Modern R in a Corporate Environment

Original materials developed for RADARS

Brian Davis

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About

Chapter 1

Introduction

> Something that will make life easier in the long-run can be the most difficult thing to do today. For coders, prioritising the long term may involve an overhaul of current practice and the learning of a new skill.

1.1 Course Philosophy

> "The best programs are written so that computing machines can perform them quickly and so that human beings can understand them clearly. A programmer is ideally an essayist who works with traditional aesthetic and literary forms as well as mathematical concepts, to communicate the way that an algorithm works and to convince a reader that the results will be correct." Donald Knuth

1.1.1 Reproducible Research

Reproducible research is the idea that data analyses, and more generally, scientific claims, are published with their data and software code so that others may verify the findings and build upon them. There are two basic reasons to be concerned about making your research reproducible. The first is *to show evidence of the correctness of your results*. The second reason to aspire to reproducibility is *to enable others to make use of our methods and results*.

Modern challenges of reproducibility in research, particularly computational reproducibility, have produced a lot of discussion in papers, blogs and videos, some of which are listed here and here.

> Conclusions in experimental psychology often are the result of null hypothesis significance testing. Unfortunately, there is evidence ((from eight major psychology journals published between 1985 and 2013) that roughly half of all published empirical psychology articles contain at least one inconsistent p-value, and around one in eight articles contain a grossly inconsistent p-value that makes a non-significant result seem significant, or vice versa. statscheck and here

> "A key component of scientific communication is sufficient information for other researchers in the field to reproduce published findings. For computational and data-enabled research, this has often been interpreted to mean making available the raw data from which results were generated, the computer code that generated the findings, and any additional information needed such as workflows and input parameters. Many journals are revising author guidelines to include data and code availability. We chose a random sample of 204 scientific papers published in the journal **Science** after the implementation of their policy in February 2011. We found that were able to

> reproduce the findings for 26%." Proceedings of the National Academy of Sciences of the United States of America
>
> "Starting September 1 2016, JASA ACS will require code and data as a minimum standard for reproducibility of statistical scientific research." JASA

1.1.2 FDA Validation

> "Establishing documented evidence which provides a high degree of assurance that a specific process will consistently produce a product meeting its predetermined specifications and quality attributes." -Validation as defined by the FDA in **Validation of Systems for 21 CFR Part 11 Compliance**

1.1.3 The SAS Myth

Contray to what we hear the FDA does not require SAS to be used *EVER*. There are instances that you have to deliver data in XPORT format though which is open and implemented in many programming languages.

> "FDA does not require use of any specific software for statistical analyses, and statistical software is not explicitly discussed in Title 21 of the Code of Federal Regulations [e.g., in 21CFR part 11]. However, the software package(s) used for statistical analyses should be fully documented in the submission, including version and build identification. As noted in the FDA guidance, E9 Statistical Principles for Clinical Trials" FDA Statistical Software Clarifying Statement

Good write up with links to several FDA talks on the subject.

1.2 Prerequisites

- We will assume you have minimal experience and knowledge of R
- IT should have installed:
  - R version 3.5
  - RStudio version 1.1
  - MiTeX
  - RTools version 3.4
- We will install other dependencies throughout the course.

1.3 Content

It is impossible to become an expert in R in only one course even a multi-week one. Yet, this course aims at giving a wide understanding on many aspects of R as used in a corporate / production environment. It will roughly be based on R for Data Science. While this is an *excellent* resource it does not cover much of what we will need on a routine basis. Some external resources will be referred to in this book for you to be able to deepen what you would have learned in this course.

This is your course so if you feel we need to hit an area deeper, or add content based on a current need, let me know an we will work to adjust it.

The **rough** topic list of the course:

1. Good programming practices
2. Basics of R Programming
3. Importing Data

4. Tiyding Data
5. Visualizing Data
6. Functions
7. Strings
8. Dates and Time
9. Communicating Results

Making Code Production Ready:

10. Functions (part II)
11. Assertions
12. Unit tests
13. Documentation
14. Communicating Results (part II)

1.4 Structure

My current thoughts are to meet an hour a week and discuss a topic. We will not be going strictly through the R4DS, but will use it as our foundation into the topic at hand. Then give an assignment due for the next week which we go over the solutions. We will incorporate these assignments into a RADARS R package(s?) so we will have a collection of usefull reusable code for the future.

Open to other ideas as we go along. I'm going to try to keep the assignments related to our current work (maybe working through Site Investigator and/or Subscriber Reports) so we can work on the class during work hours.

Chapter 2

Good practices

> "Programs must be written for people to read, and only incidentally for machines to execute." Harold Abelson
>
> "Programming is the art of telling another human being what one wants the computer to do." Donald Knuth
>
> "Let us change our traditional attitude to the construction of programs. Instead of imagining that our main task is to instruct a computer what to do, let us concentrate rather on explaining to human beings what we want a computer to do." Donald Knuth
>
> "When you write a program, think of it primarily as a work of literature. You're trying to write something that human beings are going to read. Don't think of it primarily as something a computer is going to follow. The more effective you are at making your program readable, the more effective it's going to be: You'll understand it today, you'll understand it next week, and your successors who are going to maintain and modify it will understand it."

2.1 Coding style

Good coding style is like correct punctuation: you can manage without it, butitsuremakesthingseasiertoread. When I answer questions; first, I read the title of the question to see if I can answer the question, secondly, I check the coding style of the question and if the code is too difficult to read, I just move on. Please make your code readable by following e.g. this coding style (most examples below come from this guide).

2.1.1 Comments

In code, use comments to explain the "why" not the "what" or "how". Each line of a comment should begin with the comment symbol and a single space: `#`.

2.1.2 Naming

> There are only two hard things in Computer Science: cache invalidation and naming things. – Phil Karlton

Names are not limited to 8 characters as in some other languages. Be smart with your naming; be descriptive yet concise. Think about how your names will show up in autocomplete.

Throughout the course we will point out some standard naming conventions that are used in R (and other languages). (Ex. `i` and `j` as row and column indicies)

```
# Good
average_height <- mean((feet / 12) + inches)
plot(mtcars$disp, mtcars$mpg)

# Bad
ah<-mean(x/12+y)
plot(mtcars[, 3], mtcars[, 1])
```

2.1.3 Structure

Use commented lines of `-` to create a code outline.

2.1.4 Spacing

Put a space before and after `=` when naming arguments in function calls. Most infix operators (`==`, `+`, `-`, `<-`, etc.) are also surrounded by spaces, except those with relatively high precedence: `^`, `:`, `::`, and `:::`. Always put a space after a comma, and never before (just like in regular English).

```
# Good
average <- mean((feet / 12) + inches, na.rm = TRUE)
sqrt(x^2 + y^2)
x <- 1:10
base::sum

# Bad
average<-mean(feet/12+inches,na.rm=TRUE)
sqrt(x ^ 2 + y ^ 2)
x <- 1 : 10
base :: sum
```

2.1.5 Indenting

Curly braces, `{}`, define the the most important hierarchy of R code. To make this hierarchy easy to see, always indent the code inside `{}` by two spaces.

```
# Good
if (y < 0 && debug) {
  message("y is negative")
}

if (y == 0) {
  if (x > 0) {
    log(x)
  } else {
    message("x is negative or zero")
  }
} else {
  y ^ x
}
```

```r
# Bad
if (y < 0 && debug)
message("Y is negative")

if (y == 0)
{
    if (x > 0) {
      log(x)
    } else {
  message("x is negative or zero")
    }
} else { y ^ x }
```

2.1.6 Long lines

Strive to limit your code to 80 characters per line. This fits comfortably on a printed page with a reasonably sized font. If you find yourself running out of room, this is a good indication that you should encapsulate some of the work into a separate function.

If a function call is too long to fit on a single line, use one line each for the function name, each argument, and the closing `)`. This makes the code easier to read and to change later.

```r
# Good
do_something_very_complicated(
  something = "that",
  requires  = many,
  arguments = "some of which may be long"
)

# Bad
do_something_very_complicated("that", requires, many, arguments,
                              "some of which may be long"
```

2.1.7 Other

- Use `<-`, not `=`, for assignment. Keep `=` for parameters.

```r
# Good
x <- 5
system.time(
  x <- rnorm(1e6)
)

# Bad
x = 5
system.time(
  x = rnorm(1e6)
)
```

- Don't put `;` at the end of a line, and don't use `;` to put multiple commands on one line.
- Only use `return()` for early returns. Otherwise rely on R to return the result of the last evaluated expression.

```
# Good
add_two <- function(x, y) {
  x + y
}

# Bad
add_two <- function(x, y) {
  return(x + y)
}
```

- Use `"`, not `'`, for quoting text. The only exception is when the text already contains double quotes and no single quotes.

```
# Good
"Text"
'Text with "quotes"'
'<a href="http://style.tidyverse.org">A link</a>'

# Bad
'Text'
'Text with "double" and \'single\' quotes'
```

2.2 Coding practices

2.2.1 Variables

Create variables for values that are likely to change.

2.2.2 *Rule of 3*

Try not to copy code, or copy then modify the code, more than twice.

- If a change requires you to search/replace 3 or more times make a variable.
- If you copy a code chunk 3 or more times *make a function*
- If you copy a function 3 or more times *make your function more generic*
- If you copy a function 3 or more times into a project *make a package*
- If 3 or more people will use the function *make a package*
- If 3 or more projects will use the function *make a package*

Same thing goes for lookup tables and such. The key thing to think about is; if something changes how many touch points will there be? If it is 3 or more places it is time to abstract this code a bit.

2.2.3 Path names

It is better to use relative path names instead of hard coded ones. If you must read from (or write to) paths that are not in your project directory structure create a file name variable at the highest level you can (*always end with the /*) and then use relative paths.
DO NOT EVER USE `setwd()`

```
# Good
raw_data <- read.csv("./data/mydatafile.csv")

```

```
input_file <- "./data/mydatafile.csv"
raw_data <- read.csv(input_file)

input_path <- "C:/Path/To/Some/other/project/directory/"
input_file <- paste0(input_path, "data/mydatafile.csv")
raw_data <- read.csv(input_file)

# Bad
setwd("C:/Path/To/Some/other/project/directory/data/")
raw_data <- read.csv("mydatafile.csv")
setwd("C:/Path/back/to/my/project/")
```

2.3 RStudio

Download the latest version of RStudio (> 1.1) and use it!

Learn more about new features of RStudio v1.1 there.

RStudio features:

- everything you can expect from a good IDE
- keyboard shortcuts I use frequently
  1. *Ctrl + Space* (auto-completion, better than *Tab*)
  2. *Ctrl + Up* (command history & search)
  3. *Ctrl + Enter* (execute line of code)
  4. *Ctrl + Shift + A* (reformat code)
  5. *Ctrl + Shift + C* (comment/uncomment selected lines)
  6. *Ctrl + Shift + /* (reflow comments)
  7. *Ctrl + Shift + O* (View code outline)
  8. *Ctrl + Shift + B* (build package, website or book)
  9. *Ctrl + Shift + M* (pipe)
  10. *Alt + Shift + K* to see all shortcuts…
- Panels (everything is integrated, including **Git** and a terminal)
- Interactive data importation from files and connections (see this webinar)
- Use code diagnostics:
- **R Projects**:
  - **Meaningful structure** in one folder
  - The working directory automatically switches to the project's folder
  - File tab displays the associated files and folders in the project
  - History of R commands and open files
  - Any settings associated with the project, such as Git settings, are loaded. Note that a *set-up.R* or even a *.Rprofile* file in the project's root directory enable project-specific settings to be loaded each time people work on the project.

The only two things that make @JennyBryan . Instead use projects + here::here() #rstats pic.twitter.com/GwxnHePL4n

— Hadley Wickham (@hadleywickham) December 11 2017

Read more at https://www.tidyverse.org/articles/2017/12/workflow-vs-script/ and also see chapter *Efficient set-up* of book *Efficient R programming*.

2.4 Getting help

2.4.1 Help yourself, learn how to debug

A basic solution is to print everything, but it usually does not work well on complex problems. A convenient solution to see all the variables' states in your code is to place some `browser()` anywhere you want to check the variables' states.

Learn more with this book chapter, this other book chapter, this webinar and this RStudio article.

2.4.2 External help

Can't remember useful functions? Use cheat sheets.

You can search for specific R stuff on https://rseek.org/. You should also read documentations carefully. If you're using a package, search for vignettes and a GitHub repository.

You can also use Stack Overflow. The most common use of Stack Overflow is when you have an error or a question, you google it, and most of the times the first links are Q/A on Stack Overflow.

You can ask questions on Stack Overflow (using the tag `r`). You need to make a great R reproducible example if you want your question to be answered. Most of the times, while making this reproducible example, you will find the answer to your problem.

If you're confident enough in your R skills, you can go to the next step and answer questions on Stack Overflow. It's a good way to increase your skills, or just to procrastinate while writing a scientific manuscript.

2.5 Keeping up to date

With over 10,000 packages on CRAN it is hard to keep up with the constantly changing landscape. R-Bloggers is an R forcused blog aggregator with dozens of posts per day. Checkit out.

Join the R-help mailing list. Sign up to get the daily digest and scan it for questions that interest you.

2.6 Assignement

1. See these Rstudio Tips & Tricks or these and find one that looks interesting and **practice** it all week.
2. Create an R Project for this class.
3. Create the following directories in your project (tip sheet?)
   - Bonus points if you can do it from R and not RStudio or Windows Explorer
   - Double Bonus points if you can make it a function.
4. Read Chapters 1-3 of the Tidyverse Style Guide
5. Copy one of your R scripts into your R directory. (Bonus points if you can do it from R and not RStudio or Windows Explorer)
6. Apply the style guide to your code.

7. Apply the "Rule of 3"
   - Create variables as needed
   - Identify code that is used 3 or more times to make functions
   - Identify code that would be useful in 3 or more projects to integrate into a package.
8. Read how to make a great R reproducible example

Chapter 3

R Basics

With over 10,000 packages on CRAN we can't cover everything. In general there are several ways, or packages, to accomplish a given task.

Here is a quick look at some of the basics. Next we'll dive deep into R's basic data structures and how to subset them in subsequent chapters. This will give us a good overview of base R and the background needed to dive into **R for Data Science**.

The three most important functions in R `?`, `??`, and `str`:

- `?<topic>` provides access to the documentation for <topic>.
- `??<topic>` searches the documention for <topic>.
- `str` displays the structure of an R object in human readable form.

See this vocabulary list for a good starting point on the basics functions in base R and some important libraries.

In R there three basic constructs; objects, functions, and environments:

3.1 Assignment

We saw this is Coding Style. Use `<-` for assignment and use `=` for parameters. While you can use `=` for assignment it is generally considered bad practice.

3.2 Objects

3.2.1 Vector

You create a vector with `c`.

```
v <- c("my", "first", "vector")
v
```

```
#> [1] "my"     "first"  "vector"
```

```
# length of our vector
length(v)
```

```
#> [1] 3
```

There are several shortcut functions for common vector creation.

```
# create an ordered sequence
2:10
```

```
#> [1]  2  3  4  5  6  7  8  9 10
```

```
9:3
```

```
#> [1] 9 8 7 6 5 4 3
```

```
# common mistake using 1:length(n) in loops
# but if n = 0
1:0
```

```
#> [1] 1 0
```

```
# use seq_len(n) instead and the loop won't execute
seq_len(0)
```

```
#> integer(0)
```

```
# another common mistake
n<-6
1:n+1        # is (1:n) + 1, so 2:(n + 1)
```

```
#> [1] 2 3 4 5 6 7
```

```
1:(n+1)      # usually what is meant
```

```
#> [1] 1 2 3 4 5 6 7
```

```
seq_len(n+1) # another way
```

```
#> [1] 1 2 3 4 5 6 7
```

3.2.2 Matrix

Matrices are 2D vectors, with all elements of the same type. Genearlly used for mathematics.

```
# fill in column order (default)
matrix(1:12, nrow = 3)
```

```
#>      [,1] [,2] [,3] [,4]
#> [1,]    1    4    7   10
#> [2,]    2    5    8   11
#> [3,]    3    6    9   12
```

```
# fill in row order
matrix(1:12, nrow = 3, byrow = TRUE)
```

```
#>      [,1] [,2] [,3] [,4]
#> [1,]    1    2    3    4
#> [2,]    5    6    7    8
#> [3,]    9   10   11   12
```

```
# can also specify the number of columns instead
matrix(1:12, ncol = 3)
```

```
#>      [,1] [,2] [,3]
#> [1,]    1    5    9
#> [2,]    2    6   10
#> [3,]    3    7   11
#> [4,]    4    8   12
```

You find the dimensions of a matrix with `nrow`, `ncol`, and `dim`

```
m <- matrix(1:12, ncol = 3)
dim(m)
```

```
#> [1] 4 3
```

```
nrow(m)
```

```
#> [1] 4
```

```
ncol(m)
```

```
#> [1] 3
```

3.2.3 List

A list is a generic vector containing other objects. These do **NOT** have to be the same type or the same length.

```
s <- c("aa", "bb", "cc", "dd", "ee")
b <- c(TRUE, FALSE, TRUE, FALSE, FALSE)
# x contains copies of n, s, b and our matrix from above
x <- list(n = c(2, 3, 5) , s, b, 3, m)
x
```

```
#> $n
#> [1] 2 3 5
#>
#> [[2]]
#> [1] "aa" "bb" "cc" "dd" "ee"
#>
#> [[3]]
#> [1]  TRUE FALSE  TRUE FALSE FALSE
#>
#> [[4]]
#> [1] 3
#>
#> [[5]]
#>      [,1] [,2] [,3]
#> [1,]    1    5    9
#> [2,]    2    6   10
#> [3,]    3    7   11
#> [4,]    4    8   12
```

```
# length gives you length of the list not the elements in the list
length(x)
```

```
#> [1] 5
```

We'll discuss lists in detail in the next chapter.

3.2.4 Data frame

A data frame is a list with each vector of the same length. This is the main data structure used and is analagous to a data set in SAS. While these **look** like matrices they behave very different.

```
df = data.frame(n = c(2, 3, 5),
                s = c("aa", "bb", "cc") ,
                b = c(TRUE, FALSE, TRUE),
                y = v
                )       # df is a data frame
df
```

```
#>   n  s     b      y
#> 1 2 aa  TRUE     my
#> 2 3 bb FALSE  first
#> 3 5 cc  TRUE vector
```

```
# dimensions
dim(df)
```

```
#> [1] 3 4
```

```
nrow(df)
```

```
#> [1] 3
```

```
ncol(df)
```

```
#> [1] 4
```

```
length(df)
```

```
#> [1] 4
```

We'll discuss data frames in great detail in the next chapter.

3.3 Comparision

Logical Operators include:

Operator	Description
>	greater than
>=	greater than or equal to
<	less than
<=	less than or equal to
==	exactly equal to
!=	not equal to

```
v <- 1:12
v[v > 9]
```

```
#> [1] 10 11 12
```

Equality can be tricky to test for since real numbers can't be expressed exactly in computers.

```
x <- sqrt(2)
(y <- x^2)
```

```
#> [1] 2
```

```r
y == 2
```

```
#> [1] FALSE
```

```r
print(y, digits = 20)
```

```
#> [1] 2.0000000000000004441
```

```r
all.equal(y, 2)          ## equality with some tolerance
```

```
#> [1] TRUE
```

```r
all.equal(y, 3)
```

```
#> [1] "Mean relative difference: 0.5"
```

```r
isTRUE(all.equal(y, 3))  ## if you want a boolean, use isTRUE()
```

```
#> [1] FALSE
```

3.4 Logical and sets

```r
x <- c(TRUE, FALSE)
df <- data.frame(expand.grid(x, x))
names(df) <- c("x", "y")
df$and  <- df$x & df$y     # logical and
df$or   <- df$x | df$y     # logical or
df$notx <- !df$x           # negation
df$xor  <- xor(df$x, df$y) # exlusive or
df
```

```
#>       x     y   and    or  notx   xor
#> 1  TRUE  TRUE  TRUE  TRUE FALSE FALSE
#> 2 FALSE  TRUE FALSE  TRUE  TRUE  TRUE
#> 3  TRUE FALSE FALSE  TRUE FALSE  TRUE
#> 4 FALSE FALSE FALSE FALSE  TRUE FALSE
```

R has two versions of a logical and (or) `&` and `&&` (| and `||`). The single version is the vectorized version while the the double version returns a length-one vector. Use the double version in logical control structures (if, for, while, etc).

```r
# TRUE/FALSE and each element
TRUE & c(TRUE, FALSE)
```

```
#> [1]  TRUE FALSE
```

```r
FALSE & c(TRUE, FALSE)
```

```
#> [1] FALSE FALSE
```

```r
# TRUE/FALSE and first element
TRUE && c(TRUE, FALSE)
```

```
#> [1] TRUE
```

```r
FALSE && c(TRUE, FALSE)
```

```
#> [1] FALSE
```

```
# TRUE/FALSE or each element
TRUE | c(TRUE, FALSE)
```

```
#> [1] TRUE TRUE
```

```
FALSE | c(TRUE, FALSE)
```

```
#> [1]  TRUE FALSE
```

```
# TRUE/FALSE or first element
TRUE || c(TRUE, FALSE)
```

```
#> [1] TRUE
```

```
FALSE || c(TRUE, FALSE)
```

```
#> [1] TRUE
```

It also has useful helpers `any` and `all`

```
x <- c(FALSE, FALSE, FALSE, TRUE)
any(x)
```

```
#> [1] TRUE
```

```
all(x)
```

```
#> [1] FALSE
```

```
all(!x[1:3])
```

```
#> [1] TRUE
```

And also some useful set operations intersect, union, setdiff, setequal

```
x <- 1:5
y <- 3:7

intersect(x, y)
```

```
#> [1] 3 4 5
```

```
union(x, y)
```

```
#> [1] 1 2 3 4 5 6 7
```

```
setdiff(x, y)
```

```
#> [1] 1 2
```

```
setdiff(y, x)
```

```
#> [1] 6 7
```

```
setequal(x, y)
```

```
#> [1] FALSE
```

```
z <- 5:1
setequal(x, z)
```

```
#> [1] TRUE
```

3.5 Vectorization & Recycling

3.6 Basic Looping

3.6.1 For

3.6.2 Apply

3.6.3 Others

3.7 Function Basics

3.8 Environments & Scoping

3.9 Assignment

1. Browse this vocabulary list and read the help file for functions that interest you.
2. ddd

Chapter 4

Base R Data Structures

See this vocabulary list for a good starting point on the basics functions in base R and some important libraries.

advr38book

In R there three basic constructs; objects, functions, and environments.

The three most important functions in R `?`, `??`, and `str`.

4.1 Naming Rules

R has strict rules about what constitutes a valid name. A **syntactic** name must consist of letters[1], digits, `.` and `_`, and can't begin with `_`. Additionally, it can not be one of a list of **reserved words** like `TRUE`, `NULL`, `if`, and `function` (see the complete list in `?Reserved`). Names that don't follow these rules are called **non-syntactic** names, and if you try to use them, you'll get an error:

```
_abc <- 1
#> Error: unexpected input in "_"

if <- 10
#> Error: unexpected assignment in "if <-"
```

4.2 Vectors

The most common data structure in R is the vector. R's vectors can be organised by their dimensionality (1d, 2d, or nd) and whether they're homogeneous or heterogeneous. This gives rise to the five data types most often used in data analysis:

	Homogeneous	Heterogeneous
1d	Atomic vector	List
2d	Matrix	Data frame
nd	Array	

[1] Surprisingly, what constitutes a letter is determined by your current locale. That means that the syntax of R code actually differs from computer to computer, and it's possible for a file that works on one computer to not even parse on another!

Given an object, the best way to understand what data structures it is composed of is to use `str()`. `str()` is short for structure and it gives a compact, human readable description of any R data structure.

Vectors have three common properties:

- Type, `typeof()`, what it is.
- Length, `length()`, how many elements it contains.
- Attributes, `attributes()`, additional arbitrary metadata.

They differ in the types of their elements: all elements of an atomic vector must be the same type, whereas the elements of a list can have different types.

NOTE: `is.vector()` does not test if an object is a vector. Instead it returns TRUE only if the object is a vector with no attributes apart from names. Use `is.atomic(x) || is.list(x)` to test if an object is actually a vector.

4.2.1 Atomic Vectors

There are many "atomic" types of data: `logical`, `integer`, `double` and `character` (in this order, see below). There are also `raw` and `complex` but they are rarely used.

You can't mix types in an atomic vector (you can in a list). Coercion will automatically occur if you mix types:

```r
(a <- FALSE)
```

```
#> [1] FALSE
```

```r
typeof(a)
```

```
#> [1] "logical"
```

```r
(b <- 1:10)
```

```
#>  [1]  1  2  3  4  5  6  7  8  9 10
```

```r
typeof(b)
```

```
#> [1] "integer"
```

```r
c(a, b)         ## FALSE is coerced to integer 0
```

```
#>  [1]  0  1  2  3  4  5  6  7  8  9 10
```

```r
(c <- 10.5)
```

```
#> [1] 10.5
```

```r
typeof(c)
```

```
#> [1] "double"
```

```r
(d <- c(b, c))  ## coerced to double
```

```
#>  [1]  1.0  2.0  3.0  4.0  5.0  6.0  7.0  8.0  9.0 10.0 10.5
```

```r
c(d, "a")       ## coerced to character
```

```
#>  [1] "1"    "2"    "3"    "4"    "5"    "6"    "7"    "8"    "9"    "10"   "10.5" "a"
```

```r
c(list(1), "a")
```

```
#> [[1]]
#> [1] 1
#>
#> [[2]]
#> [1] "a"
```

```
50 < "7"
```

```
#> [1] TRUE
```

You can force coercion with `as.logical`, `as.integer`, `as.double`, `as.numeric`, and `as.character`. Most of the time the coercion rules are straight forward, but not always.

```
x <- c(TRUE, FALSE)
typeof(x)
```

```
#> [1] "logical"
```

```
as.integer(x)
```

```
#> [1] 1 0
```

```
as.numeric(x)
```

```
#> [1] 1 0
```

```
as.character(x)
```

```
#> [1] "TRUE"  "FALSE"
```

However, coercion is not associative.

```
x <- c(TRUE, FALSE)

x2 <- as.integer(x)
x3 <- as.numeric(x2)
as.character(x3)
```

```
#> [1] "1" "0"
```

What would you expect this to return?

```
x <- c(TRUE, FALSE)

as.integer(as.character(x))
```

You can test for an "atomic" types of data with: `is.logical`, `is.integer`, `is.double`, `is.numeric`[2], and `is.character`.

```
x <- c(TRUE, FALSE)

is.logical(x)
```

```
#> [1] TRUE
```

```
is.integer(x)
```

```
#> [1] FALSE
```

What would you expect these to return?

[2] `is.numeric()` is a general test for the "numberliness" of a vector and returns TRUE for both integer and double vectors. It is not a specific test for double vectors, which are often called numeric.

```
x <- 2

is.integer(x)
is.numeric(x)
is.double(x)
```

Missing values are specified with `NA`, which is a logical vector of length 1. `NA` will always be coerced to the correct type if used inside `c()`, or you can create `NA`s of a specific type with `NA_real_` (a double vector), `NA_integer_` and `NA_character_`.

4.2.2 Lists

Lists are different from atomic vectors because their elements can be of any type, including other lists. Lists can contain complex objects so it's not possible to pick one visual style that works for every list. You construct lists by using `list()` instead of `c()`:

```
x <- list(1:3, "a", c(TRUE, FALSE, TRUE), c(2.3, 5.9))
str(x)
```

```
#> List of 4
#>  $ : int [1:3] 1 2 3
#>  $ : chr "a"
#>  $ : logi [1:3] TRUE FALSE TRUE
#>  $ : num [1:2] 2.3 5.9
```

Lists are sometimes called **recursive** vectors, because a list can contain other lists. This makes them fundamentally different from atomic vectors.

```
x <- list(list(list(list(1))))
str(x)
```

```
#> List of 1
#>  $ :List of 1
#>   ..$ :List of 1
#>   .. ..$ :List of 1
#>   .. .. ..$ : num 1
```

```
is.recursive(x)
```

```
#> [1] TRUE
```

`c()` will combine several lists into one. If given a combination of atomic vectors and lists, `c()` will coerce the vectors to lists before combining them. Compare the results of `list()` and `c()`:

```
x <- list(list(1, 2), c(3, 4))
y <- c(list(1, 2), c(3, 4))
str(x)
```

```
#> List of 2
#>  $ :List of 2
#>   ..$ : num 1
#>   ..$ : num 2
#>  $ : num [1:2] 3 4
```

```
str(y)
```

```
#> List of 4
#>  $ : num 1
#>  $ : num 2
#>  $ : num 3
#>  $ : num 4
```

The `typeof()` a list is `list`. You can test for a list with `is.list()` and coerce to a list with `as.list()`. You can turn a list into an atomic vector with `unlist()`. If the elements of a list have different types, `unlist()` uses the same coercion rules as `c()`.

Lists are used to build up many of the more complicated data structures in R. For example, both data frames (described in data frames) and linear models objects (as produced by `lm()`) are lists

4.2.3 NULL

Closely related to vectors is `NULL`, a singleton object often used to represent a vector of length 0. `NULL` is different than `NA`. For a good explanation of the differences see this blog post.

4.2.4 Attributes

All objects can have arbitrary additional attributes, used to store metadata about the object. Attributes can be thought of as a named list[3] (with unique names). Attributes can be accessed individually with `attr()` or all at once (as a list) with `attributes()`.

```
a <- 1:3
attr(a, "x") <- "abcdef"
attr(a, "y") <- 4:6
attr(a, "z") <- list(list())
str(attributes(a))
```

```
#> List of 3
#>  $ x: chr "abcdef"
#>  $ y: int [1:3] 4 5 6
#>  $ z:List of 1
#>   ..$ : list()
```

The `structure()` function returns a new object with modified attributes. Care must be taken with attributes since, by default, most attributes are lost when modifying a vector.

```
attributes(a[1])
```

```
#> NULL
```

```
attributes(sum(a))
```

```
#> NULL
```

The only attributes not lost are the three most important:

- Names, a character vector giving each element a name.
- Dimensions, used to turn vectors into matrices and arrays.
- Class, used to implement the S3 object system.

Each of these attributes has a specific accessor function to get and set values. When working with these attributes, use `names(x)`, `dim(x)`, and `class(x)`, not `attr(x, "names")`, `attr(x, "dim")`, and `attr(x, "class")`.

[3] The reality is a little more complicated: attributes are actually stored in something called pairlists, which can you learn more about in Advanced R

4.2.4.1 Names

You can name a vector in a couple[4] ways:

- When creating it: `x <- c(a = 1, b = 2, c = 3)`.
- By modifying an existing vector in place: `x <- 1:3; names(x) <- c("a", "b", "c")`.

Named vectors a a great way to make an easy, human readable look up table. We will see this use case extensively when we get to data visualizations.

4.2.4.2 Factors

One important use of attributes is to define factors. A factor is a vector that can contain only predefined values, and is used to store categorical data. Factors are built on top of **integer vectors** using two attributes: the `class`, "factor", which makes them behave differently from regular integer vectors, and the `levels`, which defines the set of allowed values.

Factors are useful when you know the possible values a variable may take, even if you don't see all values in a given dataset. Using a factor instead of a character vector makes it obvious when some groups contain no observations:

```
sex_char <- c("m", "m", "m")
sex_factor <- factor(sex_char, levels = c("m", "f"))

table(sex_char)
```

```
#> sex_char
#> m
#> 3
```

```
table(sex_factor)
```

```
#> sex_factor
#> m f
#> 3 0
```

While factors look like (and often behave like) character vectors, they are actually **integers**. Be careful when treating them like strings. Some string methods (like `gsub()` and `grepl()`) will coerce factors to strings, while others (like `nchar()`) will throw an error, and still others (like `c()`) will use the underlying integer values. For this reason, it is best to explicitly convert factors to character vectors if you need string-like behaviour.

Unfortunately, many base R functions (like `read.csv()` and `data.frame()`) automatically convert character vectors to factors. This is suboptimal, because there's no way for those functions to know the set of all possible levels or their optimal order. Instead, use the argument `stringsAsFactors = FALSE` to suppress this behaviour, and then manually convert character vectors to factors using your knowledge of the data only when you need the behavior of factors.

Factors tend to be most useful in data visualization and table creations where you want to report all categories but some categories may not be present in your data, or when you want to order the categories in somethin other than the default ordering. We will revisit factors and there usefulness later when we study the tidyverse and in particular the forcats package.

[4] There are a couple less common ways. See Advanced R

4.2.5 Matrices and arrays

Adding a `dim` attribute to an atomic vector allows it to behave like a multi-dimensional **array**. A special case of the array is the **matrix**, which has two dimensions. Matrices are used commonly as part of the mathematical machinery of statistics. Arrays are much rarer, but worth being aware of.

Matrices and arrays are created with `matrix()` and `array()`, or by using the assignment form of `dim()`:

```
# Two scalar arguments to specify rows and columns
a <- matrix(1:12, ncol = 3, nrow = 4)
a
```

```
#>      [,1] [,2] [,3]
#> [1,]    1    5    9
#> [2,]    2    6   10
#> [3,]    3    7   11
#> [4,]    4    8   12
```

```
# One vector argument to describe all dimensions
b <- array(1:12, c(2, 3, 2))
b
```

```
#> , , 1
#> 
#>      [,1] [,2] [,3]
#> [1,]    1    3    5
#> [2,]    2    4    6
#> 
#> , , 2
#> 
#>      [,1] [,2] [,3]
#> [1,]    7    9   11
#> [2,]    8   10   12
```

```
# You can also modify an object in place by setting dim()
vec <- 1:12
vec
```

```
#>  [1]  1  2  3  4  5  6  7  8  9 10 11 12
```

```
class(vec)
```

```
#> [1] "integer"
```

```
dim(vec) <- c(3, 4)
vec
```

```
#>      [,1] [,2] [,3] [,4]
#> [1,]    1    4    7   10
#> [2,]    2    5    8   11
#> [3,]    3    6    9   12
```

```
class(vec)
```

```
#> [1] "matrix"
```

```
dim(vec) <- c(3, 2, 2)
vec
```

```
#> , , 1
#> 
```

```
#>      [,1] [,2]
#> [1,]    1    4
#> [2,]    2    5
#> [3,]    3    6
#>
#> , , 2
#>
#>      [,1] [,2]
#> [1,]    7   10
#> [2,]    8   11
#> [3,]    9   12
```

```
class(vec)
```

```
#> [1] "array"
```

`length()` and `names()` have high-dimensional generalisations:

- `length()` generalises to `nrow()` and `ncol()` for matrices, and `dim()` for arrays.
- `names()` generalises to `rownames()` and `colnames()` for matrices, and `dimnames()`, a list of character vectors, for arrays.

`c()` generalises to `cbind()` and `rbind()` for matrices, and to `abind::abind()` for arrays. You can transpose a matrix with `t()`; the generalised equivalent for arrays is `aperm()`.

You can test if an object is a matrix or array using `is.matrix()` and `is.array()`, or by looking at the length of the `dim()`. `as.matrix()` and `as.array()` make it easy to turn an existing vector into a matrix or array.

Vectors are not the only 1-dimensional data structure. You can have matrices with a single row or single column, or arrays with a single dimension. They may print similarly, but will behave differently. The differences aren't too important, but it's useful to know they exist in case you get strange output from a function (`tapply()` is a frequent offender). As always, use `str()` to reveal the differences.

Matrices and arrays are most useful for mathematical calculations (particularly when fitting models); lists are a better fit for most other programming tasks in R.

4.2.6 Data Frames

A data frame is the most common way of storing data in R, and if used systematically makes data analysis easier. Under the hood, a data frame is a list of equal-length vectors. This makes it a 2-dimensional structure, so it shares properties of both the matrix and the list. This means that a data frame has `names()`, `colnames()`, and `rownames()`, although `names()` and `colnames()` are the same thing. The `length()` of a data frame is the length of the underlying list and so is the same as `ncol()`; `nrow()` gives the number of rows. You can subset a data frame like a 1d structure (where it behaves like a list), or a 2d structure (where it behaves like a matrix), we will discuss this further when we discuss subsetting.

4.2.6.1 Creation

You create a data frame using `data.frame()`, which takes named vectors as input:

```
df <- data.frame(x = 1:3, y = c("a", "b", "c"))
str(df)
```

```
#> 'data.frame':    3 obs. of  2 variables:
#>  $ x: int  1 2 3
#>  $ y: Factor w/ 3 levels "a","b","c": 1 2 3
```

Beware `data.frame()`'s default behaviour which turns strings into factors. Use `stringsAsFactors = FALSE` to suppress this behaviour:

```
df <- data.frame(
  x = 1:3,
  y = c("a", "b", "c"),
  stringsAsFactors = FALSE)
str(df)
```

```
#> 'data.frame':    3 obs. of  2 variables:
#>  $ x: int  1 2 3
#>  $ y: chr  "a" "b" "c"
```

4.2.6.2 Testing and coercion

Because a `data.frame` is an S3 class, its type reflects the underlying vector used to build it: the list. To check if an object is a data frame, use `is.data.frame()`:

```
is.data.frame(df)
```

```
#> [1] TRUE
```

You can coerce an object to a data frame with `as.data.frame()`:

- A vector will create a one-column data frame.
- A list will create one column for each element; it's an error if they're not all the same length.
- A matrix will create a data frame with the same number of columns and rows as the matrix.

The automatic coercion that causes the most problems is if you select a single column of a data.frame. R will coerce the column to an atomic vector, which generally is not what you want[5].

```
(x1 <- df[, "x"])
```

```
#> [1] 1 2 3
```

```
str(x1)
```

```
#>  int [1:3] 1 2 3
```

```
(x2 <- df[, "y", drop = FALSE])
```

```
#>   y
#> 1 a
#> 2 b
#> 3 c
```

```
str(x2)
```

```
#> 'data.frame':    3 obs. of  1 variable:
#>  $ y: chr  "a" "b" "c"
```

4.2.6.3 Combining data frames

You can combine data frames using `cbind()` and `rbind()`:

```
cbind(df, data.frame(z = 3:1))
```

[5] We'll revisit this when we get into R for Data Science and discuss tibbles

```
#>   x y z
#> 1 1 a 3
#> 2 2 b 2
#> 3 3 c 1
```

```
rbind(df, data.frame(x = 10, y = "z"))
```

```
#>    x y
#> 1  1 a
#> 2  2 b
#> 3  3 c
#> 4 10 z
```

When combining column-wise, the number of rows must match, but row names are ignored. When combining row-wise, both the number and names of columns must match. Use `dplyr::bind_rows()`, `data.table::rbindlist()`, or similar to combine data frames that don't have the same columns.

It's a common mistake to try and create a data frame by `cbind()`ing vectors together. This is unlikely to do what you want because `cbind()` will create a matrix unless one of the arguments is already a data frame. Instead use `data.frame()` directly:

```
# This is always a mistake
bad <- data.frame(cbind(a = 1:2, b = c("a", "b")))
str(bad)
```

```
#> 'data.frame':    2 obs. of  2 variables:
#>  $ a: Factor w/ 2 levels "1","2": 1 2
#>  $ b: Factor w/ 2 levels "a","b": 1 2
```

```
good <- data.frame(a = 1:2, b = c("a", "b"))
str(good)
```

```
#> 'data.frame':    2 obs. of  2 variables:
#>  $ a: int  1 2
#>  $ b: Factor w/ 2 levels "a","b": 1 2
```

4.2.6.4 List and matrix columns

Since a data frame is a list of vectors, it is possible for a data frame to have a column that is a list. This is a powerful technique because a list can contain any other R object. This means that you can have a column of data frames, or model objects, or even functions! We will see this again when we discuss tidy data.

```
df <- data.frame(x = 1:3)
df$y <- list(1:2, 1:3, 1:4)
df
```

```
#>   x          y
#> 1 1       1, 2
#> 2 2    1, 2, 3
#> 3 3 1, 2, 3, 4
```

However, when a list is given to `data.frame()`, it tries to put each item of the list into its own column, so this fails:

```
data.frame(x = 1:3, y = list(1:2, 1:3, 1:4))
```

```
#> Error in (function (..., row.names = NULL, check.rows = FALSE, check.names = TRUE, : arguments imply
```

A workaround is to use `I()`, which causes `data.frame()` to treat the list as one unit:

```
dfl <- data.frame(x = 1:3, y = I(list(1:2, 1:3, 1:4)))
str(dfl)
```

```
#> 'data.frame':	3 obs. of  2 variables:
#>  $ x: int  1 2 3
#>  $ y:List of 3
#>   ..$ : int  1 2
#>   ..$ : int  1 2 3
#>   ..$ : int  1 2 3 4
#>   ..- attr(*, "class")= chr "AsIs"
```

`I()` adds the `AsIs` class to its input, but this can usually be safely ignored.

Similarly, it's also possible to have a column of a data frame that's a matrix or array, as long as the number of rows matches the data frame:

```
dfm <- data.frame(x = 1:3 * 10, y = I(matrix(1:9, nrow = 3)))
str(dfm)
```

```
#> 'data.frame':	3 obs. of  2 variables:
#>  $ x: num  10 20 30
#>  $ y: 'AsIs' int [1:3, 1:3] 1 2 3 4 5 6 7 8 9
```

Use list and array columns with caution. Many functions that work with data frames assume that all columns are atomic vectors, and the printed display can be confusing.

```
dfl[2, ]
```

```
#>   x       y
#> 2 2 1, 2, 3
```

```
dfm[2, ]
```

```
#>    x y.1 y.2 y.3
#> 2 20   2   5   8
```

Chapter 5

Subsetting

R's subsetting operators are powerful and fast. Mastery of subsetting allows you to succinctly express complex operations in a way that few other languages can match. Subsetting is hard to learn because you need to master a number of interrelated concepts:

- The three subsetting operators
  - `[` select multiple elements
  - `[[`, and `$` select a single element
- The six types of subsetting.
  - **Positive integers** return elements at the specified positions
  - **Negative integers** omit elements at the specified positions
  - **Logical vectors** select elements where the corresponding logical value is `TRUE`
  - **Nothing** returns the original object.
  - **Zero** returns a zero-length object (This is not something you usually do on purpose)
  - **Character vectors** to return elements with matching names.
- Important differences in behaviour for different objects (e.g., vectors, lists, factors, matrices, and data frames).
- The use of subsetting in conjunction with assignment.

It's easiest to learn how subsetting works for atomic vectors, and then how it generalises to higher dimensions and other more complicated objects.

5.1 Selecting multiple elements [

5.1.1 Atomic vectors

Let's explore the different types of subsetting with a simple vector, `x`.

```
x <- c(2.1, 4.2, 3.3, 5.4)
```

Note that the number after the decimal point gives the original position in the vector.

There are five things that you can use to subset a vector.

- **Positive integers** return elements at the specified positions

```
x[c(3, 1)]
```

```
#> [1] 3.3 2.1
```

```
# order returns an indice
x[order(x)]
```

```
#> [1] 2.1 3.3 4.2 5.4
```

```
# Duplicated indices yield duplicated values
x[c(1, 1)]
```

```
#> [1] 2.1 2.1
```

```
# Real numbers are silently truncated (not rounded) to integers
x[c(2.1, 2.9)]
```

```
#> [1] 4.2 4.2
```

- **Negative integers** omit elements at the specified positions

```
x[-c(3, 1)]
```

```
#> [1] 4.2 5.4
```

You can't mix positive and negative integers in a single subset.

```
x[c(-1, 2)]
```

```
#> Error in x[c(-1, 2)]: only 0's may be mixed with negative subscripts
```

- **Logical vectors** select elements where the corresponding logical value is `TRUE`. This is probably the most useful type of subsetting because you write the expression that creates the logical vector:

```
x[c(TRUE, TRUE, FALSE, FALSE)]
```

```
#> [1] 2.1 4.2
```

```
x[x > 3]
```

```
#> [1] 4.2 3.3 5.4
```

If the logical vector is shorter than the vector being subsetted, it will be *recycled* to be the same length.

```
x[c(TRUE, FALSE)]
```

```
#> [1] 2.1 3.3
```

```
# Equivalent to
x[c(TRUE, FALSE, TRUE, FALSE)]
```

```
#> [1] 2.1 3.3
```

A missing value in the index always yields a missing value in the output.

```
x[c(TRUE, TRUE, NA, FALSE)]
```

```
#> [1] 2.1 4.2  NA
```

- **Nothing** returns the original vector. This is not useful for vectors but is very useful for matrices, data frames, and arrays. It can also be useful in conjunction with assignment.

```
x[]
```

```
#> [1] 2.1 4.2 3.3 5.4
```

- **Zero** returns a zero-length vector. This is not something you usually do on purpose, but it can be helpful for generating test data and testing corner cases of functions.

```
x[0]
```

```
#> numeric(0)
```

If the vector is named, you can also use:

- **Character vectors** to return elements with matching names.

```
(y <- setNames(x, letters[1:4]))
```

```
#>   a   b   c   d
#> 2.1 4.2 3.3 5.4
```

```
# subsetting by name
y[c("d", "c", "a")]
```

```
#>   d   c   a
#> 5.4 3.3 2.1
```

```
# Like integer indices, you can repeat indices
y[c("a", "a", "a")]
```

```
#>   a   a   a
#> 2.1 2.1 2.1
```

```
# When subsetting with [ names are always matched exactly
z <- c(abc = 1, def = 2)
z[c("a", "d")]
```

```
#> <NA> <NA>
#>   NA   NA
```

5.1.2 Matrices and Arrays

You can subset higher-dimensional structures in three ways:

- With multiple vectors.
- With a single vector.
- With a matrix.

The most common way of subsetting matrices (2d) and arrays (>2d) is a simple generalisation of 1d subsetting: you supply a 1d index for each dimension, separated by a comma. Blank subsetting is now useful because it lets you keep all rows or all columns.

```
a <- matrix(1:9, nrow = 3)
colnames(a) <- c("A", "B", "C")
a[1:2, ]
```

```
#>      A B C
#> [1,] 1 4 7
#> [2,] 2 5 8
```

```
a[c(TRUE, FALSE, TRUE), c("B", "A")]
```

```
#>      B A
#> [1,] 4 1
#> [2,] 6 3
```

```
a[0, -2]
```

```
#>      A C
```

By default, `[` will simplify the results to the lowest possible dimensionality. See below how to avoid this behavior.

Because matrices and arrays are implemented as vectors with special attributes, you can subset them with a single vector. In that case, they will behave like a vector. Arrays in R are stored in column-major order:

```
(vals <- outer(1:5, 1:5, FUN = "paste", sep = ","))
```

```
#>      [,1]  [,2]  [,3]  [,4]  [,5]
#> [1,] "1,1" "1,2" "1,3" "1,4" "1,5"
#> [2,] "2,1" "2,2" "2,3" "2,4" "2,5"
#> [3,] "3,1" "3,2" "3,3" "3,4" "3,5"
#> [4,] "4,1" "4,2" "4,3" "4,4" "4,5"
#> [5,] "5,1" "5,2" "5,3" "5,4" "5,5"
```

```
vals[c(4, 15)]
```

```
#> [1] "4,1" "5,3"
```

This behavior allows you to replace all missing values in one line.

```
# make a few values missing
vals[sample(1:25, 5)] <- NA_character_
vals
```

```
#>      [,1]  [,2]  [,3]  [,4]  [,5]
#> [1,] "1,1" "1,2" "1,3" "1,4" "1,5"
#> [2,] "2,1" NA    NA    "2,4" NA
#> [3,] "3,1" "3,2" NA    "3,4" "3,5"
#> [4,] "4,1" "4,2" "4,3" "4,4" "4,5"
#> [5,] "5,1" "5,2" "5,3" "5,4" NA
```

```
# replace missing values with "missing"
vals[is.na(vals)] <- "missing"
vals
```

```
#>      [,1]  [,2]      [,3]      [,4]  [,5]
#> [1,] "1,1" "1,2"     "1,3"     "1,4" "1,5"
#> [2,] "2,1" "missing" "missing" "2,4" "missing"
#> [3,] "3,1" "3,2"     "missing" "3,4" "3,5"
#> [4,] "4,1" "4,2"     "4,3"     "4,4" "4,5"
#> [5,] "5,1" "5,2"     "5,3"     "5,4" "missing"
```

You can also subset higher-dimensional data structures with an integer matrix (or, if named, a character matrix). Each row in the matrix specifies the location of one value, where each column corresponds to a dimension in the array being subsetted. This means that you use a 2 column matrix to subset a matrix, a 3 column matrix to subset a 3d array, and so on. The result is a vector of values:

```
vals <- outer(1:5, 1:5, FUN = "paste", sep = ",")
select <- matrix(ncol = 2, byrow = TRUE, c(
  1, 1,
  3, 1,
  2, 4
))
vals[select]
```

```
#> [1] "1,1" "3,1" "2,4"
```

5.1.3 Lists

Subsetting a list works in the same way as subsetting an atomic vector. Using [will always return a list; [[and $, as described below, let you pull out the components of the list.

5.1.4 Data Frames

Data frames possess the characteristics of both lists and matrices: if you subset with a single vector, they behave like lists; if you subset with two vectors, they behave like matrices.

```
df <- data.frame(x = 1:3, y = 3:1, z = letters[1:3])
df
```

```
#>   x y z
#> 1 1 3 a
#> 2 2 2 b
#> 3 3 1 c
```

```
df[df$x == 2, ]
```

```
#>   x y z
#> 2 2 2 b
```

```
df[c(1, 3), ]
```

```
#>   x y z
#> 1 1 3 a
#> 3 3 1 c
```

```
# There are two ways to select columns from a data frame
# Like a list:
df[c("x", "z")]
```

```
#>   x z
#> 1 1 a
#> 2 2 b
#> 3 3 c
```

```
# Like a matrix
df[, c("x", "z")]
```

```
#>   x z
#> 1 1 a
#> 2 2 b
#> 3 3 c
```

```
# There's an important difference if you select a single
# column: matrix subsetting simplifies by default, list
# subsetting does not.
str(df["x"])
```

```
#> 'data.frame':    3 obs. of  1 variable:
#>  $ x: int  1 2 3
```

```
str(df[, "x"])
```

```
#>  int [1:3] 1 2 3
```

5.1.5 Preserving dimensionality

By default, any subsetting 2d data structures with a single number, single name, or a logical vector containing a single `TRUE` will simplify the returned output as described below. To preserve the original dimensionality, you must use `drop = FALSE`

- For matrices and arrays, any dimensions with length 1 will be dropped:

  ```
  (a <- matrix(1:4, nrow = 2))
  ```

  ```
  #>      [,1] [,2]
  #> [1,]    1    3
  #> [2,]    2    4
  ```

  ```
  str(a[1, ])
  ```

  ```
  #>  int [1:2] 1 3
  ```

  ```
  str(a[1, , drop = FALSE])
  ```

  ```
  #>  int [1, 1:2] 1 3
  ```

- Data frames with a single column will return just that column:

  ```
  (df <- data.frame(a = 1:2, b = 1:2))
  ```

  ```
  #>   a b
  #> 1 1 1
  #> 2 2 2
  ```

  ```
  str(df[, "a"])
  ```

  ```
  #>  int [1:2] 1 2
  ```

  ```
  str(df[, "a", drop = FALSE])
  ```

  ```
  #> 'data.frame':    2 obs. of  1 variable:
  #>  $ a: int  1 2
  ```

The default `drop = TRUE` behaviour is a common source of bugs in functions: you check your code with a data frame or matrix with multiple columns, and it works. Six months later you (or someone else) uses it with a single column data frame and it fails with a mystifying error. When writing functions, get in the habit of always using `drop = FALSE` when subsetting a 2d object.

Factor subsetting also has a `drop` argument, but the meaning it rather different. It controls whether or not levels are preserved (not the dimensionality), and it defaults to `FALSE` (levels are preserved, not simplified by default). If you find you are using `drop = TRUE` a lot it's often a sign that you should be using a character vector instead of a factor.

```
z <- factor(c("a", "b"))
z[1]
```

```
#> [1] a
#> Levels: a b
```

```
z[1, drop = TRUE]
```

```
#> [1] a
#> Levels: a
```

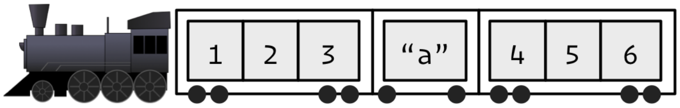
5.2 Selecting a single elements

There are two other subsetting operators: `[[` and `$`. `[[` is used for extracting single values, and `$` is a useful shorthand for `[[` combined with character subsetting. `[[` is most important working with lists because subsetting a list with `[` always returns a smaller list. To help make this easier to understand we can use a metaphor:

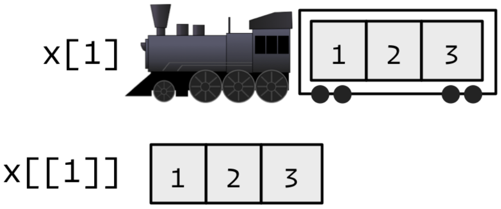
> "If list `x` is a train carrying objects, then `x[[5]]` is the object in car 5; `x[4:6]` is a train of cars 4-6."
>
> — @RLangTip, https://twitter.com/RLangTip/status/268375867468681216

Let's make a simple list and draw it as a train:

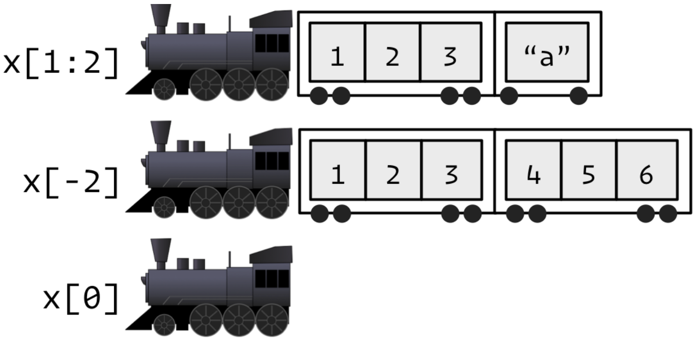
```
x <- list(1:3, "a", 4:5)
```



When extracting a single element, you have two options: you can create a smaller train, or you can extract the contents of a carriage. This is the difference between `[` and `[[`:



When extracting multiple elements (or zero!), you have to make a smaller train:



Because it can return only a single value, you must use `[[` with either a single positive integer or a string. Because data frames are lists of columns, you can use `[[` to extract a column from data frames: `mtcars[[1]]`, `mtcars[["cyl"]]`.

If you use a vector with `[[`, it will subset recursively:

```
(b <- list(a = list(b = list(c = list(d = 1)))))
```

```
#> $a
#> $a$b
#> $a$b$c
#> $a$b$c$d
#> [1] 1
```

```
b[[c("a", "b", "c", "d")]]
```

```
#> [1] 1
```

```
# Equivalent to
b[["a"]][["b"]][["c"]][["d"]]
```

```
#> [1] 1
```

[[is crucial for working with lists, but I recommend using it whenever you want your code to clearly express that it's working with a single value. That frequently arises in for loops, i.e. instead of writing:

```
for (i in 2:length(x)) {
  out[i] <- fun(x[i], out[i - 1])
}
```

It's better to write:

```
for (i in 2:length(x)) {
  out[[i]] <- fun(x[[i]], out[[i - 1]])
}
```

5.2.1 $

$ is a shorthand operator: `x$y` is roughly equivalent to `x[["y"]]`. It's often used to access variables in a data frame, as in `mtcars$cyl` or `diamonds$carat`. One common mistake with $ is to try and use it when you have the name of a column stored in a variable:

```
var <- "cyl"
# Doesn't work - mtcars$var translated to mtcars[["var"]]
mtcars$var
```

```
#> NULL
```

```
# Instead use [[
mtcars[[var]]
```

```
#>  [1] 6 6 4 6 8 6 8 4 4 6 6 8 8 8 8 8 8 4 4 4 4 8 8 8 8 4 4 4 8 6 8 4
```

There's one important difference between $ and [[. $ does partial matching:

```
x <- list(abc = 1)
x$a
```

```
#> [1] 1
```

```
x[["a"]]
```

```
#> NULL
```

It is usually a good idea to **NOT** use partial matching. It tends to to lead to hard to track down bugs and makes your code much less readable. With autocomplete in RStudio it tends not to save any time or keystrokes.

5.2.2 Missing/out of bounds indices

TL;DR version use `purrr::pluck()`, which we will get to in *R for Data Science*

It's useful to understand what happens with [and [[when you use an "invalid" index. The following tables summarise what happen when you subset a logical vector, list, and `NULL` with an out-of-bounds value (OOB), a missing value (i.e `NA_integer_`), and a zero-length object (like `NULL` or `logical()`) with `[` and `[[`. Each cell shows the result of subsetting the data structure named in the row by the type of index described in the column. I've only shown the results for logical vectors, but other atomic vectors behave similarly, returning elements of the same type.

`row[col]`	Zero-length	OOB	Missing
`NULL`	`NULL`	`NULL`	`NULL`
Logical	`logical(0)`	`NA`	`NA`
List	`list()`	`list(NULL)`	`list(NULL)`

With `[`, it doesn't matter whether the OOB index is a position or a name, but it does for `[[`:

`row[[col]]`	Zero-length	OOB (int)	OOB (chr)	Missing
`NULL`	`NULL`	`NULL`	`NULL`	`NULL`
Atomic	Error	Error	Error	Error
List	Error	Error	`NULL`	`NULL`

If the input vector is named, then the names of OOB, missing, or `NULL` components will be `"<NA>"`.

5.3 Subsetting and assignment

All subsetting operators can be combined with assignment to modify selected values of the input vector.

```
x <- 1:5
x[c(1, 2)] <- 2:3
x
```

```
#> [1] 2 3 3 4 5
```

```
# The length of the LHS needs to match the RHS
x[-1] <- 4:1
x
```

```
#> [1] 2 4 3 2 1
```

```
# Duplicated indices go unchecked and may be problematic
x[c(1, 1)] <- 2:3
x
```

```
#> [1] 3 4 3 2 1
```

```
# You can't combine integer indices with NA
x[c(1, NA)] <- c(1, 2)
```

```
#> Error in x[c(1, NA)] <- c(1, 2): NAs are not allowed in subscripted assignments
```

```
# But you can combine logical indices with NA
# (where they're treated as false).
x[c(T, F, NA)] <- 1
x
```

```
#> [1] 1 4 3 1 1
```

```r
# This is mostly useful when conditionally modifying vectors
df <- data.frame(a = c(1, 10, NA))
df$a[df$a < 5] <- 0
df$a
```

```
#> [1]  0 10 NA
```

Subsetting with nothing can be useful in conjunction with assignment because it will preserve the original object class and structure. Compare the following two expressions. In the first, `mtcars` will remain as a data frame. In the second, `mtcars` will become a list.

```r
(mtcars[] <- lapply(mtcars, as.integer))
(mtcars <- lapply(mtcars, as.integer))
```

With lists, you can use `[[` + assignment + `NULL` to remove components from a list. To add a literal `NULL` to a list, use `[` and `list(NULL)`:

```r
x <- list(a = 1, b = 2)
x[["b"]] <- NULL
str(x)
```

```
#> List of 1
#>  $ a: num 1
```

```r
y <- list(a = 1)
y["b"] <- list(NULL)
str(y)
```

```
#> List of 2
#>  $ a: num 1
#>  $ b: NULL
```

5.4 Applications

The basic principles described above give rise to a wide variety of useful applications. Some of the most important are described below. Many of these basic techniques are wrapped up into more concise functions (e.g., `subset()`, `merge()`, `dplyr::arrange()`), but it is useful to understand how they are implemented with basic subsetting. This will allow you to adapt to new situations that are not dealt with by existing functions.

5.4.1 Lookup tables (character subsetting)

Character matching provides a powerful way to make lookup tables. Say you want to convert abbreviations:

```r
x <- c("m", "f", "u", "f", "f", "m", "m")
lookup <- c(m = "Male", f = "Female", u = NA)
lookup[x]
```

```
#>        m        f        u        f        f        m        m
#>   "Male" "Female"       NA "Female" "Female"   "Male"   "Male"
```

```r
unname(lookup[x])
```

```
#> [1] "Male"   "Female" NA       "Female" "Female" "Male"   "Male"
```

If you don't want names in the result, use `unname()` to remove them.

5.4.2 Ordering (integer subsetting)

`order()` takes a vector as input and returns an integer vector describing how the subsetted vector should be ordered:

```
x <- c("b", "c", "a")
order(x)
```

```
#> [1] 3 1 2
```

```
x[order(x)]
```

```
#> [1] "a" "b" "c"
```

To break ties, you can supply additional variables to `order()`, and you can change from ascending to descending order using `decreasing = TRUE`. By default, any missing values will be put at the end of the vector; however, you can remove them with `na.last = NA` or put at the front with `na.last = FALSE`.

For two or more dimensions, `order()` and integer subsetting makes it easy to order either the rows or columns of an object:

```
(df <- data.frame(x = rep(1:3, each = 2), y = 6:1, z = letters[1:6]))
```

```
#>   x y z
#> 1 1 6 a
#> 2 1 5 b
#> 3 2 4 c
#> 4 2 3 d
#> 5 3 2 e
#> 6 3 1 f
```

```
# Randomly reorder df
df2 <- df[sample(nrow(df)), 3:1]
df2
```

```
#>   z y x
#> 2 b 5 1
#> 4 d 3 2
#> 3 c 4 2
#> 1 a 6 1
#> 5 e 2 3
#> 6 f 1 3
```

```
df2[order(df2$x), ]
```

```
#>   z y x
#> 2 b 5 1
#> 1 a 6 1
#> 4 d 3 2
#> 3 c 4 2
#> 5 e 2 3
#> 6 f 1 3
```

```
df2[, order(names(df2))]
```

```
#>   x y z
#> 2 1 5 b
#> 4 2 3 d
#> 3 2 4 c
#> 1 1 6 a
#> 5 3 2 e
#> 6 3 1 f
```

You can sort vectors directly with `sort()`, or use `dplyr::arrange()` or similar to sort a data frame.

5.4.3 Selecting rows based on a condition (logical subsetting)

Because it allows you to easily combine conditions from multiple columns, logical subsetting is probably the most commonly used technique for extracting rows out of a data frame.

```
mtcars[mtcars$gear == 5, ]
```

```
#>                 mpg cyl  disp  hp drat    wt qsec vs am gear carb
#> Porsche 914-2  26.0   4 120.3  91 4.43 2.140 16.7  0  1    5    2
#> Lotus Europa   30.4   4  95.1 113 3.77 1.513 16.9  1  1    5    2
#> Ford Pantera L 15.8   8 351.0 264 4.22 3.170 14.5  0  1    5    4
#> Ferrari Dino   19.7   6 145.0 175 3.62 2.770 15.5  0  1    5    6
#> Maserati Bora  15.0   8 301.0 335 3.54 3.570 14.6  0  1    5    8
```

```
mtcars[mtcars$gear == 5 & mtcars$cyl == 4, ]
```

```
#>                mpg cyl  disp  hp drat    wt qsec vs am gear carb
#> Porsche 914-2 26.0   4 120.3  91 4.43 2.140 16.7  0  1    5    2
#> Lotus Europa  30.4   4  95.1 113 3.77 1.513 16.9  1  1    5    2
```

Remember to use the vector boolean operators `&` and `|`, not the short-circuiting scalar operators `&&` and `||` which are more useful inside if statements. Don't forget De Morgan's laws, which can be useful to simplify negations:

- `!(X & Y)` is the same as `!X | !Y`
- `!(X | Y)` is the same as `!X & !Y`

For example, `!(X & !(Y | Z))` simplifies to `!X | !!(Y|Z)`, and then to `!X | Y | Z`.

`subset()` is a specialised shorthand function for subsetting data frames, and saves some typing because you don't need to repeat the name of the data frame..

```
subset(mtcars, gear == 5)
```

```
#>                 mpg cyl  disp  hp drat    wt qsec vs am gear carb
#> Porsche 914-2  26.0   4 120.3  91 4.43 2.140 16.7  0  1    5    2
#> Lotus Europa   30.4   4  95.1 113 3.77 1.513 16.9  1  1    5    2
#> Ford Pantera L 15.8   8 351.0 264 4.22 3.170 14.5  0  1    5    4
#> Ferrari Dino   19.7   6 145.0 175 3.62 2.770 15.5  0  1    5    6
#> Maserati Bora  15.0   8 301.0 335 3.54 3.570 14.6  0  1    5    8
```

```
subset(mtcars, gear == 5 & cyl == 4)
```

```
#>                mpg cyl  disp  hp drat    wt qsec vs am gear carb
#> Porsche 914-2 26.0   4 120.3  91 4.43 2.140 16.7  0  1    5    2
#> Lotus Europa  30.4   4  95.1 113 3.77 1.513 16.9  1  1    5    2
```

5.4.4 Boolean algebra vs. sets (logical & integer subsetting)

It's useful to be aware of the natural equivalence between set operations (integer subsetting) and boolean algebra (logical subsetting). Using set operations is more effective when:

- You want to find the first (or last) `TRUE`.

- You have very few `TRUE`s and very many `FALSE`s; a set representation may be faster and require less storage.

`which()` allows you to convert a boolean representation to an integer representation. There's no reverse operation in base R but we can easily create one:

```
x <- sample(10) < 4
which(x)
```

```
#> [1] 5 8 9
```

```
unwhich <- function(x, n) {
  out <- rep_len(FALSE, n)
  out[x] <- TRUE
  out
}
unwhich(which(x), 10)
```

```
#>  [1] FALSE FALSE FALSE FALSE  TRUE FALSE FALSE  TRUE  TRUE FALSE
```

Let's create two logical vectors and their integer equivalents and then explore the relationship between boolean and set operations.

```
(x1 <- 1:10 %% 2 == 0)
```

```
#>  [1] FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE
```

```
(x2 <- which(x1))
```

```
#> [1]  2  4  6  8 10
```

```
(y1 <- 1:10 %% 5 == 0)
```

```
#>  [1] FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE  TRUE
```

```
(y2 <- which(y1))
```

```
#> [1]  5 10
```

```
# X & Y <-> intersect(x, y)
x1 & y1
```

```
#>  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE
```

```
intersect(x2, y2)
```

```
#> [1] 10
```

```
# X | Y <-> union(x, y)
x1 | y1
```

```
#>  [1] FALSE  TRUE FALSE  TRUE  TRUE  TRUE FALSE  TRUE FALSE  TRUE
```

```
union(x2, y2)
```

```
#> [1]  2  4  6  8 10  5
```

```
# X & !Y <-> setdiff(x, y)
x1 & !y1
```

```
#>  [1] FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE FALSE
```

```
setdiff(x2, y2)
```

```
#> [1] 2 4 6 8
```

```
# xor(X, Y) <-> setdiff(union(x, y), intersect(x, y))
xor(x1, y1)
```

```
#>  [1] FALSE  TRUE FALSE  TRUE  TRUE  TRUE FALSE  TRUE FALSE FALSE
```

```
setdiff(union(x2, y2), intersect(x2, y2))
```

```
#> [1] 2 4 6 8 5
```

When first learning subsetting, a common mistake is to use `x[which(y)]` instead of `x[y]`. Here the `which()` achieves nothing: it switches from logical to integer subsetting but the result will be exactly the same. In more general cases, there are two important differences. First, when the logical vector contains NA, logical subsetting replaces these values by NA while `which()` drops these values. Second, `x[-which(y)]` is **not** equivalent to `x[!y]`: if `y` is all FALSE, `which(y)` will be `integer(0)` and `-integer(0)` is still `integer(0)`, so you'll get no values, instead of all values. In general, avoid switching from logical to integer subsetting unless you want, for example, the first or last `TRUE` value.

5.4.5 Removing columns from data frames (character subsetting)

There are two ways to remove columns from a data frame. You can set individual columns to `NULL`:

```
df <- data.frame(x = 1:3, y = 3:1, z = letters[1:3])
df$z <- NULL
```

Or you can subset to return only the columns you want:

```
df <- data.frame(x = 1:3, y = 3:1, z = letters[1:3])
df[c("x", "y")]
```

```
#>   x y
#> 1 1 3
#> 2 2 2
#> 3 3 1
```

If you know the columns you don't want, use set operations to work out which colums to keep:

```
df[setdiff(names(df), "z")]
```

```
#>   x y
#> 1 1 3
#> 2 2 2
#> 3 3 1
```

5.4.6 Matching and merging by hand (integer subsetting)

You may have a more complicated lookup table which has multiple columns of information. Suppose we have a vector of integer grades, and a table that describes their properties:

```
grades <- c(1, 2, 2, 3, 1)

info <- data.frame(
  grade = 3:1,
  desc = c("Excellent", "Good", "Poor"),
  fail = c(F, F, T)
)
```

We want to duplicate the info table so that we have a row for each value in `grades`. An elegant way to do this is by combining `match()` and integer subsetting:

```
id <- match(grades, info$grade)
info[id, ]
```

```
#>     grade      desc  fail
#> 3       1      Poor  TRUE
#> 2       2      Good FALSE
#> 2.1     2      Good FALSE
#> 1       3 Excellent FALSE
#> 3.1     1      Poor  TRUE
```

If you have multiple columns to match on, you'll need to first collapse them to a single column (with e.g. `interaction()`), but typically you are better off switching to a function design specifically for joining multiple tables like `merge()`, or `dplyr::left_join()`.

5.4.7 Random samples/bootstrap (integer subsetting)

You can use integer indices to perform random sampling or bootstrapping of a vector or data frame. `sample()` generates a vector of indices, then subsetting accesses the values:

```
(df <- data.frame(x = rep(1:3, each = 2), y = 6:1, z = letters[1:6]))
```

```
#>   x y z
#> 1 1 6 a
#> 2 1 5 b
#> 3 2 4 c
#> 4 2 3 d
#> 5 3 2 e
#> 6 3 1 f
```

```
# Randomly reorder
df[sample(nrow(df)), ]
```

```
#>   x y z
#> 3 2 4 c
#> 2 1 5 b
#> 6 3 1 f
#> 1 1 6 a
#> 5 3 2 e
#> 4 2 3 d
```

```
# Select 3 random rows
df[sample(nrow(df), 3), ]
```

```
#>   x y z
#> 4 2 3 d
#> 5 3 2 e
#> 3 2 4 c
```

```
# Select 6 bootstrap replicates
df[sample(nrow(df), 6, rep = TRUE), ]
```

```
#>     x y z
#> 4   2 3 d
#> 4.1 2 3 d
#> 3   2 4 c
#> 5   3 2 e
#> 4.2 2 3 d
#> 6   3 1 f
```

The arguments of `sample()` control the number of samples to extract, and whether sampling is performed with or without replacement.

5.4.8 Expanding aggregated counts (integer subsetting)

Sometimes you get a data frame where identical rows have been collapsed into one and a count column has been added. `rep()` and integer subsetting make it easy to uncollapse the data by subsetting with a repeated row index:

```
df <- data.frame(x = c(2, 4, 1), y = c(9, 11, 6), n = c(3, 5, 1))
df
```

```
#>   x  y n
#> 1 2  9 3
#> 2 4 11 5
#> 3 1  6 1
```

```
rep(1:nrow(df), df$n)
```

```
#> [1] 1 1 1 2 2 2 2 2 3
```

```
df[rep(1:nrow(df), df$n), ]
```

```
#>     x  y n
#> 1   2  9 3
#> 1.1 2  9 3
#> 1.2 2  9 3
#> 2   4 11 5
#> 2.1 4 11 5
#> 2.2 4 11 5
#> 2.3 4 11 5
#> 2.4 4 11 5
#> 3   1  6 1
```