can also combine this syntax sylte with the syntax styles previously discussed.

- df[1,] accesses the first row of df.
- df[1:2,] accesses the first two rows of df.
- df[,2] accesses the second column of df.
- df[1:2, 2:3] accesses the information in rows 1 and 2 of columns 2 and 3 of df.
- df[c(1, 3, 5), c("var1", "var2")] accesses the information in rows 1, 3, and 5 of the var1 and var2 variables.

We practice these techniques below.

Run the following commands in the Console. Determine what task each command is performing.

1.10.3.2 Extraction using logical expressions

Logical expressions can be used to subset a data frame.

To select specific rows of a data frame, we use the syntax df[logical vector,], where logical vector is a valid logical vector whose length matches the number of rows in the data frame. Usually, the logical vector is created using a logical expression involving one or more data frame variables. In the code below, we extract the rows of the mtcars data frame for which the hp variable is more than 250.

```
mtcars[mtcars$hp > 250,]
```

```
mpg cyl disp hp drat wt qsec vs am gear carb
Ford Pantera L 15.8 8 351 264 4.22 3.17 14.5 0 1 5 4
Maserati Bora 15.0 8 301 335 3.54 3.57 14.6 0 1 5 8
```

We can make the logical expression more complicated and also select specific variables using the syntax discussed in Section 1.10.3.1. Below, we extract the rows of mtcars with 8 cylinders and mpg > 17, while extracting only the mpg, cyl, disp, and hp variables.

```
mpg cyl disp hp
Hornet Sportabout 18.7 8 360.0 175
Merc 450SL 17.3 8 275.8 180
Pontiac Firebird 19.2 8 400.0 175
```

1.10.3.3 Extraction using the subset function

The techniques for extracting parts of a data frame discussed in Sections -Section 1.10.3.1 and -Section 1.10.3.2 are the fundamental approaches for selecting desired parts of a data frame. However, these techniques can seem complex and difficult to interpret, particularly when looking back at code we have written in the past. A sleeker approach to extracting part of a data frame is to use the subset function.

The subset function returns the parts of a data frame that meets the specified conditions. The basic usage of this function is: subset(x, subset, select, drop = FALSE)

- x is the object we want to subset.
 - x can be a vector, matrix, or data frame.
- subset is a logical expression that indicates the elements or rows of x to keep (TRUE means keep).
- select is a vector that indicates the columns to keep.
- drop is a logical value indicating whether the data frame should "drop" into a vector if only a single row or column is kept. The default is FALSE, meaning that a data frame will always be returned by the subset function by default.

There are many clever ways of using subset to select specific parts of a data frame. We encourage the reader to run?base::subset in the Console for more details.

Run the following commands in the Console to use the subset function to extract parts of the mtcars data frame.

The command below subsets the rows of mtcars that have more than 4 gears. Note that any variables referred to in the subset function are assumed to be part of the supplied data frame or are available in memory.

```
subset(mtcars, subset = gear > 4)
```

The command below will select the disp, hp, and gear variables of mtcars but will exclude the other columns.

```
subset(mtcars, select = c(disp, hp, gear))
```

Lastly, we can use the following command to perform the two previous subsetting actions in one step.

```
subset(mtcars, subset = gear > 4, select = c(disp, hp, gear))
```

An advantage of the subset function is that it makes code easily readable. Using conventional base R syntax, the final code example above would be: mtcars[mtcars\$gear>4, c("disp", "hp", "gear")].

It can be difficult to look at base R code and immediately tell what it happening, so the subset function adds clarity. This is important for collaborating with others, including our future selves!

1.11 Using the pipe operator

R's native pipe operator (|>) allows us to "pipe" the object on the left side of the operator into the first argument of the function on the right side of the operator. There are ways to modify this default behavior, but we will not discuss them.

The pipe operator is a convenient way to string together numerous steps in a string of commands. This coding style is generally considered more readable than other approaches because we can incrementally modify the object through each pipe, and each step of the pipe is easy to understand. Ultimately, it's a stylistic choice that we can decide to adopt or ignore.

Consider the following approaches to extracting part of mtcars. We choose the rows for which engine displacement is more than 400 and only keep the mpg, disp, and hp columns. We first do this in a single function call using the subset function.

Next, we use the piping approach to break the action into smaller parts.

```
mtcars |>
    subset(subset = disp > 400) |>
    subset(select = c(mpg, disp, hp))

    mpg disp hp
Cadillac Fleetwood 10.4 472 205
Lincoln Continental 10.4 460 215
Chrysler Imperial 14.7 440 230
```

When reading code with pipes, the pipe can be thought of as the word "then". In the code above, we take mtcars then subset it based on disp and then select some columns.

Most parts of the world do not use miles per gallon to measure fuel economy because they don't measure distance in miles nor volume in gallons. A common measure of fuel economy is the liters of fuel required to travel 100 kilometers. Noting that 3.8 liters is approximately equivalent to 1 U.S. gallon and 1.6 kilometers is approximately equivalent to 1 mile, we can convert fuel economy of x miles per gallon to liters per 100 kilometers by noting:

$$\frac{1}{x}\frac{\text{gal}}{\text{mi}} \times \frac{3.8}{1}\frac{\text{L}}{\text{gal}} \times \frac{1}{1.6}\frac{\text{mi}}{\text{km}} \times \frac{100 \text{ km}}{100 \text{ km}} = \frac{237.5}{x}\frac{\text{L}}{100 \text{ km}}.$$

Thus, to convert from miles per gallon to liters per 100 kilometers, we take 237.5 and divide by the number of miles per gallon.

We consider two approaches for converting the units of a variable in miles per gallon to liters per 100 km. In the first approach, we use the base::transform function create a new variable,

1p100km, in the mtcars data frame that describes the liters of fuel each car requires to travel 100 kilometers and assign it the name mtcars2. Then we select only the columns mpg and 1p100km from mtcars and assign it the name mtcars3. We then use the head function to print only the first 5 observations. Run ?base::transform in the Console for more details and examples.

```
# create new variable
mtcars2 <- transform(mtcars, lp100km = 237.5/mpg)
# select certain columns
mtcars3 <- subset(mtcars2, select = c(mpg, lp100km))
# print first 5 rows
head(mtcars3, n = 5)</pre>
```

```
mpglp100kmMazda RX421.011.30952Mazda RX4 Wag21.011.30952Datsun 71022.810.41667Hornet 4 Drive21.411.09813Hornet Sportabout18.712.70053
```

Next, we perform the actions above with pipes.

```
# create new variable, select columns, extract first 5 rows
mtcars |>
  transform(lp100km = 237.5/mpg) |>
  subset(select = c(mpg, lp100km)) |>
  head(n = 5)
```

```
mpglp100kmMazda RX421.011.30952Mazda RX4 Wag21.011.30952Datsun 71022.810.41667Hornet 4 Drive21.411.09813Hornet Sportabout18.712.70053
```

1.12 Dealing with common problems

We are going to have to deal with many errors and problems as we use R. It happens even to the best programmers.

Every problem is unique, but there are common mistakes that we try to provide insight for below.

1.12.1 Error in ...: could not find function "..."

We probably forgot to load the package needed to use the function. We may also have misspelled the function name.

1.12.2 Error: object '...' not found

The object doesn't exist in loaded memory. Perhaps we forget to assign that name to an object or misspelled the name of the object we are trying to access.

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

This typically happens because our Plots pane is too small. We should increase the size of the Plots pane and try again.

1.12.4 Code was working, but isn't anymore

We may have run code out of order. It may work if we run it in order. Or we may have run something in the Console that we don't have in our Script file. It is good practice to clear our environment (the objects R has loaded in memory) using the broom icon in the Environment pane and rerunning our entire Script file to ensure it behaves as expected. The broom icon is shown in Figure 1.4.



Figure 1.4: The broom icon can be clicked to clear the objects loaded in the Environment.

1.13 Ecosystem debate

In general, we favor performing analysis using **base** R functionality, which means we try to perform our analysis with features R offers by default. Some of the benefits of doing this include making our code easier to maintain (**base** R features change very slowly and are nearly always backwards compatible) and often result in faster code. However, more complicated aspects of regression analysis are not easy to perform using **base** R, so we will introduce new packages and functions as we progress.

Many readers may have previous experience working with the **tidyverse** (https://www.tidyverse.org) and wonder how frequently we use **tidyverse** functionality. The **tidyverse** offers a unified framework for data manipulation and visualization that tends to be more consistent than **base** R. However, there are many situations where a **base** R solution is more straightforward than a **tidyverse** solution, not to mention the fact that there are many aspects of R programming (e.g., S3 and S4 objects, method dispatch) that require knowledge of **base** R features. Because the R universe is vast and there are many competing coding styles, we will prioritize analysis approaches using **base** R, which gives users a stronger programming foundation. However, we will use parts of the **tidyverse** when it greatly simplifies analysis, data manipulation, or visualization because it provides an extremely useful feature set.

1.14 Going deeper

1.14.1 Comparing assignment operators

As previously mentioned in Section 1.3, both <- and = can mostly be used interchangeably for assignment. But there are times when using = for assignment can be problematic. Consider the examples below where we want to use system.time to time how long it takes to draw 100 values from a standard normal distribution and assign it the name result.

This code works:

```
system.time(result <- rnorm(100))
user system elapsed
0 0 0</pre>
```

This code doesn't work:

```
system.time(result = rnorm(100))
```

Error in system.time(result = rnorm(100)): unused argument (result = rnorm(100))

What's the difference? In the second case, R thinks we are setting the result argument of the system.time function (which doesn't exist) to the value produced by rnorm(100).

Thus, it is best to use <- for assigning a name to an object and reserving = for specifying function arguments.

2 Data cleaning and exploration

References

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