R for Data Science

1. Introduction

Prerequisites

R, RStudio, a collection of R packages called the **tidyverse**, and a handful of other packages. Packages are the fundamental units of reproducible R code.

R

To download R, go to CRAN, the **c**omprehensive **R** **a**rchive **n**etwork. CRAN is composed of a set of mirror servers distributed around the world and is used to distribute R and R packages.

RStudio

RStudio is an integrated development environment, or IDE, for R programming. Download and install it from http://www.rstudio.com/download (http://www.rstudio.com/download).

The tidyverse

An R *package* is a collection of functions, data, and documentation that extends the capabilities of base R. Using packages is key to the successful use of R.

You can install the complete tidyverse with a single line of code:

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

On your own computer, type that line of code in the console, and then press enter to run it. R will download the packages from CRAN and install them on to your computer. If you have problems installing, make sure that you are connected to the internet, and that https://cloud.r-project.org/ (https://cloud.r-project.org/) isn't blocked by your firewall or proxy.

You will not be able to use the functions, objects, and help files in a package until you load it with `library()`. Once you have installed a package, you can load it with the `library()` function:

```
library(tidyverse)
```

This tells you that tidyverse is loading the ggplot2, tibble, tidyr, readr, purrr, and dplyr packages. These are considered to be the **core** of the tidyverse because you'll use them in almost every analysis.

Other packages

There are many other excellent packages that are not part of the tidyverse, because they solve problems in a different domain, or are designed with a different set of underlying principles. This doesn't make them better or worse, just different. In other words, the complement to the tidyverse is not the messyverse, but many other universes of interrelated packages. As you tackle more data science projects with R, you'll learn new packages and new ways of thinking about data.

Hide

```
install.packages(c("nycflights13", "gapminder", "Lahman"))
```

These packages provide data on airline flights, world development, and baseball that we'll use to illustrate key data science ideas.

Running R code

The previous section showed you a couple of examples of running R code. Code in the book looks like this:

Hide

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

If you run the same code in your local console, it will look like this:

```
> 1 + 2
[1] 3
```

Getting help and learning more

If you get stuck, start with Google. Typically adding "R" to a query is enough to restrict it to relevant results: if the search isn't useful, it often means that there aren't any R-specific results available. Google is particularly useful for error messages. If you get an error message and you have no idea what it means, try googling it! Chances are that someone else has been confused by it in the past, and there will be help somewhere on the web. (If the error message isn't in English, run `Sys.setenv(LANGUAGE = "en")` and re-run the code; you're more likely to find help for English error messages.)

If Google doesn't help, try stackoverflow (http://stackoverflow.com). Start by spending a little time searching for an existing answer, including `[R]` restrict your search to questions and answers that use R. If you don't find anything useful, prepare a minimal reproducible example or **reprex**. A good reprex makes it easier for other people to help you, and often you'll figure out the problem yourself in the course of making it.

There are three things you need to include to make your example reproducible: required packages, data, and code.

1. **Packages** should be loaded at the top of the script, so it's easy to see which ones the example needs. This is a good time to check that you're using the latest version of each package; it's possible you've discovered a bug that's been fixed since you installed the package. For packages in the tidyverse, the easiest way to check is to run `tidyverse_update()` .

2. The easiest way to include **data** in a question is to use `dput()` to generate the R code to recreate it. For example, to recreate the `mtcars` dataset in R, I'd perform the following steps:

    1. Run `dput(mtcars)` in R
    2. Copy the output
    3. In my reproducible script, type `mtcars <-` then paste.

    Try and find the smallest subset of your data that still reveals the problem.

3. Spend a little bit of time ensuring that your **code** is easy for others to read:

    - Make sure you've used spaces and your variable names are concise, yet informative.

    - Use comments to indicate where your problem lies.

  - Do your best to remove everything that is not related to the problem.
    The shorter your code is, the easier it is to understand, and the easier it is to fix.

Finish by checking that you have actually made a reproducible example by starting a fresh R session and copying and pasting your script in.

You should also spend some time preparing yourself to solve problems before they occur. Investing a little time in learning R each day will pay off handsomely in the long run. One way is to follow what Hadley, Garrett, and everyone else at RStudio are doing on the RStudio blog (https://blog.rstudio.org).

To keep up with the R community more broadly, we recommend reading http://www.r-bloggers.com (http://www.r-bloggers.com): it aggregates over 500 blogs about R from around the world. If you're an active Twitter user, follow the `#rstats` hashtag. Twitter is one of the key tools that Hadley uses to keep up with new developments in the community.

2. Workflow: basics

Coding basics

Let's review some basics we've so far omitted in the interests of getting you plotting as quickly as possible. You can use R as a calculator:

Hide

```
1 / 200 * 30
(59 + 73 + 2) / 3
sin(pi / 2)
```

You can create new objects with `<-` :

Hide

```
x <- 3 * 4
```

All R statements where you create objects, **assignment** statements, have the same form:

Hide

```
object_name <- value
```

When reading that code say "object name gets value" in your head.

You will make lots of assignments and `<-` is a pain to type. Don't be lazy and use `=` : it will work, but it will cause confusion later. Instead, use RStudio's keyboard shortcut: Alt + - (the minus sign). Notice that RStudio automagically surrounds `<-` with spaces, which is a good code formatting practice. Code is miserable to read on a good day, so giveyoureyesabreak and use spaces.

What's in a name?

Object names must start with a letter, and can only contain letters, numbers, `_` and `.` . You want your object names to be descriptive, so you'll need a convention for multiple words. I recommend **snake_case** where you separate lowercase words with `_` .

Hide

```
i_use_snake_case
otherPeopleUseCamelCase
some.people.use.periods
And_aFew.People_RENOUNCEconvention
```

We'll come back to code style later, in [functions].

You can inspect an object by typing its name:

Hide

```
x
```

Make another assignment:

Hide

```
this_is_a_really_long_name <- 2.5
```

To inspect this object, try out RStudio's completion facility: type "this", press TAB, add characters until you have a unique prefix, then press return.

Ooops, you made a mistake! `this_is_a_really_long_name` should have value 3.5 not 2.5. Use another keyboard shortcut to help you fix it. Type "this" then press Cmd/Ctrl + ↑. That will list all the commands you've typed that start those letters. Use the arrow keys to navigate, then press enter to retype the command. Change 2.5 to 3.5 and rerun.

Make yet another assignment:

Hide

```
r_rocks <- 2 ^ 3
```

Let's try to inspect it:

Hide

```
r_rock
#> Error: object 'r_rock' not found
R_rocks
#> Error: object 'R_rocks' not found
```

There's an implied contract between you and R: it will do the tedious computation for you, but in return, you must be completely precise in your instructions. Typos matter. Case matters.

Calling functions

R has a large collection of built-in functions that are called like this:

Hide

```
function_name(arg1 = val1, arg2 = val2, ...)
```

Let's try using `seq()` which makes regular **seq**uences of numbers and, while we're at it, learn more helpful features of RStudio. Type `se` and hit TAB. A popup shows you possible completions. Specify `seq()` by typing more (a "q") to disambiguate, or by using ↑/↓ arrows to select. Notice the floating tooltip that pops up, reminding you of the function's arguments and purpose. If you want more help, press F1 to get all the details in help tab in the lower right pane.

Press TAB once more when you've selected the function you want. RStudio will add matching opening (`(`) and closing (`)`) parentheses for you. Type the arguments `1, 10` and hit return.

Hide

```
seq(1, 10)
```

Type this code and notice similar assistance help with the paired quotation marks:

Hide

```
x <- "hello world"
```

Quotation marks and parentheses must always come in a pair. RStudio does its best to help you, but it's still possible to mess up and end up with a mismatch. If this happens, R will show you the continuation character "+":

```
> x <- "hello
+
```

The `+` tells you that R is waiting for more input; it doesn't think you're done yet. Usually that means you've forgotten either a `"` or a `)` . Either add the missing pair, or press ESCAPE to abort the expression and try again.

If you make an assignment, you don't get to see the value. You're then tempted to immediately double-check the result:

Hide

```
y <- seq(1, 10, length.out = 5)
y
```

This common action can be shortened by surrounding the assignment with parentheses, which causes assignment and "print to screen" to happen.

Hide

```
(y <- seq(1, 10, length.out = 5))
```

Here you can see all of the objects that you've created.

Practice

1. Why does this code not work?

Hide

```
my_variable <- 10
my_varıable
```

Look carefully! (This may seem like an exercise in pointlessness, but training your brain to notice even the tiniest difference will pay off when programming.)

3. Data transformation

Introduction

Visualisation is an important tool for insight generation, but it is rare that you get the data in exactly the right form you need. Often you'll need to create some new variables or summaries, or maybe you just want to rename the variables or reorder the observations in order to make the data a little easier to work with. You'll learn how to do all that (and more!) in this chapter, which will teach you how to transform your data using the dplyr package and a new dataset on flights departing New York City in 2013.

Prerequisites

In this chapter we're going to focus on how to use the dplyr package, another core member of the tidyverse. We'll illustrate the key ideas using data from the nycflights13 package, and use ggplot2 to help us understand the data.

Hide

```
library(nycflights13)
library(tidyverse)
```

Take careful note of the conflicts message that's printed when you load the tidyverse. It tells you that dplyr overwrites some functions in base R. If you want to use the base version of these functions after loading dplyr, you'll need to use their full names: `stats::filter()` and `stats::lag()` .

nycflights13

To explore the basic data manipulation verbs of dplyr, we'll use `nycflights13::flights` . This data frame contains all 336,776 flights that departed from New York City in 2013. The data comes from the US Bureau of Transportation Statistics (http://www.transtats.bts.gov/DatabaseInfo.asp?DB_ID=120&Link=0), and is documented in `?flights` .

Hide

```
flights
```

You might notice that this data frame prints a little differently from other data frames you might have used in the past: it only shows the first few rows and all the columns that fit on one screen. (To see the whole dataset, you can run `View(flights)` which will open the dataset in the RStudio viewer). It prints differently because it's a **tibble**. Tibbles are data frames, but slightly tweaked to work better in the tidyverse. For now, you don't need to worry about the differences; we'll come back to tibbles in more detail in wrangle.

You might also have noticed the row of three (or four) letter abbreviations under the column names. These describe the type of each variable:

- `int` stands for integers.
- `dbl` stands for doubles, or real numbers.
- `chr` stands for character vectors, or strings.
- `dttm` stands for date-times (a date + a time).

There are three other common types of variables that aren't used in this dataset but you'll encounter later in the book:

- `lgl` stands for logical, vectors that contain only `TRUE` or `FALSE`.
- `fctr` stands for factors, which R uses to represent categorical variables with fixed possible values.
- `date` stands for dates.

dplyr basics

In this chapter you are going to learn the five key dplyr functions that allow you to solve the vast majority of your data manipulation challenges:

- Pick observations by their values (`filter()`).
- Reorder the rows (`arrange()`).
- Pick variables by their names (`select()`).
- Create new variables with functions of existing variables (`mutate()`).
- Collapse many values down to a single summary (`summarise()`).

These can all be used in conjunction with `group_by()` which changes the scope of each function from operating on the entire dataset to operating on it group-by-group. These six functions provide the verbs for a language of data manipulation.

All verbs work similarly:

1. The first argument is a data frame.
2. The subsequent arguments describe what to do with the data frame, using the variable names (without quotes).
3. The result is a new data frame.

Together these properties make it easy to chain together multiple simple steps to achieve a complex result. Let's dive in and see how these verbs work.

Filter rows with `filter()`

`filter()` allows you to subset observations based on their values. The first argument is the name of the data frame. The second and subsequent arguments are the expressions that filter the data frame. For example, we can select all flights on January 1st with:

Hide

```
filter(flights, month == 1, day == 1)
```

When you run that line of code, dplyr executes the filtering operation and returns a new data frame. dplyr functions never modify their inputs, so if you want to save the result, you'll need to use the assignment operator, `<-`:

Hide

```
jan1 <- filter(flights, month == 1, day == 1)
```

R either prints out the results, or saves them to a variable. If you want to do both, you can wrap the assignment in parentheses:

Hide

```
(dec25 <- filter(flights, month == 12, day == 25))
```

Comparisons

To use filtering effectively, you have to know how to select the observations that you want using the comparison operators. R provides the standard suite: `>`, `>=`, `<`, `<=`, `!=` (not equal), and `==` (equal).

When you're starting out with R, the easiest mistake to make is to use `=` instead of `==` when testing for equality. When this happens you'll get an informative error:

Hide

```
filter(flights, month = 1)
```

There's another common problem you might encounter when using `==`: floating point numbers. These results might surprise you!

Hide

```
sqrt(2) ^ 2 == 2
1/49 * 49 == 1
```

Computers use finite precision arithmetic (they obviously can't store an infinite number of digits!) so remember that every number you see is an approximation. Instead of relying on `==`, use `near()`:

Hide

```
near(sqrt(2) ^ 2,  2)
near(1 / 49 * 49, 1)
```

Logical operators

Multiple arguments to `filter()` are combined with "and": every expression must be true in order for a row to be included in the output. For other types of combinations, you'll need to use Boolean operators yourself: `&` is "and", `|` is "or", and `!` is "not". Figure @ref(fig:bool-ops) shows the complete set of Boolean operations.

The following code finds all flights that departed in November or December:

Hide

```
filter(flights, month == 11 | month == 12)
```

The order of operations doesn't work like English. You can't write `filter(flights, month == 11 | 12)`, which you might literally translate into "finds all flights that departed in November or December". Instead it finds all months that equal `11 | 12`, an expression that evaluates to `TRUE`. In a numeric context (like here), `TRUE` becomes one, so this finds all flights in January, not November or December. This is quite confusing!

A useful short-hand for this problem is `x %in% y`. This will select every row where `x` is one of the values in `y`. We could use it to rewrite the code above:

Hide

```
nov_dec <- filter(flights, month %in% c(11, 12))
```

Sometimes you can simplify complicated subsetting by remembering De Morgan's law: `!(x & y)` is the same as `!x | !y`, and `!(x | y)` is the same as `!x & !y`. For example, if you wanted to find flights that weren't delayed (on arrival or departure) by more than two hours, you could use either of the following two filters:

Hide

```
filter(flights, !(arr_delay > 120 | dep_delay > 120))
filter(flights, arr_delay <= 120, dep_delay <= 120)
```

As well as `&` and `|`, R also has `&&` and `||`. Don't use them here! You'll learn when you should use them in [conditional execution].

Whenever you start using complicated, multipart expressions in `filter()`, consider making them explicit variables instead. That makes it much easier to check your work. You'll learn how to create new variables shortly.

Missing values

One important feature of R that can make comparison tricky are missing values, or `NA` s ("not availables"). `NA` represents an unknown value so missing values are "contagious": almost any operation involving an unknown value will also be unknown.

Hide

```
NA > 5
10 == NA
NA + 10
NA / 2
```

The most confusing result is this one:

Hide

```
NA == NA
```

It's easiest to understand why this is true with a bit more context:

Hide

```
# Let x be Mary's age. We don't know how old she is.
x <- NA

# Let y be John's age. We don't know how old he is.
y <- NA

# Are John and Mary the same age?
x == y
# We don't know!
```

If you want to determine if a value is missing, use `is.na()`:

Hide

```
is.na(x)
```

`filter()` only includes rows where the condition is `TRUE`; it excludes both `FALSE` and `NA` values. If you want to preserve missing values, ask for them explicitly:

Hide

```
df <- tibble(x = c(1, NA, 3))
filter(df, x > 1)
filter(df, is.na(x) | x > 1)
```

Exercises

1. Find all flights that
    1. Had an arrival delay of two or more hours
    2. Flew to Houston (`IAH` or `HOU`)
    3. Were operated by United, American, or Delta
    4. Departed in summer (July, August, and September)
2. How many flights have a missing `dep_time` ? What other variables are missing?

Arrange rows with `arrange()`

`arrange()` works similarly to `filter()` except that instead of selecting rows, it changes their order. It takes a data frame and a set of column names (or more complicated expressions) to order by. If you provide more than one column name, each additional column will be used to break ties in the values of preceding columns:

Hide

```
arrange(flights, year, month, day)
```

Use `desc()` to re-order by a column in descending order:

Hide

```
arrange(flights, desc(arr_delay))
```

Missing values are always sorted at the end:

Hide

```
df <- tibble(x = c(5, 2, NA))
arrange(df, x)
arrange(df, desc(x))
```

Select columns with `select()`

It's not uncommon to get datasets with hundreds or even thousands of variables. In this case, the first challenge is often narrowing in on the variables you're actually interested in. `select()` allows you to rapidly zoom in on a useful subset using operations based on the names of the variables.

`select()` is not terribly useful with the flights data because we only have 19 variables, but you can still get the general idea:

Hide

```
# Select columns by name
select(flights, year, month, day)
# Select all columns between year and day (inclusive)
select(flights, year:day)
# Select all columns except those from year to day (inclusive)
select(flights, -(year:day))
```

There are a number of helper functions you can use within `select()`:

- `starts_with("abc")`: matches names that begin with "abc".
- `ends_with("xyz")`: matches names that end with "xyz".
- `contains("ijk")`: matches names that contain "ijk".
- `matches("(.)\\1")`: selects variables that match a regular expression. This one matches any variables that contain repeated characters. You'll learn more about regular expressions in [strings].
- `num_range("x", 1:3)` matches `x1`, `x2` and `x3`.

See `?select` for more details.

`select()` can be used to rename variables, but it's rarely useful because it drops all of the variables not explicitly mentioned. Instead, use `rename()`, which is a variant of `select()` that keeps all the variables that aren't explicitly mentioned:

Hide

```
rename(flights, tail_num = tailnum)
```

Another option is to use `select()` in conjunction with the `everything()` helper. This is useful if you have a handful of variables you'd like to move to the start of the data frame.

Hide

```
select(flights, time_hour, air_time, everything())
```

Exercises

1. Does the result of running the following code surprise you? How do the select helpers deal with case by default? How can you change that default?

Hide

```
select(flights, contains("TIME"))
?select_helper
```

Add new variables with `mutate()`

Besides selecting sets of existing columns, it's often useful to add new columns that are functions of existing columns. That's the job of `mutate()`.

`mutate()` always adds new columns at the end of your dataset so we'll start by creating a narrower dataset so we can see the new variables. Remember that when you're in RStudio, the easiest way to see all the columns is `View()`.

Hide

```
flights_sml <- select(flights,
  year:day,
  ends_with("delay"),
  distance,
  air_time
)
mutate(flights_sml,
  gain = arr_delay - dep_delay,
  speed = distance / air_time * 60
)
```

Note that you can refer to columns that you've just created:

Hide

```
mutate(flights_sml,
  gain = arr_delay - dep_delay,
  hours = air_time / 60,
  gain_per_hour = gain / hours
)
```

If you only want to keep the new variables, use `transmute()` :

Hide

```
transmute(flights,
  gain = arr_delay - dep_delay,
  hours = air_time / 60,
  gain_per_hour = gain / hours
)
```

Useful creation functions

There are many functions for creating new variables that you can use with `mutate()` . The key property is that the function must be vectorised: it must take a vector of values as input, return a vector with the same number of values as output. There's no way to list every possible function that you might use, but here's a selection of functions that are frequently useful:

- Arithmetic operators: `+` , `-` , `*` , `/` , `^` . These are all vectorised, using the so called "recycling rules". If one parameter is shorter than the other, it will be automatically extended to be the same length. This is most useful when one of the arguments is a single number: `air_time / 60` , `hours * 60 + minute` , etc.

  Arithmetic operators are also useful in conjunction with the aggregate functions you'll learn about later. For example, `x / sum(x)` calculates the proportion of a total, and `y - mean(y)` computes the difference from the mean.

- Modular arithmetic: `%/%` (integer division) and `%%` (remainder), where `x == y * (x %/% y) + (x %% y)` . Modular arithmetic is a handy tool because it allows you to break integers up into pieces. For example, in the flights dataset, you can compute `hour` and `minute` from `dep_time` with:

Hide

```
transmute(flights,
  dep_time,
  hour = dep_time %/% 100,
  minute = dep_time %% 100
)
```

- Logs: `log()`, `log2()`, `log10()`. Logarithms are an incredibly useful transformation for dealing with data that ranges across multiple orders of magnitude. They also convert multiplicative relationships to additive, a feature we'll come back to in modelling.

  All else being equal, I recommend using `log2()` because it's easy to interpret: a difference of 1 on the log scale corresponds to doubling on the original scale and a difference of -1 corresponds to halving.

- Offsets: `lead()` and `lag()` allow you to refer to leading or lagging values. This allows you to compute running differences (e.g. `x - lag(x)`) or find when values change (`x != lag(x))`. They are most useful in conjunction with `group_by()`, which you'll learn about shortly.

Hide

```
(x <- 1:10)
lag(x)
lead(x)
```

- Cumulative and rolling aggregates: R provides functions for running sums, products, mins and maxes: `cumsum()`, `cumprod()`, `cummin()`, `cummax()`; and dplyr provides `cummean()` for cumulative means. If you need rolling aggregates (i.e. a sum computed over a rolling window), try the RcppRoll package.

Hide

```
x
cumsum(x)
cummean(x)
```

- Logical comparisons, `<`, `<=`, `>`, `>=`, `!=`, which you learned about earlier. If you're doing a complex sequence of logical operations it's often a good idea to store the interim values in new variables so you can check that each step is working as expected.

Grouped summaries with `summarise()`

The last key verb is `summarise()`. It collapses a data frame to a single row:

Hide

```
summarise(flights, delay = mean(dep_delay, na.rm = TRUE))
```

(We'll come back to what that `na.rm = TRUE` means very shortly.)

`summarise()` is not terribly useful unless we pair it with `group_by()`. This changes the unit of analysis from the complete dataset to individual groups. Then, when you use the dplyr verbs on a grouped data frame they'll be automatically applied "by group". For example, if we applied exactly the same code to a data frame grouped by date, we get the average delay per date:

Hide

```
by_day <- group_by(flights, year, month, day)
summarise(by_day, delay = mean(dep_delay, na.rm = TRUE))
```

Together `group_by()` and `summarise()` provide one of the tools that you'll use most commonly when working with dplyr: grouped summaries. But before we go any further with this, we need to introduce a powerful new idea: the pipe.

Combining multiple operations with the pipe

Imagine that we want to explore the relationship between the distance and average delay for each location. Using what you know about dplyr, you might write code like this:

Hide

```
by_dest <- group_by(flights, dest)
delay <- summarise(by_dest,
  count = n(),
  dist = mean(distance, na.rm = TRUE),
  delay = mean(arr_delay, na.rm = TRUE)
)
delay <- filter(delay, count > 20, dest != "HNL")

# It looks like delays increase with distance up to ~750 miles
# and then decrease. Maybe as flights get longer there's more
# ability to make up delays in the air?
ggplot(data = delay, mapping = aes(x = dist, y = delay)) +
  geom_point(aes(size = count), alpha = 1/3) +
  geom_smooth(se = FALSE)
```

There are three steps to prepare this data:

1. Group flights by destination.
2. Summarise to compute distance, average delay, and number of flights.
3. Filter to remove noisy points and Honolulu airport, which is almost twice as far away as the next closest airport.

This code is a little frustrating to write because we have to give each intermediate data frame a name, even though we don't care about it. Naming things is hard, so this slows down our analysis.

There's another way to tackle the same problem with the pipe, `%>%` :

Hide

```
delays <- flights %>%
  group_by(dest) %>%
  summarise(
    count = n(),
    dist = mean(distance, na.rm = TRUE),
    delay = mean(arr_delay, na.rm = TRUE)
  ) %>%
  filter(count > 20, dest != "HNL")
```

This focuses on the transformations, not what's being transformed, which makes the code easier to read. You can read it as a series of imperative statements: group, then summarise, then filter. As suggested by this reading, a good way to pronounce `%>%` when reading code is "then".

Behind the scenes, `x %>% f(y)` turns into `f(x, y)`, and `x %>% f(y) %>% g(z)` turns into `g(f(x, y), z)` and so on. You can use the pipe to rewrite multiple operations in a way that you can read left-to-right, top-to-bottom. We'll use piping frequently from now on because it considerably improves the readability of code, and we'll come back to it in more detail in [pipes].

Working with the pipe is one of the key criteria for belonging to the tidyverse. The only exception is ggplot2: it was written before the pipe was discovered. Unfortunately, the next iteration of ggplot2, ggvis, which does use the pipe, isn't quite ready for prime time yet.

Missing values

You may have wondered about the `na.rm` argument we used above. What happens if we don't set it?

Hide

```
flights %>%
  group_by(year, month, day) %>%
  summarise(mean = mean(dep_delay))
```

We get a lot of missing values! That's because aggregation functions obey the usual rule of missing values: if there's any missing value in the input, the output will be a missing value. Fortunately, all aggregation functions have an `na.rm` argument which removes the missing values prior to computation:

Hide

```
flights %>%
  group_by(year, month, day) %>%
  summarise(mean = mean(dep_delay, na.rm = TRUE))
```

In this case, where missing values represent cancelled flights, we could also tackle the problem by first removing the cancelled flights. We'll save this dataset so we can reuse in the next few examples.

Hide

```
not_cancelled <- flights %>%
  filter(!is.na(dep_delay), !is.na(arr_delay))

not_cancelled %>%
  group_by(year, month, day) %>%
  summarise(mean = mean(dep_delay))
```

Counts

Whenever you do any aggregation, it's always a good idea to include either a count (`n()`), or a count of non-missing values (`sum(!is.na(x))`). That way you can check that you're not drawing conclusions based on very small amounts of data. For example, let's look at the planes (identified by their tail number) that have the highest average delays:

Hide

```
delays <- not_cancelled %>%
  group_by(tailnum) %>%
  summarise(
    delay = mean(arr_delay)
  )

ggplot(data = delays, mapping = aes(x = delay)) +
  geom_freqpoly(binwidth = 10)
```

Wow, there are some planes that have an *average* delay of 5 hours (300 minutes)!

The story is actually a little more nuanced. We can get more insight if we draw a scatterplot of number of flights vs. average delay:

Hide

```
delays <- not_cancelled %>%
  group_by(tailnum) %>%
  summarise(
    delay = mean(arr_delay, na.rm = TRUE),
    n = n()
  )

ggplot(data = delays, mapping = aes(x = n, y = delay)) +
  geom_point(alpha = 1/10)
```

Not surprisingly, there is much greater variation in the average delay when there are few flights. The shape of this plot is very characteristic: whenever you plot a mean (or other summary) vs. group size, you'll see that the variation decreases as the sample size increases.

When looking at this sort of plot, it's often useful to filter out the groups with the smallest numbers of observations, so you can see more of the pattern and less of the extreme variation in the smallest groups. This is what the following code does, as well as showing you a handy pattern for integrating ggplot2 into dplyr flows. It's a bit painful that you have to switch from `%>%` to `+`, but once you get the hang of it, it's quite convenient.

Hide

```
delays %>%
  filter(n > 25) %>%
  ggplot(mapping = aes(x = n, y = delay)) +
    geom_point(alpha = 1/10)
```

RStudio tip: a useful keyboard shortcut is Cmd/Ctrl + Shift + P. This resends the previously sent chunk from the editor to the console. This is very convenient when you're (e.g.) exploring the value of `n` in the example above. You send the whole block once with Cmd/Ctrl + Enter, then you modify the value of `n` and press Cmd/Ctrl + Shift + P to resend the complete block.

Useful summary functions

Just using means, counts, and sum can get you a long way, but R provides many other useful summary functions:

- Measures of location: we've used `mean(x)`, but `median(x)` is also useful. The mean is the sum divided by the length; the median is a value where 50% of `x` is above it, and 50% is below it.

It's sometimes useful to combine aggregation with logical subsetting. We haven't talked about this sort of subsetting yet, but you'll learn more about it in subsetting.

Hide

```
not_cancelled %>%
  group_by(year, month, day) %>%
  summarise(
    avg_delay1 = mean(arr_delay),
    avg_delay2 = mean(arr_delay[arr_delay > 0]) # the average positive delay
  )
```

- Measures of spread: `sd(x)` , `IQR(x)` , `mad(x)` . The mean squared deviation, or standard deviation or sd for short, is the standard measure of spread. The interquartile range `IQR()` and median absolute deviation `mad(x)` are robust equivalents that may be more useful if you have outliers.

Hide

```
# Why is distance to some destinations more variable than to others?
not_cancelled %>%
  group_by(dest) %>%
  summarise(distance_sd = sd(distance)) %>%
  arrange(desc(distance_sd))
```

- Measures of rank: `min(x)` , `quantile(x, 0.25)` , `max(x)` . Quantiles are a generalisation of the median. For example, `quantile(x, 0.25)` will find a value of `x` that is greater than 25% of the values, and less than the remaining 75%.

Hide

```
# When do the first and last flights leave each day?
not_cancelled %>%
  group_by(year, month, day) %>%
  summarise(
    first = min(dep_time),
    last = max(dep_time)
  )
```

- Measures of position: `first(x)` , `nth(x, 2)` , `last(x)` . These work similarly to `x[1]` , `x[2]` , and `x[length(x)]` but let you set a default value if that position does not exist (i.e. you're trying to get the 3rd element from a group that only has two elements). For example, we can find the first and last departure for each day:

Hide

```
not_cancelled %>%
  group_by(year, month, day) %>%
  summarise(
    first_dep = first(dep_time),
    last_dep = last(dep_time)
  )
```

```
These functions are complementary to filtering on ranks. Filtering gives
you all variables, with each observation in a separate row:
```

Hide

```
not_cancelled %>%
  group_by(year, month, day) %>%
  mutate(r = min_rank(desc(dep_time))) %>%
  filter(r %in% range(r))
```

- Counts: You've seen `n()`, which takes no arguments, and returns the size of the current group. To count the number of non-missing values, use `sum(!is.na(x))`. To count the number of distinct (unique) values, use `n_distinct(x)`.

Hide

```
# Which destinations have the most carriers?
not_cancelled %>%
  group_by(dest) %>%
  summarise(carriers = n_distinct(carrier)) %>%
  arrange(desc(carriers))
```

```
Counts are so useful that dplyr provides a simple helper if all you want is
a count:
```

Hide

```
not_cancelled %>%
  count(dest)
```

```
You can optionally provide a weight variable. For example, you could use
this to "count" (sum) the total number of miles a plane flew:
```

Hide

```
not_cancelled %>%
  count(tailnum, wt = distance)
```

- Counts and proportions of logical values: `sum(x > 10)`, `mean(y == 0)`. When used with numeric functions, `TRUE` is converted to 1 and `FALSE` to 0. This makes `sum()` and `mean()` very useful: `sum(x)` gives the number of `TRUE`s in `x`, and `mean(x)` gives the proportion.

Hide

```
# How many flights left before 5am? (these usually indicate delayed
# flights from the previous day)
not_cancelled %>%
  group_by(year, month, day) %>%
  summarise(n_early = sum(dep_time < 500))
```

Hide

```
# What proportion of flights are delayed by more than an hour?
not_cancelled %>%
  group_by(year, month, day) %>%
  summarise(hour_perc = mean(arr_delay > 60))
```

Grouping by multiple variables

When you group by multiple variables, each summary peels off one level of the grouping. That makes it easy to progressively roll up a dataset:

Hide

```
daily <- group_by(flights, year, month, day)
(per_day   <- summarise(daily, flights = n()))
(per_month <- summarise(per_day, flights = sum(flights)))
(per_year  <- summarise(per_month, flights = sum(flights)))
```

Be careful when progressively rolling up summaries: it's OK for sums and counts, but you need to think about weighting means and variances, and it's not possible to do it exactly for rank-based statistics like the median. In other words, the sum of groupwise sums is the overall sum, but the median of groupwise medians is not the overall median.

Ungrouping

If you need to remove grouping, and return to operations on ungrouped data, use `ungroup()`.

Hide

```
daily %>%
  ungroup() %>%             # no longer grouped by date
  summarise(flights = n())  # all flights
```

Grouped mutates (and filters)

Grouping is most useful in conjunction with `summarise()`, but you can also do convenient operations with `mutate()` and `filter()`:

- Find the worst members of each group:

Hide

```
flights_sml %>%
  group_by(year, month, day) %>%
  filter(rank(desc(arr_delay)) < 10)
```

- Find all groups bigger than a threshold:

Hide

```
popular_dests <- flights %>%
  group_by(dest) %>%
  filter(n() > 365)
popular_dests
```

- Standardise to compute per group metrics:

Hide

```
popular_dests %>%
  filter(arr_delay > 0) %>%
  mutate(prop_delay = arr_delay / sum(arr_delay)) %>%
  select(year:day, dest, arr_delay, prop_delay)
```

A grouped filter is a grouped mutate followed by an ungrouped filter. I generally avoid them except for quick and dirty manipulations: otherwise it's hard to check that you've done the manipulation correctly.

Functions that work most naturally in grouped mutates and filters are known as window functions (vs. the summary functions used for summaries). You can learn more about useful window functions in the corresponding vignette: `vignette("window-functions")`.

4. Workflow: scripts

So far you've been using the console to run code. That's a great place to start, but you'll find it gets cramped pretty quickly as you create more complex ggplot2 graphics and dplyr pipes. To give yourself more room to work, it's a great idea to use the script editor. Open it up either by clicking the File menu, and selecting New File, then R script, or using the keyboard shortcut Cmd/Ctrl + Shift + N. Now you'll see four panes:

The script editor is a great place to put code you care about. Keep experimenting in the console, but once you have written code that works and does what you want, put it in the script editor. RStudio will automatically save the contents of the editor when you quit RStudio, and will automatically load it when you re-open. Nevertheless, it's a good idea to save your scripts regularly and to back them up.

Instead of running expression-by-expression, you can also execute the complete script in one step: Cmd/Ctrl + Shift + S. Doing this regularly is a great way to check that you've captured all the important parts of your code in the script.

I recommend that you always start your script with the packages that you need. That way, if you share your code with others, they can easily see what packages they need to install. Note, however, that you should never include `install.packages()` or `setwd()` in a script that you share. It's very antisocial to change settings on someone else's computer!

When working through future chapters, I highly recommend starting in the editor and practicing your keyboard shortcuts. Over time, sending code to the console in this way will become so natural that you won't even think about it.

5. Tibbles

Introduction

Throughout this book we work with "tibbles" instead of R's traditional `data.frame`. Tibbles *are* data frames, but they tweak some older behaviours to make life a little easier. R is an old language, and some things that were useful 10 or 20 years ago now get in your way. It's difficult to change base R without breaking existing code, so most innovation occurs in packages. Here we will describe the **tibble** package, which provides opinionated data frames that make working in the tidyverse a little easier. In most places, I'll use the term tibble and data frame interchangeably; when I want to draw particular attention to R's built-in data frame, I'll call them `data.frame`s.

If this chapter leaves you wanting to learn more about tibbles, you might enjoy `vignette("tibble")`.

Prerequisites

In this chapter we'll explore the **tibble** package, part of the core tidyverse.

Creating tibbles

Almost all of the functions that you'll use in this book produce tibbles, as tibbles are one of the unifying features of the tidyverse. Most other R packages use regular data frames, so you might want to coerce a data frame to a tibble. You can do that with `as_tibble()` :

Hide

```
as_tibble(iris)
```

You can create a new tibble from individual vectors with `tibble()` . `tibble()` will automatically recycle inputs of length 1, and allows you to refer to variables that you just created, as shown below.

Hide

```
tibble(
  x = 1:5,
  y = 1,
  z = x ^ 2 + y
)
```

If you're already familiar with `data.frame()` , note that `tibble()` does much less: it never changes the type of the inputs (e.g. it never converts strings to factors!), it never changes the names of variables, and it never creates row names.

It's possible for a tibble to have column names that are not valid R variable names, aka **non-syntactic** names. For example, they might not start with a letter, or they might contain unusual characters like a space. To refer to these variables, you need to surround them with backticks, ` ` ` :

:) <chr>	 <chr>	**2000** <chr>
smile	space	number

1 row

You'll also need the backticks when working with these variables in other packages, like ggplot2, dplyr, and tidyr.

Tibbles vs. data.frame

There are two main differences in the usage of a tibble vs. a classic `data.frame` : printing and subsetting.

Printing

Tibbles have a refined print method that shows only the first 10 rows, and all the columns that fit on screen. This makes it much easier to work with large data. In addition to its name, each column reports its type, a nice feature borrowed from `str()` :

a <S3: POSIXct>	**b** <function () ,.Internal(date())>	**c** <int>	**d** <dbl>	**e** <ch
2017-02-11 23:44:19	2017-03-06	1	0.043220683	l
2017-02-12 12:53:10	2017-02-28	2	0.112494377	t
2017-02-11 23:19:08	2017-02-17	3	0.502094967	c

a <S3: POSIXct>	b <function () ,.Internal(date())>	c <int>	d <dbl>	e <ch
2017-02-11 23:23:22	2017-02-16	4	0.590418844	y
2017-02-12 11:46:41	2017-03-12	5	0.068116747	l
2017-02-12 00:30:59	2017-02-17	6	0.775143211	z
2017-02-12 21:27:44	2017-02-19	7	0.285312797	r
2017-02-12 14:49:05	2017-02-11	8	0.265565257	n
2017-02-12 02:44:10	2017-02-13	9	0.482958248	k
2017-02-12 21:45:49	2017-03-08	10	0.841403625	r

1-10 of 1,000 rows Previous **1** 2 3 4 5 6 ... 100 Next

Tibbles are designed so that you don't accidentally overwhelm your console when you print large data frames. But sometimes you need more output than the default display. There are a few options that can help.

First, you can explicitly `print()` the data frame and control the number of rows (`n`) and the `width` of the display. `width = Inf` will display all columns:

Hide

```
nycflights13::flights %>%
  print(n = 10, width = Inf)
```

You can also control the default print behaviour by setting options:

- `options(tibble.print_max = n, tibble.print_min = m)` : if more than `m` rows, print only `n` rows. Use `options(dplyr.print_min = Inf)` to always show all rows.
- Use `options(tibble.width = Inf)` to always print all columns, regardless of the width of the screen.

You can see a complete list of options by looking at the package help with `package?tibble` .

A final option is to use RStudio's built-in data viewer to get a scrollable view of the complete dataset. This is also often useful at the end of a long chain of manipulations.

Hide

```
nycflights13::flights %>%
  View()
```

Subsetting

So far all the tools you've learned have worked with complete data frames. If you want to pull out a single variable, you need some new tools, `$` and `[[` . `[[` can extract by name or position; `$` only extracts by name but is a little less typing.

Hide

```
df <- tibble(
  x = runif(5),
  y = rnorm(5)
)

# Extract by name
df$x
df[["x"]]

# Extract by position
df[[1]]
```

To use these in a pipe, you'll need to use the special placeholder `.` :

Hide

```
df %>% .$x
df %>% .[["x"]]
```

Compared to a `data.frame` , tibbles are more strict: they never do partial matching, and they will generate a warning if the column you are trying to access does not exist.

Interacting with older code

Some older functions don't work with tibbles. If you encounter one of these functions, use `as.data.frame()` to turn a tibble back to a `data.frame` :

Hide

```
class(as.data.frame(tb))
```

The main reason that some older functions don't work with tibble is the `[` function. We don't use `[` much in this book because `dplyr::filter()` and `dplyr::select()` allow you to solve the same problems with clearer code (but you will learn a little about it in vector subsetting). With base R data frames, `[` sometimes returns a data frame, and sometimes returns a vector. With tibbles, `[` always returns another tibble.

6. Data import

Introduction

Working with data provided by R packages is a great way to learn the tools of data science, but at some point you want to stop learning and start working with your own data. In this chapter, you'll learn how to read plain-text rectangular files into R. Here, we'll only scratch the surface of data import, but many of the principles will translate to other forms of data. We'll finish with a few pointers to packages that are useful for other types of data.

Prerequisites

In this chapter, you'll learn how to load flat files in R with the **readr** package, which is part of the core tidyverse.

Getting started

Most of readr's functions are concerned with turning flat files into data frames:

- `read_csv()` reads comma delimited files, `read_csv2()` reads semicolon separated files (common in countries where `,` is used as the decimal place), `read_tsv()` reads tab delimited files, and `read_delim()` reads in files with any delimiter.
- `read_fwf()` reads fixed width files. You can specify fields either by their widths with `fwf_widths()` or their position with `fwf_positions()`. `read_table()` reads a common variation of fixed width files where columns are separated by white space.
- `read_log()` reads Apache style log files. (But also check out webreadr (https://github.com/Ironholds/webreadr) which is built on top of `read_log()` and provides many more helpful tools.)

These functions all have similar syntax: once you've mastered one, you can use the others with ease. For the rest of this chapter we'll focus on `read_csv()`. Not only are csv files one of the most common forms of data storage, but once you understand `read_csv()`, you can easily apply your knowledge to all the other functions in readr.

The first argument to `read_csv()` is the most important: it's the path to the file to read.

Hide

```
heights <- read_csv("heights.csv")
```

When you run `read_csv()` it prints out a column specification that gives the name and type of each column.

Compared to base R

If you've used R before, you might wonder why we're not using `read.csv()`. There are a few good reasons to favour readr functions over the base equivalents:

- They are typically much faster (~10x) than their base equivalents. Long running jobs have a progress bar, so you can see what's happening. If you're looking for raw speed, try `data.table::fread()`. It doesn't fit quite so well into the tidyverse, but it can be quite a bit faster.
- They produce tibbles, they don't convert character vectors to factors, use row names, or munge the column names. These are common sources of frustration with the base R functions.
- They are more reproducible. Base R functions inherit some behaviour from your operating system and environment variables, so import code that works on your computer might not work on someone else's.

Writing to a file

readr also comes with two useful functions for writing data back to disk: `write_csv()` and `write_tsv()`. Both functions increase the chances of the output file being read back in correctly by:

- Always encoding strings in UTF-8.
- Saving dates and date-times in ISO8601 format so they are easily parsed elsewhere.

If you want to export a csv file to Excel, use `write_excel_csv()` — this writes a special character (a "byte order mark") at the start of the file which tells Excel that you're using the UTF-8 encoding.

The most important arguments are `x` (the data frame to save), and `path` (the location to save it). You can also specify how missing values are written with `na`, and if you want to `append` to an existing file.

Hide

```
write_csv(heights, "heights1.csv")
```

Other types of data

To get other types of data into R, we recommend starting with the tidyverse packages listed below. They're certainly not perfect, but they are a good place to start. For rectangular data:

- **haven** reads SPSS, Stata, and SAS files.
- **readxl** reads excel files (both `.xls` and `.xlsx`).
- **DBI**, along with a database specific backend (e.g. **RMySQL**, **RSQLite**, **RPostgreSQL** etc) allows you to run SQL queries against a database and return a data frame.

For hierarchical data: use **jsonlite** (by Jeroen Ooms) for json, and **xml2** for XML. Jenny Bryan has some excellent worked examples at https://jennybc.github.io/purrr-tutorial/examples.html (https://jennybc.github.io/purrr-tutorial/examples.html).

For other file types, try the R data import/export manual (https://cran.r-project.org/doc/manuals/r-release/R-data.html) and the **rio** (https://github.com/leeper/rio) package.

7. Tidy data

Introduction

In this chapter, you will learn a consistent way to organise your data in R, an organisation called **tidy data**. Getting your data into this format requires some upfront work, but that work pays off in the long term. Once you have tidy data and the tidy tools provided by packages in the tidyverse, you will spend much less time munging data from one representation to another, allowing you to spend more time on the analytic questions at hand.

This chapter will give you a practical introduction to tidy data and the accompanying tools in the **tidyr** package. If you'd like to learn more about the underlying theory, you might enjoy the *Tidy Data* paper published in the Journal of Statistical Software, http://www.jstatsoft.org/v59/i10/paper (http://www.jstatsoft.org/v59/i10/paper).

Prerequisites

In this chapter we'll focus on tidyr, a package that provides a bunch of tools to help tidy up your messy datasets. tidyr is a member of the core tidyverse.

Tidy data

You can represent the same underlying data in multiple ways. The example below shows the same data organised in four different ways. Each dataset shows the same values of four variables *country*, *year*, *population*, and *cases*, but each dataset organises the values in a different way.

Hide

```
table1
table2
table3

# Spread across two tibbles
table4a  # cases
table4b  # population
```

These are all representations of the same underlying data, but they are not equally easy to use. One dataset, the tidy dataset, will be much easier to work with inside the tidyverse.

There are three interrelated rules which make a dataset tidy:

1. Each variable must have its own column.
2. Each observation must have its own row.
3. Each value must have its own cell.

These three rules are interrelated because it's impossible to only satisfy two of the three. That interrelationship leads to an even simpler set of practical instructions:

1. Put each dataset in a tibble.
2. Put each variable in a column.

In this example, only `table1` is tidy. It's the only representation where each column is a variable.

Why ensure that your data is tidy? There are two main advantages:

1. There's a general advantage to picking one consistent way of storing data. If you have a consistent data structure, it's easier to learn the tools that work with it because they have an underlying uniformity.

2. There's a specific advantage to placing variables in columns because it allows R's vectorised nature to shine. As you learned in mutate and summary functions, most built-in R functions work with vectors of values. That makes transforming tidy data feel particularly natural.

dplyr, ggplot2, and all the other packages in the tidyverse are designed to work with tidy data. Here are a couple of small examples showing how you might work with `table1`.

Hide

```
# Compute rate per 10,000
table1 %>%
  mutate(rate = cases / population * 10000)

# Compute cases per year
table1 %>%
  count(year, wt = cases)

# Visualise changes over time
library(ggplot2)
ggplot(table1, aes(year, cases)) +
  geom_line(aes(group = country), colour = "grey50") +
  geom_point(aes(colour = country))
```

Spreading and gathering

The principles of tidy data seem so obvious that you might wonder if you'll ever encounter a dataset that isn't tidy. Unfortunately, however, most data that you will encounter will be untidy. There are two main reasons:

1. Most people aren't familiar with the principles of tidy data, and it's hard to derive them yourself unless you spend a *lot* of time working with data.
2. Data is often organised to facilitate some use other than analysis. For example, data is often organised to make entry as easy as possible.

This means for most real analyses, you'll need to do some tidying. The first step is always to figure out what the variables and observations are. Sometimes this is easy; other times you'll need to consult with the people who originally generated the data. The second step is to resolve one of two common problems:

1. One variable might be spread across multiple columns.
2. One observation might be scattered across multiple rows.

Typically a dataset will only suffer from one of these problems; it'll only suffer from both if you're really unlucky! To fix these problems, you'll need the two most important functions in tidyr: `gather()` and `spread()`.

Gathering

A common problem is a dataset where some of the column names are not names of variables, but *values* of a variable. Take `table4a`: the column names `1999` and `2000` represent values of the `year` variable, and each row represents two observations, not one.

Hide

```
table4a
```

To tidy a dataset like this, we need to **gather** those columns into a new pair of variables. To describe that operation we need three parameters:

- The set of columns that represent values, not variables. In this example, those are the columns `1999` and `2000`.
- The name of the variable whose values form the column names. I call that the `key`, and here it is `year`.
- The name of the variable whose values are spread over the cells. I call that `value`, and here it's the number of `cases`.

Together those parameters generate the call to `gather()`:

Hide

```
table4a %>%
  gather(`1999`, `2000`, key = "year", value = "cases")
```

The columns to gather are specified with `dplyr::select()` style notation. Here there are only two columns, so we list them individually. Note that "1999" and "2000" are non-syntactic names so we have to surround them in backticks. To refresh your memory of the other ways to select columns, see select.

In the final result, the gathered columns are dropped, and we get new `key` and `value` columns. Otherwise, the relationships between the original variables are preserved. Visually, this is shown in Figure @ref(fig:tidy-gather). We can use `gather()` to tidy `table4b` in a similar fashion. The only difference is the variable stored in the cell values:

Hide

```
table4b %>%
  gather(`1999`, `2000`, key = "year", value = "population")
```

To combine the tidied versions of `table4a` and `table4b` into a single tibble, we need to use `dplyr::left_join()`, which you'll learn about in [relational data].

Hide

```
tidy4a <- table4a %>%
  gather(`1999`, `2000`, key = "year", value = "cases")
tidy4b <- table4b %>%
  gather(`1999`, `2000`, key = "year", value = "population")
left_join(tidy4a, tidy4b)
```

Spreading

Spreading is the opposite of gathering. You use it when an observation is scattered across multiple rows. For example, take `table2`: an observation is a country in a year, but each observation is spread across two rows.

Hide

```
table2
```

To tidy this up, we first analyse the representation in similar way to `gather()`. This time, however, we only need two parameters:

- The column that contains variable names, the `key` column. Here, it's `type`.
- The column that contains values forms multiple variables, the `value` column. Here it's `count`.

Once we've figured that out, we can use `spread()`, as shown programmatically below, and visually in Figure @ref(fig:tidy-spread).

Hide

```
spread(table2, key = type, value = count)
```

As you might have guessed from the common `key` and `value` arguments, `spread()` and `gather()` are complements. `gather()` makes wide tables narrower and longer; `spread()` makes long tables shorter and wider.

Separating and uniting

So far you've learned how to tidy `table2` and `table4`, but not `table3`. `table3` has a different problem: we have one column (`rate`) that contains two variables (`cases` and `population`). To fix this problem, we'll need the `separate()` function. You'll also learn about the complement of `separate()`: `unite()`, which you use if a single variable is spread across multiple columns.

Separate

`separate()` pulls apart one column into multiple columns, by splitting wherever a separator character appears. Take `table3`:

Hide

```
table3
```

The `rate` column contains both `cases` and `population` variables, and we need to split it into two variables. `separate()` takes the name of the column to separate, and the names of the columns to separate into, as shown in Figure @ref(fig:tidy-separate) and the code below.

Hide

```
table3 %>%
  separate(rate, into = c("cases", "population"))
```

By default, `separate()` will split values wherever it sees a non-alphanumeric character (i.e. a character that isn't a number or letter). For example, in the code above, `separate()` split the values of `rate` at the forward slash characters. If you wish to use a specific character to separate a column, you can pass the character to the `sep` argument of `separate()`. For example, we could rewrite the code above as:

Hide

```
table3 %>%
  separate(rate, into = c("cases", "population"), sep = "/")
```

Look carefully at the column types: you'll notice that `case` and `population` are character columns. This is the default behaviour in `separate()`: it leaves the type of the column as is. Here, however, it's not very useful as those really are numbers. We can ask `separate()` to try and convert to better types using `convert = TRUE`:

Hide

```
table3 %>%
  separate(rate, into = c("cases", "population"), convert = TRUE)
```

You can also pass a vector of integers to `sep`. `separate()` will interpret the integers as positions to split at. Positive values start at 1 on the far-left of the strings; negative value start at -1 on the far-right of the strings. When using integers to separate strings, the length of `sep` should be one less than the number of names in `into`.

You can use this arrangement to separate the last two digits of each year. This make this data less tidy, but is useful in other cases, as you'll see in a little bit.

Hide

```
table3 %>%
  separate(year, into = c("century", "year"), sep = 2)
```

Unite

`unite()` is the inverse of `separate()`: it combines multiple columns into a single column. You'll need it much less frequently than `separate()`, but it's still a useful tool to have in your back pocket.

We can use `unite()` to rejoin the *century* and *year* columns that we created in the last example. That data is saved as `tidyr::table5`. `unite()` takes a data frame, the name of the new variable to create, and a set of columns to combine, again specified in `dplyr::select()` style:

Hide

```
table5 %>%
  unite(new, century, year)
```

In this case we also need to use the `sep` argument. The default will place an underscore (_) between the values from different columns. Here we don't want any separator so we use `""` :

Hide

```
table5 %>%
  unite(new, century, year, sep = "")
```

Missing values

Changing the representation of a dataset brings up an important subtlety of missing values. Surprisingly, a value can be missing in one of two possible ways:

- **Explicitly**, i.e. flagged with `NA` .
- **Implicitly**, i.e. simply not present in the data.

Let's illustrate this idea with a very simple data set:

Hide

```
stocks <- tibble(
  year   = c(2015, 2015, 2015, 2015, 2016, 2016, 2016),
  qtr    = c(   1,    2,    3,    4,    2,    3,    4),
  return = c(1.88, 0.59, 0.35,   NA, 0.92, 0.17, 2.66)
)
```

There are two missing values in this dataset:

- The return for the fourth quarter of 2015 is explicitly missing, because the cell where its value should be instead contains `NA` .
- The return for the first quarter of 2016 is implicitly missing, because it simply does not appear in the dataset.

One way to think about the difference is with this Zen-like koan: An explicit missing value is the presence of an absence; an implicit missing value is the absence of a presence.

The way that a dataset is represented can make implicit values explicit. For example, we can make the implicit missing value explicit by putting years in the columns:

Hide

```
stocks %>%
  spread(year, return)
```

Because these explicit missing values may not be important in other representations of the data, you can set `na.rm = TRUE` in `gather()` to turn explicit missing values implicit:

Hide

```
stocks %>%
  spread(year, return) %>%
  gather(year, return, `2015`:`2016`, na.rm = TRUE)
```

Another important tool for making missing values explicit in tidy data is `complete()` :

Hide

```
stocks %>%
  complete(year, qtr)
```

`complete()` takes a set of columns, and finds all unique combinations. It then ensures the original dataset contains all those values, filling in explicit `NA` s where necessary.

8. Data visualisation

Introduction

This chapter will teach you how to visualise your data using ggplot2. R has several systems for making graphs, but ggplot2 is one of the most elegant and most versatile. ggplot2 implements the **grammar of graphics**, a coherent system for describing and building graphs. With ggplot2, you can do more faster by learning one system and applying it in many places.

If you'd like to learn more about the theoretical underpinnings of ggplot2 before you start, I'd recommend reading "The Layered Grammar of Graphics", http://vita.had.co.nz/papers/layered-grammar.pdf (http://vita.had.co.nz/papers/layered-grammar.pdf).

The `mpg` data frame

You can test your answer with the `mpg` **data frame** found in ggplot2 (aka `ggplot2::mpg`). A data frame is a rectangular collection of variables (in the columns) and observations (in the rows). `mpg` contains observations collected by the US Environment Protection Agency on 38 models of cars.

Hide

```
mpg
```

Among the variables in `mpg` are:

1. `displ` , a car's engine size, in litres.
2. `hwy` , a car's fuel efficiency on the highway, in miles per gallon (mpg). A car with a low fuel efficiency consumes more fuel than a car with a high fuel efficiency when they travel the same distance.

To learn more about `mpg` , open its help page by running `?mpg` .

Creating a ggplot

To plot `mpg` , run this code to put `displ` on the x-axis and `hwy` on the y-axis:

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy))
```

The plot shows a negative relationship between engine size (`displ`) and fuel efficiency (`hwy`). In other words, cars with big engines use more fuel. Does this confirm or refute your hypothesis about fuel efficiency and engine size?

With ggplot2, you begin a plot with the function `ggplot()` . `ggplot()` creates a coordinate system that you can add layers to. The first argument of `ggplot()` is the dataset to use in the graph. So `ggplot(data = mpg)` creates an empty graph, but it's not very interesting so I'm not going to show it here.

You complete your graph by adding one or more layers to `ggplot()` . The function `geom_point()` adds a layer of points to your plot, which creates a scatterplot. ggplot2 comes with many geom functions that each add a different type of layer to a plot. You'll learn a whole bunch of them throughout this chapter.

Each geom function in ggplot2 takes a `mapping` argument. This defines how variables in your dataset are mapped to visual properties. The `mapping` argument is always paired with `aes()` , and the `x` and `y` arguments of `aes()` specify which variables to map to the x and y axes. ggplot2 looks for the mapped variable in the `data` argument, in this case, `mpg` .

A graphing template

Let's turn this code into a reusable template for making graphs with ggplot2. To make a graph, replace the bracketed sections in the code below with a dataset, a geom function, or a collection of mappings.

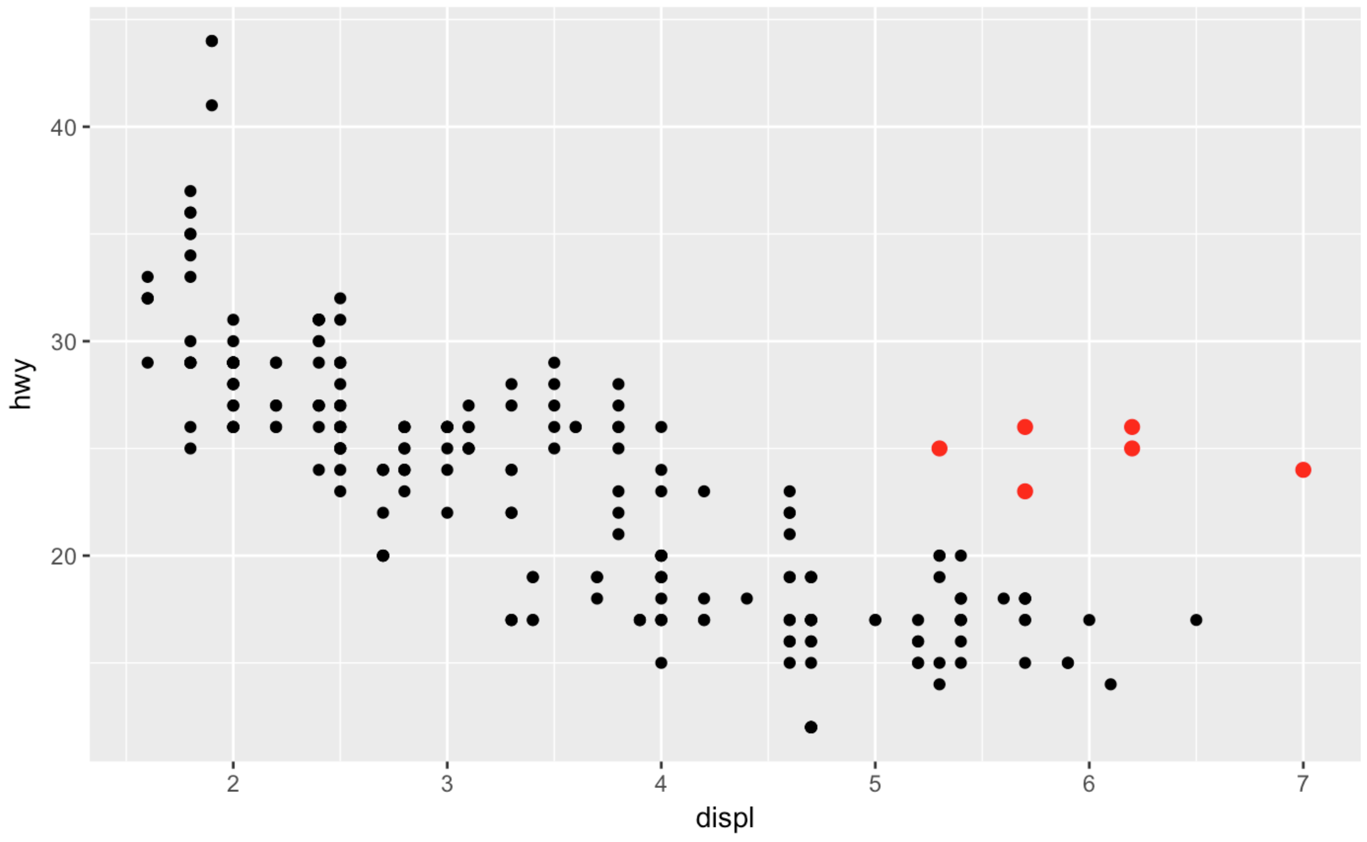
Hide

```
ggplot(data = <DATA>) +
  <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>))
```

The rest of this chapter will show you how to complete and extend this template to make different types of graphs. We will begin with the `<MAPPINGS>` component.

Aesthetic mappings

In the plot below, one group of points (highlighted in red) seems to fall outside of the linear trend. These cars have a higher mileage than you might expect. How can you explain these cars?



Let's hypothesize that the cars are hybrids. One way to test this hypothesis is to look at the `class` value for each car. The `class` variable of the `mpg` dataset classifies cars into groups such as compact, midsize, and SUV. If the outlying points are hybrids, they should be classified as compact cars or, perhaps, subcompact cars (keep in mind that this data was collected before hybrid trucks and SUVs became popular).

You can add a third variable, like `class` , to a two dimensional scatterplot by mapping it to an **aesthetic**. An aesthetic is a visual property of the objects in your plot. Aesthetics include things like the size, the shape, or the color of your points. You can display a point (like the one below) in different ways by changing the values of its aesthetic properties. Since we already use the word "value" to describe data, let's use the word "level" to describe aesthetic properties. Here we change the levels of a point's size, shape, and color to make the point small, triangular, or blue:

You can convey information about your data by mapping the aesthetics in your plot to the variables in your dataset. For example, you can map the colors of your points to the `class` variable to reveal the class of each car.

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy, color = class))
```

To map an aesthetic to a variable, associate the name of the aesthetic to the name of the variable inside `aes()` . ggplot2 will automatically assign a unique level of the aesthetic (here a unique color) to each unique value of the variable, a process known as **scaling**. ggplot2 will also add a legend that explains which levels correspond to which values.

The colors reveal that many of the unusual points are two-seater cars. These cars don't seem like hybrids, and are, in fact, sports cars! Sports cars have large engines like SUVs and pickup trucks, but small bodies like midsize and compact cars, which improves their gas mileage. In hindsight, these cars were unlikely to be hybrids since they have large engines.

In the above example, we mapped `class` to the color aesthetic, but we could have mapped `class` to the size aesthetic in the same way. In this case, the exact size of each point would reveal its class affiliation. We get a *warning* here, because mapping an unordered variable (`class`) to an ordered aesthetic (`size`) is not a good idea.

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy, size = class))
```

Or we could have mapped `class` to the *alpha* aesthetic, which controls the transparency of the points, or the shape of the points.

Hide

```
# Left
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy, alpha = class))

# Right
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy, shape = class))
```

What happened to the SUVs? ggplot2 will only use six shapes at a time. By default, additional groups will go unplotted when you use the shape aesthetic.

For each aesthetic, you use `aes()` to associate the name of the aesthetic with a variable to display. The `aes()` function gathers together each of the aesthetic mappings used by a layer and passes them to the layer's mapping argument. The syntax highlights a useful insight about `x` and `y` : the x and y locations of a point are themselves aesthetics, visual properties that you can map to variables to display information about the data.

Once you map an aesthetic, ggplot2 takes care of the rest. It selects a reasonable scale to use with the aesthetic, and it constructs a legend that explains the mapping between levels and values. For x and y aesthetics, ggplot2 does not create a legend, but it creates an axis line with tick marks and a label. The axis line acts as a legend; it explains the mapping between locations and values.

You can also *set* the aesthetic properties of your geom manually. For example, we can make all of the points in our plot blue:

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy), color = "blue")
```

Here, the color doesn't convey information about a variable, but only changes the appearance of the plot. To set an aesthetic manually, set the aesthetic by name as an argument of your geom function; i.e. it goes *outside* of `aes()` . You'll need to pick a value that makes sense for that aesthetic:

Common problems

As you start to run R code, you're likely to run into problems. Don't worry — it happens to everyone. I have been writing R code for years, and every day I still write code that doesn't work!

Start by carefully comparing the code that you're running to the code in the book. R is extremely picky, and a misplaced character can make all the difference. Make sure that every `(` is matched with a `)` and every `"` is paired with another `"` . Sometimes you'll run the code and nothing happens. Check the left-hand of your console: if it's a `+` , it means that R doesn't think you've typed a complete expression and it's waiting for you to finish it. In this case, it's usually easy to start from scratch again by pressing ESCAPE to abort processing the current command.

One common problem when creating ggplot2 graphics is to put the `+` in the wrong place: it has to come at the end of the line, not the start. In other words, make sure you haven't accidentally written code like this:

Hide

```
ggplot(data = mpg)
+ geom_point(mapping = aes(x = displ, y = hwy))
```

If you're still stuck, try the help. You can get help about any R function by running `?function_name` in the console, or selecting the function name and pressing F1 in RStudio. Don't worry if the help doesn't seem that helpful - instead skip down to the examples and look for code that matches what you're trying to do.

If that doesn't help, carefully read the error message. Sometimes the answer will be buried there! But when you're new to R, the answer might be in the error message but you don't yet know how to understand it. Another great tool is Google: trying googling the error message, as it's likely someone else has had the same problem, and has gotten help online.

Facets

One way to add additional variables is with aesthetics. Another way, particularly useful for categorical variables, is to split your plot into **facets**, subplots that each display one subset of the data.

To facet your plot by a single variable, use `facet_wrap()` . The first argument of `facet_wrap()` should be a formula, which you create with `~` followed by a variable name (here "formula" is the name of a data structure in R, not a synonym for "equation"). The variable that you pass to `facet_wrap()` should be discrete.

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy)) +
  facet_wrap(~ class, nrow = 2)
```

To facet your plot on the combination of two variables, add `facet_grid()` to your plot call. The first argument of `facet_grid()` is also a formula. This time the formula should contain two variable names separated by a `~`.

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy)) +
  facet_grid(drv ~ cyl)
```

If you prefer to not facet in the rows or columns dimension, use a `.` instead of a variable name, e.g. `+ facet_grid(. ~ cyl)`.

Geometric objects

How are these two plots similar?

Both plots contain the same x variable, the same y variable, and both describe the same data. But the plots are not identical. Each plot uses a different visual object to represent the data. In ggplot2 syntax, we say that they use different **geoms**.

A **geom** is the geometrical object that a plot uses to represent data. People often describe plots by the type of geom that the plot uses. For example, bar charts use bar geoms, line charts use line geoms, boxplots use boxplot geoms, and so on. Scatterplots break the trend; they use the point geom. As we see above, you can use different geoms to plot the same data. The plot on the left uses the point geom, and the plot on the right uses the smooth geom, a smooth line fitted to the data.

To change the geom in your plot, change the geom function that you add to `ggplot()`. For instance, to make the plots above, you can use this code:

Hide

```
# left
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy))

# right
ggplot(data = mpg) +
  geom_smooth(mapping = aes(x = displ, y = hwy))
```

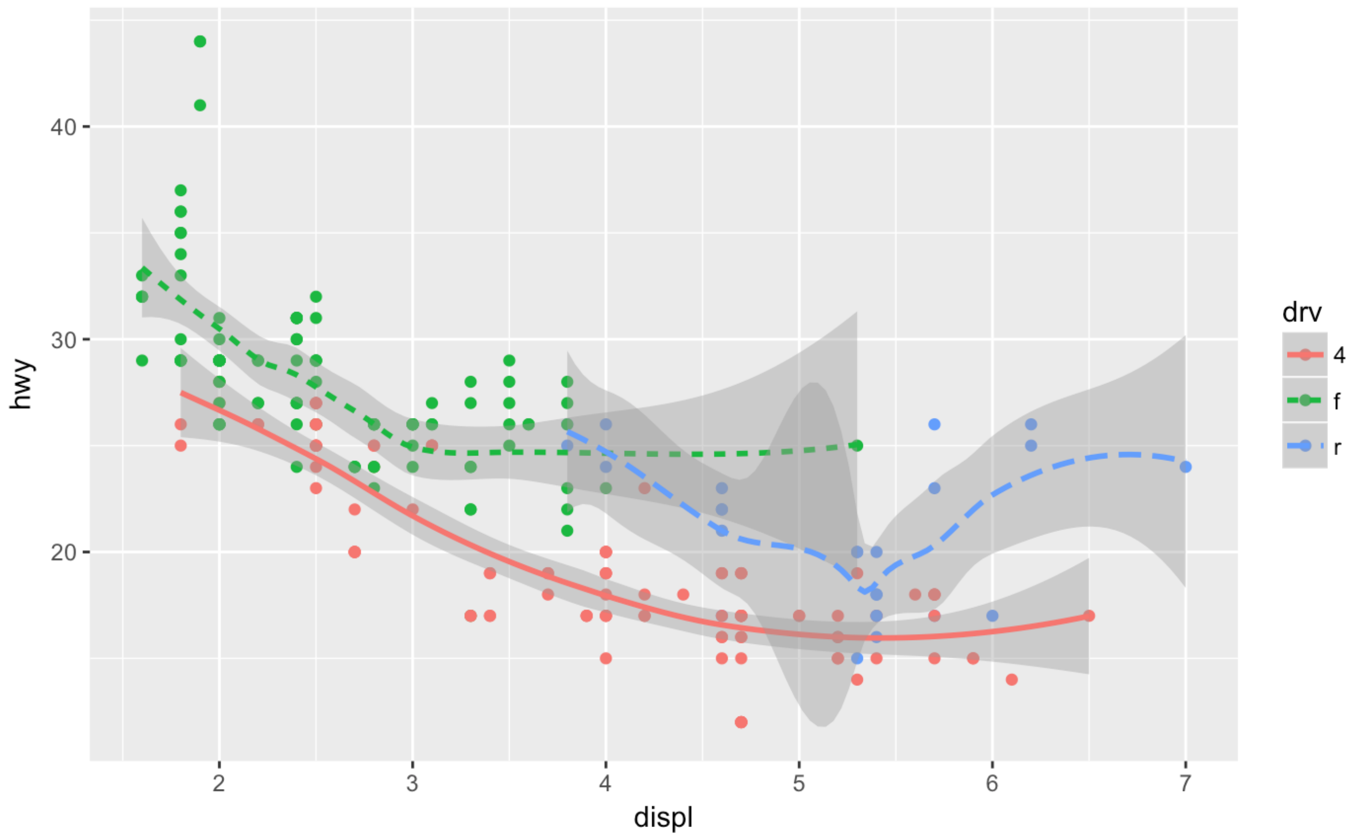
Every geom function in ggplot2 takes a `mapping` argument. However, not every aesthetic works with every geom. You could set the shape of a point, but you couldn't set the "shape" of a line. On the other hand, you *could* set the linetype of a line. `geom_smooth()` will draw a different line, with a different linetype, for each unique value of the variable that you map to linetype.

Hide

```
ggplot(data = mpg) +
  geom_smooth(mapping = aes(x = displ, y = hwy, linetype = drv))
```

Here `geom_smooth()` separates the cars into three lines based on their `drv` value, which describes a car's drivetrain. One line describes all of the points with a `4` value, one line describes all of the points with an `f` value, and one line describes all of the points with an `r` value. Here, `4` stands for four-wheel drive, `f` for front-wheel drive, and `r` for rear-wheel drive.

If this sounds strange, we can make it more clear by overlaying the lines on top of the raw data and then coloring everything according to `drv`.



Notice that this plot contains two geoms in the same graph! If this makes you excited, buckle up. In the next section, we will learn how to place multiple geoms in the same plot.

ggplot2 provides over 30 geoms, and extension packages provide even more (see https://www.ggplot2-exts.org (https://www.ggplot2-exts.org) for a sampling). The best way to get a comprehensive overview is the ggplot2 cheatsheet, which you can find at http://rstudio.com/cheatsheets (http://rstudio.com/cheatsheets). To learn more about any single geom, use help: `?geom_smooth`.

Many geoms, like `geom_smooth()`, use a single geometric object to display multiple rows of data. For these geoms, you can set the `group` aesthetic to a categorical variable to draw multiple objects. ggplot2 will draw a separate object for each unique value of the grouping variable. In practice, ggplot2 will automatically group the data for these geoms whenever you map an aesthetic to a discrete variable (as in the `linetype` example). It is convenient to rely on this feature because the group aesthetic by itself does not add a legend or distinguishing features to the geoms.

To display multiple geoms in the same plot, add multiple geom functions to `ggplot()`:

Hide

```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy)) +
  geom_smooth(mapping = aes(x = displ, y = hwy))
```

This, however, introduces some duplication in our code. Imagine if you wanted to change the y-axis to display `cty` instead of `hwy`. You'd need to change the variable in two places, and you might forget to update one. You can avoid this type of repetition by passing a set of mappings to `ggplot()`. ggplot2 will treat these mappings as global mappings that apply to each geom in the graph. In other words, this code will produce the same plot as the previous code:

Hide

```
ggplot(data = mpg, mapping = aes(x = displ, y = hwy)) +
  geom_point() +
  geom_smooth()
```

If you place mappings in a geom function, ggplot2 will treat them as local mappings for the layer. It will use these mappings to extend or overwrite the global mappings *for that layer only*. This makes it possible to display different aesthetics in different layers.

Hide

```
ggplot(data = mpg, mapping = aes(x = displ, y = hwy)) +
  geom_point(mapping = aes(color = class)) +
  geom_smooth()
```

Exercises

Hide

```
install.packages(c("quantmod","zoo"))
library(quantmod)
library(zoo)

# Get data
getSymbols(c("MSFT", "SBUX", "IBM", "AAPL", "^GSPC", "AMZN"))

# Assign to dataframe
# Get adjusted prices
prices.data <- merge.zoo(MSFT[,6], SBUX[,6], IBM[,6], AAPL[,6], GSPC[,6], AMZN[,6])

prices.tidy <- mutate(as_tibble(prices.data), Date = index(prices.data)) %>%
  select(Date, everything()) %>%
  gather(Ticker, Price, -Date)

ggplot(prices.tidy) +
  geom_line(mapping = aes(x = Date, y = Price, color = Ticker)) +
  theme_bw()

# Calculate returns
returns.data <- diff(log(prices.data))

returns.tidy <- mutate(as_tibble(returns.data), Date = index(returns.data)) %>%
  select(Date, everything()) %>%
  gather(Ticker, Return, -Date)

ggplot(returns.tidy) +
  geom_line(mapping = aes(x = Date, y = Return, color = Ticker)) +
  facet_wrap(~Ticker)
```