Working in the Tidyverse

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Chapter 1

Preface

Hello! This is the manual and workbook for **Working in the Tidyverse**, an HIE Advanced R workshop. The website for the HIE R Course is at <http://www.hiercourse.com>, where you can view and download this manual and its related materials.

Workshop goals

In this workshop, you will:

1. Learn about the Tidyverse, the concept of *tidy data*, and how it can benefit you.
2. Get an overview of the core Tidyverse packages and what their most useful functions do.
3. Reshape, clean, and recode/recalculate a real-world dataset using `dplyr`, `tidyr`, and `janitor`.
4. Make layered and interactive graphs with `ggplot2` and `plotly`.
5. Have a brief introduction to how grouped dataframes can be used to fit multiple models.
6. Learn where to go to find further resources and help.

Assumed knowledge

This workshop is meant for people who have a basic working knowledge of R. You should:

- Know about the most common *atomic types*: `logical`, `integer`, `numeric`/`double`, and `character`.
- Know how to create lists and data frames, and how to access and inspect their elements.
- Know about `names`/`symbols`, which are the identifiers used to refer to objects like variables and functions.
- Know how to install and attach packages, and how to call functions by namespace (e.g. the difference between `stats::filter()` and `dplyr::filter()`).
- Know how to define basic functions (using the `function()` declaration) and how that relates to *anonymous* functions (they're simply functions that are not assigned to a name).

If you would like a quick refresher, RStudio has a great Base R Cheatsheet at <http://bit.ly/base-r-cheatsheet>. For a beginner's R course, we suggest the book 'Data analysis and visualization with R', which is available for download from <http://www.hiercourse.com>.

Conventions in this manual

- When we refer to the technical meaning of R terms, we will typeset it `in monospace text`. For example, `data.frame` refers to a specific object type in R, but data frame refers to the general concept of data stored in a tabular format.
- Function names in text are indicated with brackets, like `mean()` or `median()`.
- Features of RStudio will be typeset in italics. Interactions will be shown as a series of arrow-linked steps. For example, *Help* → *Cheatsheets* means that you can follow the *Help* toolbar item to an entry called *Cheatsheets*.
- Comments from the authors are preceded by `#`. Console output from R is preceded by `##`.

Chapter 2

Setting up the Tidyverse

This chapter will run through the software that you need to install for this workshop, and how to do it.

Software to install

- **R**, downloaded from <https://cran.r-project.org>. This manual was compiled with R version 3.6.0 (2019-04-26).
- **RStudio Open Source Edition**, an IDE for R, downloaded from <https://www.rstudio.com/products/rstudio>.

Installing course material and packages

We provide the course materials via the `usethis` package, so please run this code:

```
install.packages("usethis")

usethis::use_course("http://www.hiercourse.com/docs/hie_tidy.zip")
```

The course materials will download and put themselves on your desktop, by default. You will be asked to acknowledge this new folder, and then the folder will open.

Inside this new `hie_tidy/` folder, double-click the file `working_in_tidyverse.Rproj`. A new instance of RStudio will open with `hie_tidy` set as the project. If you are new to 'projects' in RStudio, see the 'Project-based workflow' section below.

Now open the script called `install_course_packages.R` and 'source' it (run it) by clicking the *Source* button in the top-right of the editor pane. This will install the packages you need for this workshop. A full list of the packages used in this manual can be found in Chapter 15.

Within the *hie_tidy/* folder, there are three other folders you should be aware of.

- `_answers/` contains the answers to exercises as `.rds` files that can be imported with `readr::read_rds()`. This lets you skip exercises if you get stuck.
- `_data/` contains the datasets that we will be using.
  - `_data/incomplete_data` is a fictional dataset with implicit zero values.

  - `_data/light_trap/` is 18 years of insect light trapping conducted on the roof of the Zoological Museum in the University of Copenhagen.
  - `_data/mongolia_livestock/` is the number of livestock (camels, cattle, goats, horses, sheep) recorded in Mongolia over 47 years.
  - `_data/wood_blocks/` is an experiment where blocks of wood were left in the field for a year, and then collected afterwards to assess how they decayed.

- `_output/` is an empty folder for writing your results and other output to.

Workflow suggestions

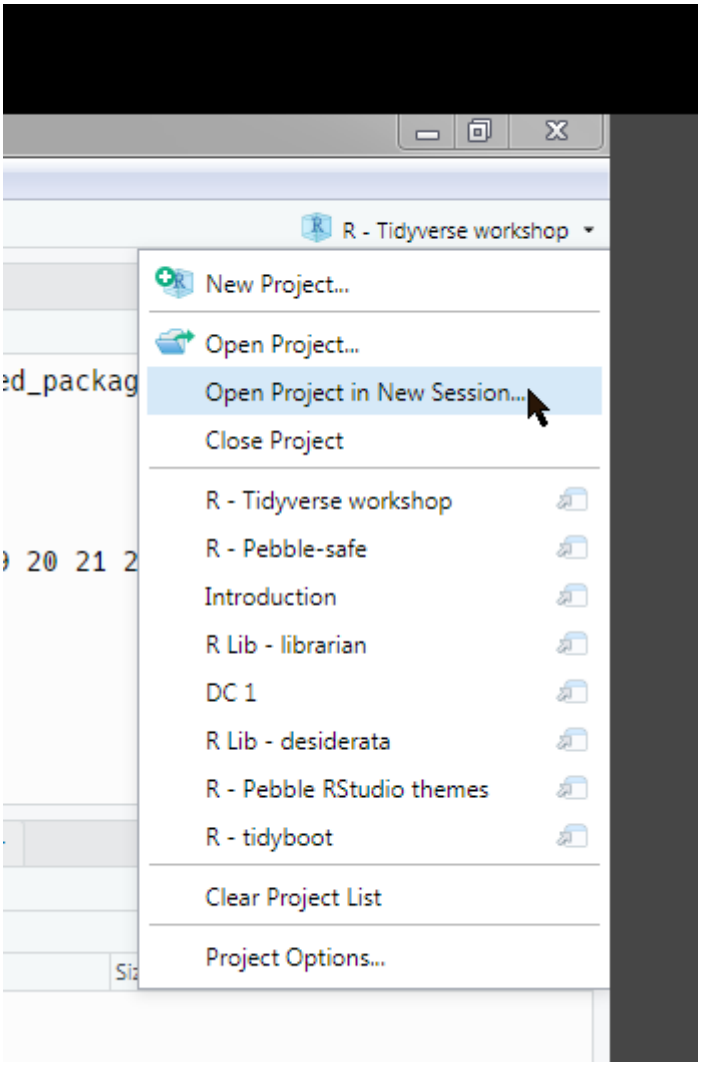
While these workflows are not mandatory for the Tidyverse, they are *strongly recommended* as best-practices that will save you some headaches and help you write more reliable, reproducible code. They are a **project-based workflow** and literate programming via **Rmarkdown**.

Project-based workflow

In the next chapter, we will use the `usethis` package to download the course materials. These course materials are packaged in an *RStudio Project*, which is simply a folder with a special `.RProj` file inside it. Working inside projects has several advantages:

1. **Projects set the working directory for you.** You do not set a path to your working directory using `setwd("Path/that/only/my/computer/has")`. The working directory for the project is automatically set to the folder that has the `.RProj` file.
2. **Projects (with the `here` package) let you organise files as you like.** Even if your script is in a subfolder, you can always access your root folder with `here()`. Even if you reorganise and move your scripts around, they will just work without you having to edit the paths to fix them.
3. **Remove side-effects from unrelated scripts.** Loading a new project clears the environment so that objects in memory are not carried between sessions.
4. **Projects give you version control.** Version control through Git or SVN is integrated into RStudio via projects.

You can open and create projects by clicking the drop-down in the top right of the RStudio window.



You can have multiple projects open in multiple RStudio windows by choosing *Open Project in New Session*, or clicking the "arrow window" icon to the right of the listed project names.

Literate programming via Rmarkdown

Rmarkdown lets you work in a style called *literate programming*, mixing formatted text and code together in the same document so that you can record your decisions and process as you go. You can also pull data from your analysis and put it into your text, like reporting the R^2 of a model without having to replace that number every time you tweak the model.

Rmarkdown lets you create a single document that includes your text, code, tables, and plots, and then you can share this document with your collaborators or revisit it later. Rmarkdown documents can be 'knitted' to many different file formats including HTML, PDF, DOCX (Word), even Beamer or Powerpoint slides. This manual was written entirely with Rmarkdown too.

In the workshop, we will demonstrate using *R Notebooks*. This is a kind of Rmarkdown document that saves its output to a self-contained HTML file (the images and graphs are encoded into the file as text). R Notebooks are a convenient kind of Rmarkdown document because the HTML output is automatically built every time you save the source file, unlike other Rmarkdown variants that need to be 'knitted' explicitly to build their output. Another advantage of R Notebooks is that HTML files are interactive — which means that if you have an interactive graph (we'll get to it in Chapter 5), the reader can interact with it.

We provide a short example of an R Notebook below (with the code that generated it following after), and you can read the Rmarkdown cheatsheet at <https://www.rstudio.com/resources/cheatsheets/#rmarkdown> for more information.

An example of a small Rmarkdown document

Aim

I will summarise the `iris` dataset that is built into *R*.

```
output <-
    iris %>%
    select(-ends_with("Width")) %>%  # Note - for removing these columns.
    group_by(Species) %>%
    summarise_if(is.numeric, list(~mean(.), ~median(.)))
```

Now I would like to format the table nicely instead of just printing it as console output.

NOTE: The `kable()` function is from the package `knitr`, it does basic conversion of data frames to neatly-formatted tables. There are many other options out there, but `kable` is built in.

Table 2.1: Summary of petal and sepal length in the 'iris' dataset.

Iris species	Mean sepal length	Mean petal length	Median sepal length	Median petal length
setosa	5.006	1.462	5.0	1.50
versicolor	5.936	4.260	5.9	4.35
virginica	6.588	5.552	6.5	5.55

````
    ---
    title: "An example R Notebook"
    output: html_notebook
    ---

    # An example of a small R Notebook document

     ```{r setup, warning=FALSE, message=FALSE}
    library(knitr)
    library(dplyr)
    ```

    ## Aim

    I will summarise the `iris` dataset that is built into _R_.

     ```{r summarise_iris}
    output <-
        iris %>%
````
````

```
    select(-ends_with("Width")) %>%  # Note - for removing these columns.
    group_by(Species) %>%
    summarise_if(is.numeric, list(~mean, ~median))
```

Now I would like to format the table nicely instead of just printing it as console output.

NOTE: The `kable()` function is from the package `knitr`, it does basic conversion of data frames to neatly-formatted tables. There are many other options out there, but `kable` is built in.

```{r print_table, echo=FALSE}
kable(output,
      col.names = c("Iris species", "Mean sepal length", "Mean petal length",
                    "Median sepal length", "Median petal length"),
      caption = "Summary of petal and sepal length in the 'iris' dataset.")
```

Chapter 3

Tidyverse: What, why, when?

This chapter will introduce the Tidyverse, its concept of *tidy data*, and the advantages of a tidy-centric workflow.

What is the Tidyverse?

"The Tidyverse" is the nickname for a family of packages that have agreed on one way to represent tabular data (they call it "tidy data"; covered in Chapter 7). The functions in these packages accept tidy data frames as input and return tidy data frames as output. Since the input and output are the same type of data, a series of simple functions can be chained one-after-the-other to perform complex tasks.

In this following example, functions from four different Tidyverse packages (`janitor`, `tibble`, `tidyr`, and `dplyr`) are working together in a single "pipeline", where the **output** from each line is passed to the next line where it is used as the **input**. The concept of pipes is explained properly in Chapter 4.

```
library(tibble)
library(tidyr)
library(dplyr)
library(janitor)

mtcars %>%
    janitor::clean_names() %>%                                  # Standardise column names
    tibble::rownames_to_column("model") %>%                     # Put rownames in the table
    tidyr::separate(model,                                      # Split 'model' into 2 cols
                    into = c("manufacturer", "model")) %>%
    dplyr::top_n(5, wt = mpg) %>%                               # Get cars with best mileage
    dplyr::select(manufacturer, model, mpg:disp)                # Keep only some columns
```

```
##   manufacturer   model  mpg cyl disp
## 1         Fiat     128 32.4   4 78.7
## 2        Honda   Civic 30.4   4 75.7
## 3       Toyota Corolla 33.9   4 71.1
## 4         Fiat      X1 27.3   4 79.0
## 5        Lotus  Europa 30.4   4 95.1
```

Table 3.1: Relative run-times of data frame operations performed in Base R versus 'dplyr' (lower is better). Data from <http://datascience.la/dplyr-and-a-very-basic-benchmark/>.

Operation	Base R	dplyr
Filter	2	1
Sort	30-60	20-30
New col	1	1
Aggregate	8-100	4-30
Join	>100	4-15

What are the advantages of Tidyverse over base R?

1. Tidyverse packages are built around a common convention and workflow, so it's easier to understand new packages and slot them into your existing workflow.
2. Many existing data structures can be used as-is with the Tidyverse (e.g. base R's `data.frame`), or transformed to a tidy format. For example, `broom::tidy()` can take many types of statistical output (`lm()`, `glm()`, `t.test()`, and more) and turn it into a tidy data frame.
3. Pipelines make each step of data manipulation and analysis very clear, even to people who are rusty at R.
4. The pipeline interface is a great introduction to functional programming, and you can bring that knowledge with you to other frameworks and languages.
5. `dplyr` is faster than Base R for nearly all data frame operations (Table 3.1).

What are the disadvantages of the Tidyverse?

In general, Tidyverse packages value the clarity and ease-of-use of non-standard interfaces (e.g. referring to a column as `Sepal.Width` instead of having to quote it as `"Sepal.Width"`). While this makes the functions easier to approach, it also makes it a little trickier to write your own functions that work with them.

Regarding `dplyr`, the core data manipulation package, it is faster than base R but slower than other solutions like `data.table`. This is usually not a problem for ecologists even with metabarcoding data; if you need something faster, you will know it very quickly. You can use `data.table` keyed structures with `dplyr` for a speed improvement, or use `data.table` for expensive operations and `dplyr` for everything else, or transition to `data.table` entirely.

Chapter 4

The Pipeline

This chapter will introduce the concept of 'piping' data from one function to the next to create 'pipelines' of functions that incrementally transform your data.

What does the pipe %>% do?

```
library(dplyr)  # dplyr imports the pipe '%>%' from the package 'magrittr'.

# 'warpbreaks' is a built-in dataset gives the number of warp breaks on 9 looms for
# 6 combinations of wool type (A and B) and thread tension (L, M, H).

head(warpbreaks)
```

```
##   breaks wool tension
## 1     26    A       L
## 2     30    A       L
## 3     54    A       L
## 4     25    A       L
## 5     70    A       L
## 6     52    A       L
```

```
warpbreaks %>%
    group_by(wool, tension) %>%
    summarise_at(vars(breaks), list(~mean(.), ~median(.), ~sd(.)))
```

```
## # A tibble: 6 x 5
## # Groups:   wool [2]
##   wool  tension  mean median    sd
##   <fct> <fct>   <dbl>  <dbl> <dbl>
## 1 A     L        44.6     51 18.1
## 2 A     M        24       21  8.66
## 3 A     H        24.6     24 10.3
## 4 B     L        28.2     29  9.86
## 5 B     M        28.8     28  9.43
## 6 B     H        18.8     17  4.89
```

To newcomers, the most striking thing about a Tidyverse workflow is the pipeline. It certainly looks different from base R, but the concept is simple.

> "We should have some ways of coupling programs like garden hose — screw in another segment when it becomes necessary to massage data in another way."
>
> — Doug McIlroy, 1964 <http://doc.cat-v.org/unix/pipes/>

The pipe operator `%>%` means, "Take the output from the thing to my left, and deliver it as input to the thing on my right." When you chain functions together with the pipe, it is called a *pipeline*.

RStudio has a handy keyboard shortcut for inserting the pipe operator: *Ctrl + Shift + M* on Windows/Linux, or *Cmd + Shift + M* on Mac. Rstudio also has a shortcut for the arrow assignment operator (`<-`): *Alt + -* or *Option + -*.

```
library(stringr)

"ATMOSPHERE" %>% str_replace("SPHERE", "SQUARE") %>% str_to_lower() %>% print()
```

```
## [1] "atmosquare"
```

Spacing and linebreaks around the pipes do not matter (except for readability), and the pipes can be used with any function, not just the ones that come with Tidyverse packages. Here are some base R functions:

```
month.abb %>%                # Built-in dataset of month names (Jan, Feb...)
    sample(6) %>%            # Randomly choose 6 months
    tolower() %>%            # Lowercase their names
    paste0(collapse = "|")   # And combine them into one string, separated by '|'
```

```
## [1] "dec|oct|nov|jan|jun|jul"
```

In both examples, the process of what is happening to the initial data is easy to follow and reads nearly like a sequence of steps in a recipe. In base R without pipes, the sequence of functions actually reads in reverse of what is happening:

```
paste0(tolower(sample(month.abb, 6)), collapse = "|")
```

```
## [1] "dec|oct|nov|jan|jun|jul"
```

Using the pipe

The pipe outputs to the first argument by default

In the simplest sense, `%>%` assigns the output of the left-hand side to `.` (hereafter `dot` for readability) and then puts `dot` in the first argument of the left-hand side.

```
. <- c(1, 3, 4, 5, NA)
mean(., na.rm = TRUE)

  # Is doing the same thing as

c(1, 3, 4, 5, NA) %>% mean(., na.rm = TRUE)
```

You don't need to type `dot` for the first argument; it's there implicitly. This manual omits the first `dot` unless it makes the code more understandable, in keeping with the Tidyverse Style Guide.

```
                  #  Implicit dot
                  #        ↓
c(1, 3, 4, 5, NA) %>% mean(na.rm = TRUE)
```

The output can be used more than once on the right-hand side

`dot` can be used multiple times in the right-hand function call:

```
                  #  Here as x-value   And here as plot title
                  #     ↓                 ↓
c(1, 3, 4, 5) %>% plot(., main = paste(., collapse = ", "))
```

You don't need to write the first `dot`, but subsequent uses of `dot` must be written.

```
                 #  Implicit dot    Required dot
                 #     ↓              ↓
c(1, 3, 4, 5) %>% plot(main = paste(., collapse = ", "))
```

Passing `dot` to an argument *other than* the first one

If the first argument of the function isn't the one that accepts data (common with plotting and statistical functions outside the Tidyverse), you will need to put `dot` in manually.

```
iris %>% plot(Sepal.Width ~ Petal.Width)

## Error in text.default(x, y, txt, cex = cex, font = font) :
##   invalid mathematical annotation

  # Because it was trying to run this:

plot(x = iris, y = Sepal.Width ~ Petal.Width)
```

```
                                    # Place the dot
                                    #            ↓
iris %>% plot(Sepal.Width ~ Petal.Width, data = .)
```

Functions from pipelines

Sometimes you may want to write anonymous functions inside a pipeline. You can use the shorthand `{...}` to do it.

```
month.abb %>%
    {.[1:3]}

  # Is identical to

month.abb %>%
    (function(.) {.[1:3]})
```

```
## [1] "Jan" "Feb" "Mar"
```

You can also turn an entire pipeline into a function by passing `dot` as the first value in the pipeline and assigning the whole pipeline to a name (which will be used as the function's name).

```
random_sepal_data <-                              # The name of the new function
    . %>%                                         # Using 'dot' as the start of the pipeline
    select(Species, starts_with("Sepal")) %>%     # Subset columns by name
    sample_n(5) %>%                               # Randomly choose 5 rows
    arrange(desc(Sepal.Length))                   # Sort rows with biggest Sepal.Length first

iris %>%
    random_sepal_data()
```

```
##      Species Sepal.Length Sepal.Width
## 1 versicolor          7.0         3.2
## 2  virginica          6.9         3.1
## 3 versicolor          6.4         2.9
## 4 versicolor          5.8         2.6
## 5 versicolor          4.9         2.4
```

NOTE: Pipeline functions are always unary; they can only accept one argument, and in a pipeline that argument is `dot`. If you want to pass multiple arguments into a pipeline then you will need to declare the function in the usual way with `function()`.

Pipeline-friendly aliases for common actions

You may want to access the contents of `dot` by using `[` or `[[` or `$`. For example, perhaps you have subsetted a data frame, and you want to view the values of one of the columns in a histogram. You can use these functions in their prefix form, but it's not easy to read:

```
iris %>%
    filter(Petal.Length > 2, Petal.Width > 2) %>%
    `[[`("Sepal.Length") %>%
    hist(main = "Histogram of 'Sepal.Length' after subsetting")
```

Instead, `magrittr` (the package where the `%>%` operator comes from) includes aliases for common actions that work well inside a pipeline. The most useful are:

Function name	Performs
`magrittr::extract()`	`[`
`magrittr::extract2()`	`[[`
`magrittr::use_series()`	`$`
`magrittr::is_in()`	`%in%`
`magrittr::set_colnames()`	`colnames<-`
`magrittr::set_rownames()`	`rownames<-`
`magrittr::set_names()`	`names<-`

A full list of these aliases can be found with `?extract` if `magrittr` is already attached to the session, or `help("extract", package = "magrittr")` if it is not.

```
library(magrittr)

# Just like in base R, iris["Sepal.Length"] returns a data.frame with one column.
iris %>%
    head() %>%
    extract("Sepal.Length") %>%
    class()
```

```
## [1] "data.frame"
```

```
# And iris[["Sepal.Length"]] extracts the column as an atomic vector.
iris %>%
    head() %>%
    extract2("Sepal.Length") %>%
    class()
```

```
## [1] "numeric"
```

Functions that mask other functions

When two packages are loaded that both contain functions with identical names, the function in the most-recently loaded package is the one that is referred to by default. This is called **masking**.

Tidyverse packages sometimes mask the functions of other packages, and `magrittr` is one common example. The function name `extract` is used by both `magrittr` and `tidyr`, so the version of `extract` that is used by default is the one from the package that you attached most recently. Here's what happens when I accidentally call the wrong function:

```
  # We will attach `tidyr` AFTER `magrittr` is already loaded:

library(tidyr)

## Attaching package: tidyr
##
## The following object is masked from package:magrittr:
##
##     extract

iris %>%
    head() %>%
    extract("Sepal.Length") %>%  # Calls tidyr::extract, not magrittr::extract.
    class()

## Error in is_character(into) : argument "into" is missing, with no default
```

R warns you about this name masking, so pay attention to it if your code mysteriously stops working after you've attached a new package. Other very common name conflicts are between `dplyr::select()` and `MASS::select()`, and `lubridate::here()` and `here::here()`. You can resolve name conflicts in two ways:

1. Load the packages in a different order so that the one you prefer is attached more recently.
2. Preferably, namespace the function with `magrittr::extract()` to be sure you are getting the right one.

Debugging a pipeline

Pipelines can be debugged by looking at their stepwise progress or interrupting their execution. These debugging solutions are presented in the order of most useful/efficient to least useful.

Use the `ViewPipeSteps` RStudio addin

The simplest way to debug a pipeline is to look at what is happening to your data at each step, for which we have the `ViewPipeSteps` addin for RStudio by David Ranzolin <https://github.com/daranzolin/ViewPipeSteps>.

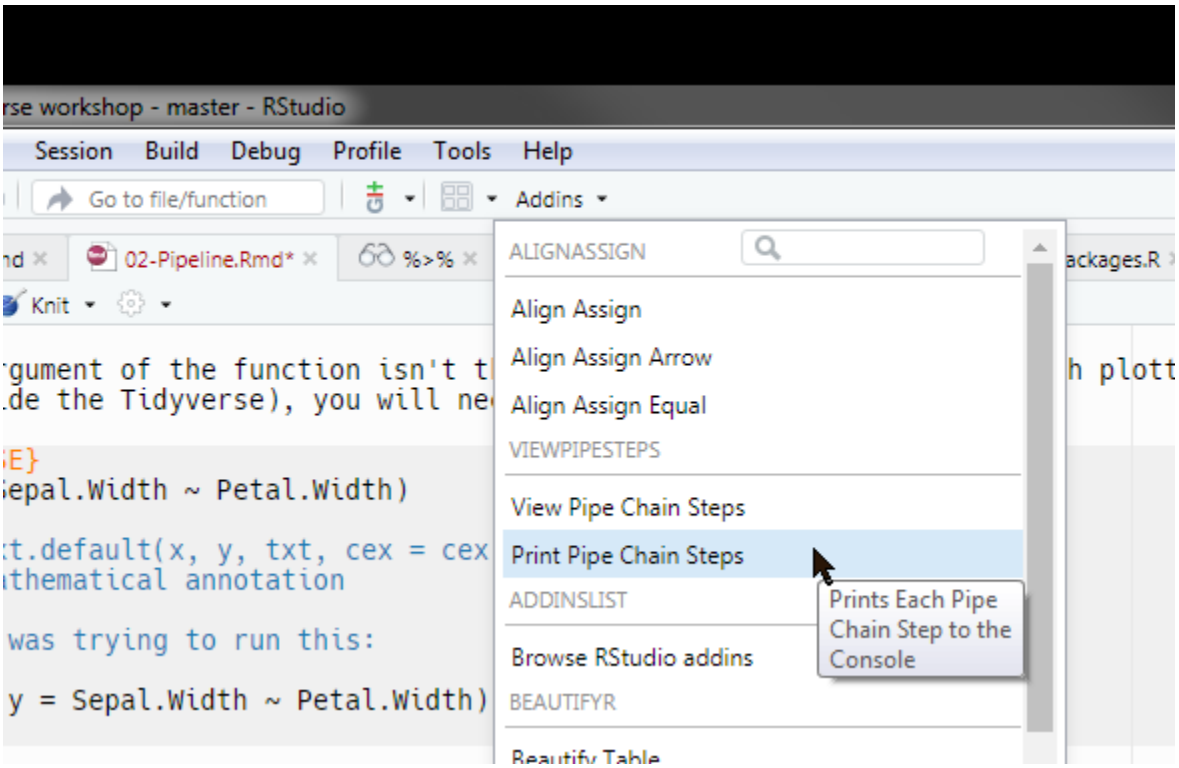
If you used the package installation script in Chapter 2 then this should already be installed, but if you want to install it yourself, you do it like any other GitHub package:

```
install.packages("remotes")

remotes::install_github("daranzolin/ViewPipeSteps")

# And then restart RStudio
```

To use the addin, highlight a pipeline and choose one of the *ViewPipeSteps* options in the *Addins* drop-down, underneath *Help* on the top toolbar.




```
month.abb %>%  # Built-in abbreviations of month names (Jan, Feb...)
    sample(6) %>%
    tolower() %>%
    paste0(collapse = "|")
```

```
# After highlighting the pipeline above and clicking Addins → Print Pipe Chain Steps

## 1. month.abb
##  [1] "Jan" "Feb" "Mar" "Apr" "May" "Jun" "Jul" "Aug" "Sep" "Oct" "Nov" "Dec"
##
## 2. sample(6)
## [1] "Aug" "Nov" "Jul" "Dec" "Jan" "Oct"
##
## 3. tolower()
## [1] "aug" "nov" "jul" "dec" "jan" "oct"
##
## 4. paste0(collapse = "|")
## [1] "aug|nov|jul|dec|jan|oct"
```

Comment out pipelines with `identity()`

You can't comment out the last entry in a pipeline because it leaves the last `%>%` with nothing to pipe into, which is a shame because the last entry in the pipeline is often the one you want to get rid of!

```
month.abb %>%
    sample(6) %>%
    tolower() %>%  # A hanging pipe
    # paste0(collapse = "|")

## Error: attempt to use zero-length variable name
```

You can end your in-development pipelines with `identity()` to stop this from ever happening. `identity()` just returns what it was passed (`function(x) {x}`).

```
month.abb %>%
    sample(6) %>%
    tolower() %>%
    # paste0(collapse = "|") %>%
    identity()
```

```
## [1] "aug" "feb" "jun" "oct" "jul" "sep"
```

Manual inspection by interrupting the pipeline

Finally, you can manually inspect the state of a pipeline by interrupting it with a function like `View()` or `print()` or `dplyr::glimpse()` and then executing from the start of the chain.

```
month.abb %>%
    sample(6) %>% print()
    tolower() %>%
    paste0(collapse = "|")

# The pipeline stops at print()

## [1] "Nov" "Jan" "Apr" "Jul" "Jun" "Oct"
```

We discourage this debugging method because it is easy to forget to remove your change, thus creating an error that makes the rest of your code behave unpredictably:

```
month.abb %>%
    sample(6) %>% print()
    tolower() %>%
    paste0(collapse = "|")

## [1] "Nov" "Jan" "Apr" "Jul" "Jun" "Oct"

## Error in tolower() : argument "x" is missing, with no default
```

Chapter 5

What do all these packages do?

Analysis tasks in the Tidyverse are split across many domain-specific packages. This chapter will help you understand what each package does, and where you might start looking if you have a task that you want to accomplish.

This page lists only the most frequently-used functions, but the packages themselves contain many more. You should always read the function list for a package so that you know what it can do. You can access the function list for `dplyr`, for example, with `help(package = "dplyr")`.

Importing data

`tibble`

A modern replacement for R's data frames. It never converts strings to factors, never renames columns, is more intelligent about printing its contents, and subsetting a tibble always returns a tibble (in base R, accessing one column returned a vector).

- Inspecting data frames: `glimpse()`
- Building data frames: `tibble()` and `tribble()` (rowwise tibble)
- Coercing to a data frame: `as_tibble()` and `enframe()`
- Working with row names: `rownames_to_column()` and `column_to_rownames()`

`readr`

Read and write delimited text files such as CSV and TSV. Also reads and writes RDS, which is a serialised R object. If you want to save a dataset and load it up later, RDS will preserve the meta-data and state of that object too, like its groupings and data types.

- Reading into a data frame: `read_csv()` and `read_tsv()`
- Reading European-format data (`;` for field separator and `,` for decimal place): `read_csv2()` and `read_tsv2()`
- Reading and writing RDS: `read_rds()` and `write_rds()`
- Writing to a spreadsheet: `write_csv()`, `write_tsv()`, `write_csv2()`, `write_tsv2()`
- Converting data types: `parse_number()`, `parse_logical()`, `parse_factor()`, and others.

readxl

Read proprietary Excel files, including different sheets in the same workbook. You cannot write to the proprietary Excel format, use `readr::write_csv()` instead.

- `read_excel()` to auto-detect the file extension, otherwise `read_xls()` or `read_xlsx()`

haven

Read and write SPSS, Stata, and SASS files.

- Reading: `read_spss()`, `read_stata()`, `read_sas()`
- Writing: `write_spss()`, `write_stata()`, `write_sas()`

readtext

Read the contents of entire text files into a dataframe, one row per document. This is useful for things like language analysis or data harvesting.

- It has only one function: `readtext()`

Manipulating data frames

janitor

Convenience functions for cleaning data frames and reporting on their contents.

- Fix bad column names: `clean_names()`
- Fix Excel dates (e.g. *42370* to *2016-01-01*): `excel_numeric_to_date()`
- Remove rows/columns with only `NA` values: `remove_empty()`
- Add row/column totals to a data frame: `adorn_totals()`

tidyr

Get imported data into the 'tidy data' shape.

- Reshape from wide to long and vice versa: `gather()`, `spread()`
- Split the contents of one column into several columns: `separate()` or `extract()`
- Split the contents of one column into several rows: `separate_rows()`
- Combine the contents of several columns into one column: `unite()`
- Fill `NA`s with adjacent values: `fill()`
- Replace `NA`s: `replace_na()`
- Complete a table with missing variable combinations: `complete()`, `full_seq()`
- Duplicate a row `n` times: `uncount()`

dplyr

Once the data frame is tidied, `dplyr` can be used to subset, calculate, and manipulate it.

- Choose, omit, or rearrange columns: `select()`
- Subset a data frame: `filter()`
- Sort rows by value: `arrange()`, `desc()`
- Perform calculations within groups: `group_by()`, `rowwise()`, `ungroup()`
- Summarise by group: `summarise()`
- Create or re-calculate columns: `mutate()`, `recode()`
- Add a column for group counts/sums: `add_count()`, `add_tally()`
- Make a new data frame with group counts/sums: `count()`, `tally()`
- Keep unique rows: `distinct()`
- Keep top (or bottom) rows in a group: `top_n()`
- Randomly choose rows: `sample()`, `sample_n()`, `sample_frac()`
- Join data frames with matching values: `left_join()`, `inner_join()`, `full_join()`
- Filter a data frame with the contents of another: `semi_join()`, `anti_join()`
- Row-bind or column-bind: `bind_rows()`, `bind_cols()`
- Get values from the next/previous row: `lag()`, `lead()`
- Decision-making: `if_else()`, `case_when()`
- Replace `NA` with first non-`NA` value: `coalesce()`
- The basic verbs `arrange()`, `distinct()`, `filter()`, `group_by()`, and `select()` also have 'scoped' variants. For example:
  - Choose all columns: `select_all()`
  - Choose specific columns: `select_at()`
  - Choose columns by condition (e.g. all numeric columns): `select_if()`

Modifying vectors

These packages are most often used inside `dplyr::mutate()` and `dplyr::summarise()`.

stringr

Consistent functions for working with strings.

- Does a string match a search query? `str_detect()`
- Get regular expression matches (with separate capture groups): `str_match_all()`
- Delete text from a string: `str_remove_all()`
- Replace text in a string: `str_replace_all()`
- Get a substring by position: `str_sub()`

forcats

Functions for working with factors.

- Drop unused levels: `fct_drop()`
- Combine rare or abundant levels together as 'other': `fct_lump()`, `fct_other()`
- Reorder levels: `fct_reorder()`
- Reverse factor order (useful for plotting): `fct_rev()`
- Anonymise levels (randomly reorder and replace names with numbers): `fct_anon()`

lubridate

Parse strings into dates, times, and intervals. Extract components from them and do maths with them.

- Parse a string as a date-time object: `dmy()`, `dmy_hms()`, `mdy_h()`, `ymd_hms()` ...
- Get components of a date-time object: `year()`, `month()`, `week()`, `day()`, `hour()`, `minute()`, `second()`
- Convert date to international standard week number: `isoweek()`, `epiweek()`

Iterating and functional programming

purrr

`purrr` provides sensible replacements for base R's `apply` family of functions. The interfaces of `purrr` are easier to remember and behave more predictably.

I will only list the basic functions, but nearly all of them have typed versions as well. For example `flatten()` will return a list, but `flatten_chr()` will return a Character vector and `flatten_dfc()` will column-bind its inputs and return it as a data frame.

- Remove one nesting layer from a list of lists: `flatten()`
- Apply a function to every element of a vector: `map()`
- Apply a function to parallel elements from multiple vectors: `map2()`, `pmap()`
- Apply a list of functions to a each element in a vector: `invoke_map()`
- Join lists: `append()`, `prepend()`, `splice()`
- Drop empty (`NULL` or length 0) entries in a vector: `compact()`

magrittr

Used to create pipelines of functions, as you know! `magrittr` comes with some prefix functions that perform the same jobs as infix functions, but are easier to read. For example, `extract2()` replaces `[[`. It also has some specialised pipes which, to avoid confusing the new learner, we will leave to you to investigate later. This manual will only use the most basic pipe, `%>%`.

- Alias for `[`: `extract()` (note that there is also an `extract()` in `tidyr`!)
- Alias for `[[`: `extract2()`
- Alias for `$`: `use_series()`
- Alias for `%in%`: `is_in()`
- Alias for `colnames <-`: `set_colnames()`
- Alias for `rownames <-`: `set_rownames()`
- Alias for `names <-`: `set_names()`

assertr

Check that a dataframe meets some assumptions about its quality. For example, does it have the same number of rows after a manipulation as it did before? Does a column have less than 5 % NA values? Does a factor have the expected number of levels?

- Check a condition and halt if it returns FALSE: verify()
- Check a condition for several columns and halt if it returns FALSE: assert()

Graphing

ggplot2

Build plots by layering their individual components: A dataset, a coordinate system, and marks on that coordinate system that represent the datapoints. There is too much to cover in a small note like this, so ggplot2 has its own chapter, in Chapter 13.

plotly

Create interactive graphs that can be viewed on the web. You can zoom, rotate, and hover over data points to see the information they represent. Most importantly, lets you convert ggplot2 objects into interactive graphs.

- Make a ggplot2 graph interactive: ggplotly()

Statistical modelling

broom and broom.mixed

Extract information from statistical model output into a tidy dataframe.

- Add model information to a data frame (predicted values, residuals, and so on): augment()
- Get model summary (r^2, p-values, and so on): glance()
- Get components of a model (intercepts, SE, F stat, and so on): tidy()

rsample

A resampling framework that is compatible with tidy data and iteration. Use it with purrr to iterate through every bootstrap resample.

- Split a data frame into train/test sets: initial_split(), training(), testing()
- Bootstrap resampling: bootstraps()

`parsnip`

A unified tidy interface for a variety of machine learning methods. Developed by Max Kuhn, the author of the popular `caret` package. Max is slowly working through `caret` to break it into smaller packages with a tidy workflow.

- Decision trees: `decision_tree()`, `boost_tree()`, `rand_forest()`, `xgb_train()`
- Regression: `linear_reg()`, `logistic_reg()`, `multinom_reg()`
- Neural networks: `mlp()`
- K-Nearest Neighbours (KNN): `nearest_neighbour()`
- Support Vector Machines (SVM): `svm_poly()`, `svm_rbf()`

Chapter 6

Importing data

In this chapter we will cover importing a dataset, whether that dataset is in a single spreadsheet, or spread across multiple files.

All of your import needs will probably by covered by `readxl` or `readr`. `readxl` imports data from the proprietary *.XLS* and *.XLSX* formats that Microsoft Excel creates. `readr` imports plain-text files like *.CSV* and *.TSV* spreadsheets, where each column is separated by a character (i.e. *comma-separated values*) and each row appears on a new line. `readr` also writes data into these formats.

`readr` also imports and writes *.RDS* files, which are R objects that have been saved with all of their metadata. This is the format that you will be using in our exercises.

Importing one CSV spreadsheet

We can import one spreadsheet easily:

```
library(readr)

trap_ins <-
    read_csv("_data/light_trap/1992.csv")
```

```
## Parsed with column specification:
## cols(
##   order = col_character(),
##   family = col_character(),
##   date1 = col_character(),
##   date2 = col_character(),
##   individuals = col_double()
## )
```

```
# Space-efficient way of looking at a dataframe. Lists one column per line.
glimpse(trap_ins)
```

```
## Observations: 429
## Variables: 5
## $ order       <chr> "COLEOPTERA", "COLEOPTERA", "COLEOPTERA", "COLEOPT...
## $ family      <chr> "ANOBIIDAE", "ANOBIIDAE", "ANOBIIDAE", "CANTHARIDA...
```

```
## $ date1       <chr> "7/13/92", "7/6/92", "8/6/92", "6/29/92", "7/17/92...
## $ date2       <chr> "7/16/92", "7/8/92", "8/9/92", "7/2/92", "7/20/92"...
## $ individuals <dbl> 1, 2, 1, 3, 1, 1, 1, 5, 12, 4, 155, 37, 27, 84, 1,...
```

Notice that `readr` tries to guess the data type of each column (numeric, character, etc.), but it is conservative with its guesses to avoid losing information. In this case, it saved the `date` columns as `Character` (`<chr>`) because it doesn't recognise the dates' formatting, and it has saved the `individuals` column as a `Double` (a number that is allowed to have decimal places) instead of an integer. It is often preferable to fix these data types later using `dplyr`.

Importing several CSV spreadsheets

It's common to have a single dataset split into several spreadsheets. Perhaps you've started a different spreadsheet for every year of the study, or perhaps you're pooling results that were collected by different research groups.

The bad approach: Copy-paste

Assuming that each spreadsheet has the same structure, you could import all of them and row-bind them together:

```
library(dplyr)

all_ins <-
    bind_rows(
        read_csv("_data/light_trap/1992.csv"),
        read_csv("_data/light_trap/1993.csv"),
        read_csv("_data/light_trap/1994.csv"),
        ...
    )
```

But this is a poor approach. Firstly, it takes a long time to copy-paste-edit this code. Secondly — and most importantly — this code is not future-proof. If you add another year of observations, you'll need to remember to come back and add that spreadsheet to this list too.

The better approach: Iteration with `purrr`

Instead, let's make R do the hard work of listing the CSV files in `_data/light_trap/`.

```
list_of_files <-
    list.files("_data/light_trap/", pattern = "csv", full.names = TRUE)

list_of_files
```

```
##  [1] "_data/light_trap/1992.csv" "_data/light_trap/1993.csv"
##  [3] "_data/light_trap/1994.csv" "_data/light_trap/1995.csv"
##  [5] "_data/light_trap/1996.csv" "_data/light_trap/1997.csv"
##  [7] "_data/light_trap/1998.csv" "_data/light_trap/1999.csv"
##  [9] "_data/light_trap/2000.csv" "_data/light_trap/2001.csv"
## [11] "_data/light_trap/2002.csv" "_data/light_trap/2003.csv"
```

```
## [13] "_data/light_trap/2004.csv" "_data/light_trap/2005.csv"
## [15] "_data/light_trap/2006.csv" "_data/light_trap/2007.csv"
## [17] "_data/light_trap/2008.csv" "_data/light_trap/2009.csv"
```

Now that we have this list we can iterate over it, applying `read_csv()` to each file and then row-binding at the end.

You have probably used base R's `apply` family of functions to iterate in the past (`apply()`, `sapply()`, `vapply()`, `lapply()`, etc.). In the Tidyverse we use prefer to use `purrr` because its user interface is easier to remember, it returns a predictable data type, and it can be used in a pipeline.

In this case, we can use the function `map_dfr()`:

```
map_dfr(.x, .f, .id = "id_col")
```

It applies a function `.f` to every entry of the list or vector in `.x`. Then it creates a data frame by row-binding (hence "`dfr`") every result, and adds a new column called `id_col` to it that describes which file the rows came from.

```
library(dplyr)
library(purrr)

light_trap <-
    map_dfr(.x = set_names(list_of_files),  # The names are used in .id
            .f = read_csv,
            .id = "source_file")

glimpse(light_trap)
```

```
## Observations: 10,534
## Variables: 6
## $ source_file <chr> "_data/light_trap/1992.csv", "_data/light_trap/199...
## $ order       <chr> "COLEOPTERA", "COLEOPTERA", "COLEOPTERA", "COLEOPT...
## $ family      <chr> "ANOBIIDAE", "ANOBIIDAE", "ANOBIIDAE", "CANTHARIDA...
## $ date1       <chr> "7/13/92", "7/6/92", "8/6/92", "6/29/92", "7/17/92...
## $ date2       <chr> "7/16/92", "7/8/92", "8/9/92", "7/2/92", "7/20/92"...
## $ individuals <dbl> 1, 2, 1, 3, 1, 1, 1, 5, 12, 4, 155, 37, 27, 84, 1,...
```

One of the common problems you might encounter is if the columns in your spreadsheets are given different data types. For example, maybe in one of the sheets, presence/absence has been recorded as `1/0`, and on another sheet is has been recorded as `TRUE/FALSE`. These columns can't be row-bound because R doesn't know how to convert between these types:

```
bind_rows(
    data.frame(presabs = c(1, 0)),
    data.frame(presabs = c(TRUE, FALSE))
)

## Error: Column `presabs` can't be converted from numeric to logical
```

In this case, you can tell `read_csv()` to import all columns as `Character` so that you can handle the type conversion later.

```
light_trap <-
    map_dfr(.x = set_names(list_of_files),
            .f = ~ read_csv(.x, col_types = cols(.default = "c")),
            #    ↑ This is purrr's shorthand for anonymous functions.
            #      This is identical to:
            # .f = function(.x) {read_csv(.x, col_types = ...)}
            .id = "source_file")

glimpse(light_trap)
```

```
## Observations: 10,534
## Variables: 6
## $ source_file <chr> "_data/light_trap/1992.csv", "_data/light_trap/199...
## $ order       <chr> "COLEOPTERA", "COLEOPTERA", "COLEOPTERA", "COLEOPT...
## $ family      <chr> "ANOBIIDAE", "ANOBIIDAE", "ANOBIIDAE", "CANTHARIDA...
## $ date1       <chr> "7/13/92", "7/6/92", "8/6/92", "6/29/92", "7/17/92...
## $ date2       <chr> "7/16/92", "7/8/92", "8/9/92", "7/2/92", "7/20/92"...
## $ individuals <chr> "1", "2", "1", "3", "1", "1", "1", "5", "12", "4",...
```

Saving (exporting) to a .RDS file

You can save a data frame to a file with `readr::write_csv()` and `readr::write_rds()`. In this manual we will be using `write_rds()` because it saves the data frame together with its meta data, such as its data types and its groupings (if any). As an example, here is how to write the built-in dataset `iris` to a file called `my_iris.rds` in the working directory.

```
iris %>%
    write_rds("my_iris.rds")
```

And here is how to import that .RDS file:

```
my_import <- read_rds("my_iris.rds")
```

Chapter 7

Reshaping and completing

This chapter covers how to reshape a newly-imported data frame into the 'tidy' format that Tidyverse packages expect.

What is tidy data?

There are many perspectives on what data *should* look like when it is ready for exploration, but the one that's relevant to us is the concept of **tidy data**, presented by Hadley Wickham <http://www.jstatsoft.org/v59/i10/>. You may know these concepts already by the names 'wide table' and 'long table'. Wickham writes that messy/untidy data (an example is given in Table 7.1) tends to have these attributes:

- Column headers are values, not variable names.
- Multiple variables are stored in one column.
- Variables are stored in both rows and columns.
- Multiple types of observational units are stored in the same table.
- A single observational unit is stored in multiple tables.

Table 7.1: An example of 'Untidy' data in 'wide' format. The 'observation' column holds two different variables and each species × measurement pair is in its own column.

observation	spp_A_count	spp_B_count	spp_A_dbh_cm	spp_B_dbh_cm
Richmond (Sam)	7	2	100	110
Windsor (Ash)	10	5	80	87
Bilpin (Jules)	5	8	95	99

Conversely, tidy data (see Table 7.2) has these attributes:

1. Each variable forms a column.
2. Each observation forms a row.
3. Each type of observational unit forms a table.

Tidyverse packages and functions know how to work with this standard form. It becomes easier to recode your variables, sort them, compute with them, and eventually, transform them into the different subsets that you'll need for analysis.

In this manual we will use the names 'wide' and 'long' to refer to table shapes because they are more commonly used among analysts than 'tidy' and 'untidy'.

Table 7.2: 'Tidy' data. Each column holds one variable. Each row holds one observation of that variable.

site	surveyor	species	count	dbh_cm
Richmond	Sam	A	7	100
Richmond	Sam	B	2	110
Windsor	Ash	A	10	80
Windsor	Ash	B	5	87
Bilpin	Jules	A	5	95
Bilpin	Jules	B	8	99

Preparing a practice dataset for reshaping

There is a small dataset in `_data/mongolia_livestock` that we will use to illustrate reshaping. It describes the number of domesticated animals (in thousands of head) that was recorded in Mongolia between 1970 and 2017.

```
library(tidyverse)

animals <-
    read_csv("_data/mongolia_livestock/animal_numbers.csv",
             # For a small/simple dataset, setting data types is easy with this:
             # c = Character, i = Integer, d = Double. See ?cols for more.
             col_types = "cid") %>%
    glimpse()
```

```
## Observations: 228
## Variables: 3
## $ `Type of livestock` <chr> "Sheep", "Cattle", "Camel", "Camel", "Came...
## $ Year                <int> 2015, 1972, 1985, 1995, 1997, 1977, 1979, ...
## $ `Heads (Thousands)` <dbl> 24943.127, 2189.381, 559.000, 367.500, 355...
```

This dataset has three variables and each variable is represented with its own column, which means that it is already in long format.

Renaming columns

The column names of this dataset are quoted with backticks because they contain spaces and brackets. The same thing would happen if a column name started with a number. We always clean up our data frames with the `janitor::clean_names()` function to automatically produce names that are consistent and easy to type.

```
library(janitor)

animals <-
    animals %>%
    clean_names() %>%
    glimpse()
```

```
## Observations: 228
## Variables: 3
```

```
## $ type_of_livestock <chr> "Sheep", "Cattle", "Camel", "Camel", "Camel"...
## $ year              <int> 2015, 1972, 1985, 1995, 1997, 1977, 1979, 20...
## $ heads_thousands   <dbl> 24943.127, 2189.381, 559.000, 367.500, 355.4...
```

We can also rename columns directly using `dplyr::rename()` (to refer to columns by name), or `purrr::set_names()` (to give every column a new name).

```
# To change all column names
animals %>%
    set_names("livestock", "year", "heads_1k") %>%
    glimpse()
```

```
## Observations: 228
## Variables: 3
## $ livestock <chr> "Sheep", "Cattle", "Camel", "Camel", "Camel", "Goat"...
## $ year      <int> 2015, 1972, 1985, 1995, 1997, 1977, 1979, 2014, 1996...
## $ heads_1k  <dbl> 24943.127, 2189.381, 559.000, 367.500, 355.400, 4411...
```

```
# To change some column names
animals <-
    animals %>%
    rename(livestock = type_of_livestock, heads_1k = heads_thousands) %>%
    glimpse()
```

```
## Observations: 228
## Variables: 3
## $ livestock <chr> "Sheep", "Cattle", "Camel", "Camel", "Camel", "Goat"...
## $ year      <int> 2015, 1972, 1985, 1995, 1997, 1977, 1979, 2014, 1996...
## $ heads_1k  <dbl> 24943.127, 2189.381, 559.000, 367.500, 355.400, 4411...
```

Spreading a long data frame into wide

To convert a data frame from long to wide, use the `tidyr::spread()` function:

```
spread(data = df, key = "col_names", value = "cell_contents", fill = NA)
```

This function will create new columns, where the column names come from `key` and the values placed into each column come from `value`. If there are any missing values in the new table, they will be filled with `fill`.

```
animals_wide <-
    animals %>%
    spread(key = "livestock", value = "heads_1k")

head(animals_wide)
```

```
## # A tibble: 6 x 6
##    year Camel Cattle  Goat Horse  Sheep
##   <int> <dbl>  <dbl> <dbl> <dbl>  <dbl>
## 1  1970  633.  2108. 4207. 2315. 13311.
## 2  1971  632.  2176. 4195. 2270. 13420.
```

```
## 3  1972  625.  2189. 4338. 2239. 13716.
## 4  1973  603.  2235. 4442. 2185. 14073.
## 5  1974  607.  2364. 4574. 2265. 14504.
## 6  1975  617.  2427. 4595.   NA  14458.
```

Notice that we have some new `NA` values. These are year × livestock combinations that were not included in `animals`; the change from a long format to a wide format has turned these **implicit missing values** into **explicit** ones.

Gathering a wide data frame into long

To convert a data frame from wide to long, use the `tidyr::gather()` function.

```
gather(data = df, key = "col_names", value = "cell_contents", ...)
```

You'll recognise that it's very similar to `spread()`, but with a special argument called `...` (called `dots` in R lingo, see the next section for an explanation of how `dots` works).

You define the columns that will be gathered in the `...` argument, and those columns will be condensed into two new columns. The first new column, `key`, contains the names of the original columns. The second new column, `value`, contains the contents of the table cells.

```
animals_long <-
    animals_wide %>%
    # Since we want to gather every column except year, we can use -year.
    gather(key = "livestock", value = "heads_1k", -year)

head(animals_long)
```

```
## # A tibble: 6 x 3
##    year livestock heads_1k
##   <int> <chr>        <dbl>
## 1  1970 Camel         633.
## 2  1971 Camel         632.
## 3  1972 Camel         625.
## 4  1973 Camel         603.
## 5  1974 Camel         607.
## 6  1975 Camel         617.
```

By default, the `NA` values that were created during the `spread()` operation are kept by `gather()`.

A quick word about `dots`

`dots` is an argument that you'll see often in the Tidyverse, so it deserves some explaining. Normal function arguments accept one object only. Even when you don't name the arguments, they are filled by each object in the order you provide them:

```
my_sum <- function(x, y) {
    sum(x, y)
}

my_sum(1, 2)
```

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

```
# Identical to
my_sum(x = 1, y = 2)
```

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

But what happens if you want to add 3 numbers together? You get an error because there's no argument, no box, for the third number to fit into:

```
my_sum(1, 2, 3)

## Error in my_sum(1, 2, 3) : unused argument (3)
```

`dots` is a special argument that can accept any number of objects and pass them on as a single list:

```
dots_sum <- function(...) {
    sum(...)
}

dots_sum(1)
```

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

```
dots_sum(1, 2, 3, 4, 5)
```

```
## [1] 15
```

Nearly every function in R uses `dots` to pass data like this. For example, `sum()` itself uses `dots`, and `plot()` uses `dots` to pass graphical parameters such as the graph title, the shape of points, and so on. The Tidyverse is no exception to this — for example, see `?dplyr::rename`.

The one catch to using `dots` is that sometimes, there may be other function arguments that come after it that you also want to use. If you want to use them, you need to name them so that R knows that `dots` is finished:

```
dots_sum <- function(..., multiply_by = 1) {
    sum(...) * multiply_by
}

dots_sum(1, 2, 3, 4, 5)  # dots is still being filled
```

```
## [1] 15
```

```
dots_sum(1, 2, 3, 4, multiply_by = 5)  # dots stops when an argument is named
```

```
## [1] 50
```

Separating one column into several

Sometimes, one column will contain several pieces of information that you would like to separate into their own columns. For example, you may want to separate the area code from a phone number, or a first name from a last name. Use `tidyr::separate()` for this. Let's generate a small example of insects and their taxa names:

```
example_ids <-
    tibble::tribble(
        ~sample_id,                                          ~names,
           "BIL01",          "Hymenoptera; Apoidea; Ampulicidae",
           "BIL02",         "Lepidoptera; Pyraloidea; Pyralidae",
           "KAT03", "Hymenoptera; Ichneumonoidea; Ichneumonidae",
           "KAT04",         "Diptera; Sciaroidea; Cecidomyiidae"
        )

example_ids
```

```
## # A tibble: 4 x 2
##   sample_id names
##   <chr>     <chr>
## 1 BIL01     Hymenoptera; Apoidea; Ampulicidae
## 2 BIL02     Lepidoptera; Pyraloidea; Pyralidae
## 3 KAT03     Hymenoptera; Ichneumonoidea; Ichneumonidae
## 4 KAT04     Diptera; Sciaroidea; Cecidomyiidae
```

The column `names` contains the insect's order, superfamily, and family. The default behaviour of `separate()` is to split each alphanumeric group (i.e. each word or group of numbers) into a separate column. Since the values in `names` are separated by a semicolon and a space, this default behaviour will work fine:

```
example_ids <-
    example_ids %>%
    separate(names, into = c("order", "superfamily", "family")) %>%
    glimpse()
```

```
## Observations: 4
## Variables: 4
## $ sample_id   <chr> "BIL01", "BIL02", "KAT03", "KAT04"
## $ order       <chr> "Hymenoptera", "Lepidoptera", "Hymenoptera", "Dipt...
## $ superfamily <chr> "Apoidea", "Pyraloidea", "Ichneumonoidea", "Sciaro...
## $ family      <chr> "Ampulicidae", "Pyralidae", "Ichneumonidae", "Ceci...
```

The input column is removed by default. In this next case, we will split the `sample_id` column into two columns, but we will keep the `sample_id` column in case it is useful. In this example there is no separator to use, but we can see that the site name is always 3 letters long (`BIL` or `KAT`) so we can separate *by position*:

```
example_ids <-
    example_ids %>%
    separate(sample_id, into = c("site", "insect_id"),
             sep = 3,        # Separate at the 3rd character
             remove = FALSE  # Don't remove the sample_id column
             ) %>%
    glimpse()
```

```
## Observations: 4
## Variables: 6
## $ sample_id   <chr> "BIL01", "BIL02", "KAT03", "KAT04"
## $ site        <chr> "BIL", "BIL", "KAT", "KAT"
## $ insect_id   <chr> "01", "02", "03", "04"
## $ order       <chr> "Hymenoptera", "Lepidoptera", "Hymenoptera", "Dipt...
## $ superfamily <chr> "Apoidea", "Pyraloidea", "Ichneumonoidea", "Sciaro...
## $ family      <chr> "Ampulicidae", "Pyralidae", "Ichneumonidae", "Ceci...
```

Combining columns into one

The opposite of `tidyr::separate()` is `tidyr::unite()`:

```
example_ids %>%
    unite(taxa, order:family, sep = " / ") %>%
    glimpse()
```

```
## Observations: 4
## Variables: 4
## $ sample_id <chr> "BIL01", "BIL02", "KAT03", "KAT04"
## $ site      <chr> "BIL", "BIL", "KAT", "KAT"
## $ insect_id <chr> "01", "02", "03", "04"
## $ taxa      <chr> "Hymenoptera / Apoidea / Ampulicidae", "Lepidoptera ...
```

Completing a table

'Completing' a table means finding any missing combinations of variables and representing them as `NA` in the data frame. For example, if you went bird-watching at the same place every month and only wrote down the birds that were present, then all of the missing rows are actually true absences. It's valuable to have a complete table because we can replace those `NA`s by predicting new values for them, or represent periods of missing data in our graphs.

We saw that the `animals` data frame has missing observations (counts of a particular livestock on a particular year). We also saw that `spread()` and `gather()` can be used to make these implicitly-missing observations into explicitly-missing ones. However, while this approach is fine for a combination of two variables (livestock vs year), it doesn't work for combinations for 3 or more. Instead, we use `tidyr::complete()`.

```
incomplete <-
    read_csv("_data/incomplete_data/incomplete.csv", col_types = "ccci") %>%
    glimpse()
```

```
## Observations: 36
## Variables: 4
## $ city      <chr> "Sydney", "Brisbane", "Melbourne", "Melbourne", "Syd...
## $ survey_id <chr> "Syd_2019", "Bri_2017", "Mel_2016", "Mel_2018", "Syd...
## $ order     <chr> "Coleoptera", "Coleoptera", "Hemiptera", "Hemiptera"...
## $ count     <int> 30, 25, 0, 12, 46, 21, 39, 13, 38, 39, 17, 46, 28, 3...
```

This dataset is missing data in both structured and random ways:

1. Sydney has no monitoring data for 2016.

2. Brisbane is not equipped to monitor Hemipterans.
3. There are rows missing at random (implicit zeroes).

All cases can be filled like this (compare the number of observations):

```
explicit <-
    incomplete %>%
    complete(survey_id, city, order) %>%
    glimpse()
```

```
## Observations: 132
## Variables: 4
## $ survey_id <chr> "Bri_2016", "Bri_2016", "Bri_2016", "Bri_2016", "Bri...
## $ city      <chr> "Brisbane", "Brisbane", "Brisbane", "Brisbane", "Mel...
## $ order     <chr> "Coleoptera", "Diptera", "Hemiptera", "Lepidoptera",...
## $ count     <int> 40, 25, NA, 43, NA, NA, NA, NA, NA, NA, NA, 25, ...
```

The above code finds **all** combinations of `survey_id` × `city` × `order`. However, it doesn't make very much sense to duplicate `survey_id` entries from Sydney across all the other cities! Instead, we can tell R that `survey_id` and `city` are *nested* within each other using `nesting()`:

```
explicit <-
    incomplete %>%
    complete(nesting(survey_id, city), order) %>%
    glimpse()
```

```
## Observations: 44
## Variables: 4
## $ survey_id <chr> "Bri_2016", "Bri_2016", "Bri_2016", "Bri_2016", "Bri...
## $ city      <chr> "Brisbane", "Brisbane", "Brisbane", "Brisbane", "Bri...
## $ order     <chr> "Coleoptera", "Diptera", "Hemiptera", "Lepidoptera",...
## $ count     <int> 40, 25, NA, 43, 25, NA, NA, 46, 45, 28, NA, NA, NA, ...
```

Chapter 8

Joining data frames together

This chapter covers how to join two data frames together. Although the examples that we present involve only two data frames at a time, they can be iterated with `purrr` to perform complex joins.

Classic row-binding and column-binding

The most basic methods of joining data frames are to *row-bind* them by stacking their rows on top of each other (if their columns are identical), or *column-bind* them by putting their columns beside each other (if they have the same number of columns). In the Tidyverse, these are performed by `dplyr::bind_rows()` and `dplyr::bind_rows()` respectively. Their advantage over the base functions `rbind()` and `cbind()` is that you can pass many data frames to them at once:

```
library(tidyverse)

bind_rows(
    sample_n(iris, 10),
    sample_n(iris, 10),
    sample_n(iris, 10)
    ) %>%
    glimpse()  # 30 observations (i.e. rows)
```

```
## Observations: 30
## Variables: 5
## $ Sepal.Length <dbl> 5.8, 7.2, 5.0, 5.8, 5.6, 4.5, 5.7, 5.5, 6.8, 5.2,...
## $ Sepal.Width  <dbl> 4.0, 3.6, 2.3, 2.8, 2.9, 2.3, 4.4, 3.5, 3.2, 4.1,...
## $ Petal.Length <dbl> 1.2, 6.1, 3.3, 5.1, 3.6, 1.3, 1.5, 1.3, 5.9, 1.5,...
## $ Petal.Width  <dbl> 0.2, 2.5, 1.0, 2.4, 1.3, 0.3, 0.4, 0.2, 2.3, 0.1,...
## $ Species      <fct> setosa, virginica, versicolor, virginica, versico...
```

```
bind_cols(
    sample_n(iris, 10),
    sample_n(iris, 10),
    sample_n(iris, 10)
    ) %>%
    glimpse()  # 15 variables (i.e. columns). Columns are given unique names.
```

```
## Observations: 10
## Variables: 15
## $ Sepal.Length  <dbl> 4.8, 6.3, 5.0, 4.9, 4.8, 6.3, 5.6, 5.4, 6.9, 5.8
## $ Sepal.Width   <dbl> 3.0, 3.4, 3.3, 3.1, 3.4, 2.8, 2.5, 3.9, 3.2, 2.8
## $ Petal.Length  <dbl> 1.4, 5.6, 1.4, 1.5, 1.9, 5.1, 3.9, 1.3, 5.7, 5.1
## $ Petal.Width   <dbl> 0.1, 2.4, 0.2, 0.2, 0.2, 1.5, 1.1, 0.4, 2.3, 2.4
## $ Species       <fct> setosa, virginica, setosa, setosa, setosa, virgi...
## $ Sepal.Length1 <dbl> 6.8, 5.1, 7.6, 6.7, 4.9, 5.2, 5.2, 7.4, 5.0, 6.5
## $ Sepal.Width1  <dbl> 3.2, 3.3, 3.0, 3.0, 3.1, 3.4, 4.1, 2.8, 3.4, 3.0
## $ Petal.Length1 <dbl> 5.9, 1.7, 6.6, 5.0, 1.5, 1.4, 1.5, 6.1, 1.5, 5.5
## $ Petal.Width1  <dbl> 2.3, 0.5, 2.1, 1.7, 0.2, 0.2, 0.1, 1.9, 0.2, 1.8
## $ Species1      <fct> virginica, setosa, virginica, versicolor, setosa...
## $ Sepal.Length2 <dbl> 6.3, 7.4, 6.6, 7.2, 5.1, 5.0, 6.7, 4.6, 5.5, 6.7
## $ Sepal.Width2  <dbl> 2.9, 2.8, 3.0, 3.0, 3.4, 3.5, 3.0, 3.4, 2.4, 3.0
## $ Petal.Length2 <dbl> 5.6, 6.1, 4.4, 5.8, 1.5, 1.6, 5.2, 1.4, 3.7, 5.0
## $ Petal.Width2  <dbl> 1.8, 1.9, 1.4, 1.6, 0.2, 0.6, 2.3, 0.3, 1.0, 1.7
## $ Species2      <fct> virginica, virginica, versicolor, virginica, set...
```

We performed row-binding behind-the-scenes in Chapter @ref{importing-data} when we imported multiple spreadsheets using `purrr::map_dfr()`:

```
list_of_files <-
    list.files("_data/light_trap/", pattern = "csv", full.names = TRUE)

light_trap <-
    map_dfr(list_of_files, read_csv, col_types = "ccccd") %>%
    glimpse()
```

```
## Observations: 10,534
## Variables: 5
## $ order       <chr> "COLEOPTERA", "COLEOPTERA", "COLEOPTERA", "COLEOPT...
## $ family      <chr> "ANOBIIDAE", "ANOBIIDAE", "ANOBIIDAE", "CANTHARIDA...
## $ date1       <chr> "7/13/92", "7/6/92", "8/6/92", "6/29/92", "7/17/92...
## $ date2       <chr> "7/16/92", "7/8/92", "8/9/92", "7/2/92", "7/20/92"...
## $ individuals <dbl> 1, 2, 1, 3, 1, 1, 1, 5, 12, 4, 155, 37, 27, 84, 1,...
```

You can also perform column-binding in a similar way with `map_dfc()`.

Joining data frames by value

There are seven different kinds of join operations provided by `dplyr`, which you can read more of in `?dplyr::join`. Here we draw attention to the three most useful ones:

- `left_join(x, y)`: Column-bind values from `y` to their matching rows in `x`.
- `semi_join(x, y)`: Only keep rows from `x` if they also appear in `y`.
- `anti_join(x, y)`: Only keep rows from `x` if they **do not** appear in `y`.

We will demonstrate these joining methods by using a dataset called `starwars` that is included with `dplyr`. It includes canon information about characters from the Star Wars franchise, but remember that these built-in examples are useful for their structure and data types, and not for the information they actually hold. If you prefer, you can imagine that we are joining by site names, or bioregion, or country.

First we have the `starwars` dataset itself, but we will only keep some of the columns:

```
sw_all <-
    starwars %>%
    select(name, homeworld, species) %>%  # More select() in the next chapter
    glimpse()
```

```
## Observations: 87
## Variables: 3
## $ name      <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", "...
## $ homeworld <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Aldera...
## $ species   <chr> "Human", "Droid", "Droid", "Human", "Human", "Human"...
```

Then we will create a subset of `starwars` for use with `semi_join()` and `anti_join()`, and keep a different set of columns:

```
set.seed(1287540661)  # So we draw the same rows every time

sw_subset <-
    starwars %>%
    select(name, height:eye_color, species) %>%
    sample_frac(0.20) %>%  # Pick 20 % of the total rows.
    glimpse()
```

```
## Observations: 17
## Variables: 7
## $ name       <chr> "Dud Bolt", "BB8", "Saesee Tiin", "Zam Wesell", "Jo...
## $ height     <int> 94, NA, 188, 168, 167, 66, 178, 79, 157, 97, 183, 1...
## $ mass       <dbl> 45, NA, NA, 55, NA, 17, 57, 15, NA, 32, NA, NA, 79,...
## $ hair_color <chr> "none", "none", "none", "blonde", "white", "white",...
## $ skin_color <chr> "blue, grey", "none", "pale", "fair, green, yellow"...
## $ eye_color  <chr> "yellow", "black", "orange", "yellow", "blue", "bro...
## $ species    <chr> "Vulptereen", "Droid", "Iktotchi", "Clawdite", "Hum...
```

Joining tables requires at least one column to be the same between them, but here we have two: `name` and `species`.

Merge with `left_join()`

The most-used method is `left_join()`, which can be used to merge data from two tables together. For example, we have extra information about 17 of our characters:

```
left_join(x = sw_all, y = sw_subset) %>%
    glimpse()
```

```
## Joining, by = c("name", "species")
```

```
## Observations: 87
## Variables: 8
## $ name       <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", ...
## $ homeworld  <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Alder...
## $ species    <chr> "Human", "Droid", "Droid", "Human", "Human", "Human...
```

```
## $ height     <int> NA, NA, NA, NA, NA, NA, NA, 97, NA, NA, NA, NA, NA,...
## $ mass       <dbl> NA, NA, NA, NA, NA, NA, NA, 32, NA, NA, NA, NA, NA,...
## $ hair_color <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,...
## $ skin_color <chr> NA, NA, NA, NA, NA, NA, NA, "white, red", NA, NA, N...
## $ eye_color  <chr> NA, NA, NA, NA, NA, NA, NA, "red", NA, NA, NA, NA, ...
```

By default, join operations will automatically try to use every identically-named column in both data frames, and then raise a message to tell you so. If you manually define the `by` argument, you can get control over this behaviour while removing this message:

```
left_join(x = sw_all, y = sw_subset, by = "name") %>%
    glimpse()
```

```
## Observations: 87
## Variables: 9
## $ name       <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", ...
## $ homeworld  <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Alder...
## $ species.x  <chr> "Human", "Droid", "Droid", "Human", "Human", "Human...
## $ height     <int> NA, NA, NA, NA, NA, NA, NA, 97, NA, NA, NA, NA, NA,...
## $ mass       <dbl> NA, NA, NA, NA, NA, NA, NA, 32, NA, NA, NA, NA, NA,...
## $ hair_color <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,...
## $ skin_color <chr> NA, NA, NA, NA, NA, NA, NA, "white, red", NA, NA, N...
## $ eye_color  <chr> NA, NA, NA, NA, NA, NA, NA, "red", NA, NA, NA, NA, ...
## $ species.y  <chr> NA, NA, NA, NA, NA, NA, NA, "Droid", NA, NA, NA, NA...
```

Note that in this last example, we chose to only join by `name`. The behaviour of `left_join()` is to keep all columns from both `x` and `y`, which is why `species` has been duplicated in the resulting data frame. This does not happen with `semi_join()` or `anti_join()`, which only keep the columns from `x`.

Intersect with `semi_join()`

Use `semi_join()` when you only want to keep rows that occur in two data frames.

```
sw_all %>%
    left_join(sw_subset, by = c("name", "species")) %>%
    semi_join(sw_subset, by = "name") %>%
    glimpse()
```

```
## Observations: 17
## Variables: 8
## $ name       <chr> "R5-D4", "Yoda", "Dud Bolt", "Saesee Tiin", "Mas Am...
## $ homeworld  <chr> "Tatooine", NA, "Vulpter", "Iktotch", "Champala", "...
## $ species    <chr> "Droid", "Yoda's species", "Vulptereen", "Iktotchi"...
## $ height     <int> 97, 66, 94, 188, 196, 157, 183, 191, 183, 168, 167,...
## $ mass       <dbl> 32, 17, 45, NA, NA, NA, NA, NA, 79, 55, NA, 15, NA,...
## $ hair_color <chr> NA, "white", "none", "none", "none", "brown", "brow...
## $ skin_color <chr> "white, red", "green", "blue, grey", "pale", "blue"...
## $ eye_color  <chr> "red", "brown", "yellow", "orange", "blue", "brown"...
```

Difference with 'anti_join()

Use `anti_join()` when you only want to find rows that **don't** occur in both data frames.

```
anti_join(sw_all, sw_subset, by = c("name", "species")) %>%
    glimpse()
```

```
## Observations: 70
## Variables: 3
## $ name      <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", "...
## $ homeworld <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Aldera...
## $ species   <chr> "Human", "Droid", "Droid", "Human", "Human", "Human"...
```

Chapter 9

Choosing and renaming columns

In this chapter, we will cover how to select, reorder, and rename the columns of a data frame.

Choosing columns by name

Manual naming

You can choose columns using `dplyr::select()`. The most basic method of choosing columns is to name them:

```
library(tidyverse)

starwars %>%
    select(name, height, mass) %>%
    glimpse()
```

```
## Observations: 87
## Variables: 3
## $ name   <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", "Lei...
## $ height <int> 172, 167, 96, 202, 150, 178, 165, 97, 183, 182, 188, 18...
## $ mass   <dbl> 77.0, 75.0, 32.0, 136.0, 49.0, 120.0, 75.0, 32.0, 84.0,...
```

Another method is to name a set of adjacent columns using the `:` operator, just as you would create a range of numbers from 1 to 4 with `1:4`:

```
starwars %>%
    select(name:mass) %>%
    glimpse()
```

```
## Observations: 87
## Variables: 3
## $ name   <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", "Lei...
## $ height <int> 172, 167, 96, 202, 150, 178, 165, 97, 183, 182, 188, 18...
## $ mass   <dbl> 77.0, 75.0, 32.0, 136.0, 49.0, 120.0, 75.0, 32.0, 84.0,...
```

Using a helper function to name

The Tidyverse comes with a set of functions that can be used to programatically select columns by name. They can be viewed in `?tidyselect::select_helpers`, but the ones we use most often are:

Helper	Chooses column names that...
`starts_with()`	Start with a literal string
`ends_with()`	End with a literal string
`contains()`	Contains a literal string
`matches()`	Match a regular expression
`num_range()`	Are part of a numerical range (x1, x2, ...)
`everything()`	Selects all columns.

For example, we can select all columns from `iris` that measure `Petal`, or all columns that measure `Length`, or any column that has a `.`:

```
iris %>%
    select(starts_with("Petal")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 2
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
```

```
iris %>%
    select(ends_with("Length")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 2
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
```

```
iris %>%
    select(contains(".")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 4
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
```

Reordering columns

Columns will be returned in the order they are chosen:

```
iris %>%
    select(ends_with("Length"), Species, ends_with("Width")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 5
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
```

The `everything()` selector returns every column that isn't already selected, which makes it useful for reordering a data frame's columns:

```
iris %>%
    select(Species, everything()) %>%  # Reorder 'Species' to the first column
    glimpse()
```

```
## Observations: 150
## Variables: 5
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
```

Omitting columns

With any of the above methods, you can **omit** a column by putting a `-` in front of the selection:

```
iris %>%
    #   Negate the selector to omit its results
    #      ↓
    select(-Species, -Petal.Length) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 3
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
```

```
iris %>%
    select(-ends_with("Length")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 3
## $ Sepal.Width <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, ...
## $ Petal.Width <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, ...
## $ Species     <fct> setosa, setosa, setosa, setosa, setosa, setosa, se...
```

Negating `everything()` will, of course, return no columns.

Note that because `everything()` chooses all unselected columns, any omitted columns will be returned. If you use `everything()`, do your omissions after it:

```
iris %>%
    select(Species, everything(), -ends_with("Length")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 3
## $ Species     <fct> setosa, setosa, setosa, setosa, setosa, setosa, se...
## $ Sepal.Width <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, ...
## $ Petal.Width <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, ...
```

Choosing columns by value

You can choose columns based on whether they satisfy a logical test by using the special verb `select_if()`. For example, we can choose columns by data type:

```
starwars %>%
    select_if(is.numeric) %>%  # Using the base R function is.numeric()
    glimpse()
```

```
## Observations: 87
## Variables: 3
## $ height     <int> 172, 167, 96, 202, 150, 178, 165, 97, 183, 182, 188...
## $ mass       <dbl> 77.0, 75.0, 32.0, 136.0, 49.0, 120.0, 75.0, 32.0, 8...
## $ birth_year <dbl> 19.0, 112.0, 33.0, 41.9, 19.0, 52.0, 47.0, NA, 24.0...
```

Or we can choose columns that meet some arbitrary check by writing our own function that returns `TRUE` or `FALSE`:

```
colSums(iris[1:4])
```

```
## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##        876.5        458.6        563.7        179.9
```

```
less_than_500 <- function(x) {
    sum(x) < 500
}

iris[1:4] %>%
    select_if(less_than_500) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 2
## $ Sepal.Width <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, ...
## $ Petal.Width <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, ...
```

Just as we mentioned in Chapter @ref{the-pipeline}, you can use the tilde (~) as a shortcut to write an anonymous function, so the above could be expressed like this:

```
iris[1:4] %>%
    #    dot holds the contents of the column being checked
    #                ↓
    select_if(~ sum(.) < 500) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 2
## $ Sepal.Width <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, ...
## $ Petal.Width <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, ...
```

The `select_if()` verb is one of several "scoped verbs" that `dplyr` provides, which we will explore more in the following chapters.

Renaming columns

In Chapter @ref{reshaping-and-completing} we covered basic column renaming. As a reminder:

```
library(janitor)
```

```
##
## Attaching package: 'janitor'
```

```
## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test
```

```
# Standardise names with janitor::clean_names()
iris %>%
    clean_names() %>%
    names()  # Print the column names
```

```
## [1] "sepal_length" "sepal_width"  "petal_length" "petal_width"
## [5] "species"
```

```
# Replace all names with purrr::set_names()
iris %>%
    set_names("sep_len", "sep_wid", "pet_len", "pet_wid", "spp") %>%
    names()
```

```
## [1] "sep_len" "sep_wid" "pet_len" "pet_wid" "spp"
```

```
# Replace some names with dplyr::rename()
iris %>%
    rename(sep_length = Sepal.Length, sep_width = Sepal.Width) %>%
    names()
```

```
## [1] "sep_length"   "sep_width"    "Petal.Length" "Petal.Width"
## [5] "Species"
```

Chapter 10

Choosing rows

In the previous chapter, we look at how to subset a data frame to keep and remove columns. In this chapter, we will learn how to subset a data frame to keep and remove rows, and how to reorder those rows.

Building a dataset with duplicated rows

To illustrate subsetting, we will make a special version of the built-in `starwars` dataset that contains some duplicated rows:

```
set.seed(896)

sw_dup <-
    starwars %>%
    select(-(films:starships)) %>%  # Omit the last 3 columns (they are lists)
    sample_n(100, replace = TRUE) %>%  # replace = TRUE to get duplicate rows.
    glimpse()
```

```
## Observations: 100
## Variables: 10
## $ name       <chr> "Sly Moore", "Mon Mothma", "Finn", "Roos Tarpals", ...
## $ height     <int> 178, 150, NA, 224, NA, NA, 188, 200, 264, 180, 163,...
## $ mass       <dbl> 48, NA, NA, 82, NA, NA, NA, 140, NA, 110, 65, 80, 8...
## $ hair_color <chr> "none", "auburn", "black", "none", "brown", "none",...
## $ skin_color <chr> "pale", "fair", "dark", "grey", "fair", "none", "pa...
## $ eye_color  <chr> "white", "blue", "dark", "orange", "brown", "black"...
## $ birth_year <dbl> NA, 48, NA, NA, NA, NA, NA, 15, NA, NA, NA, NA, 72,...
## $ gender     <chr> "female", "female", "male", "male", "male", "none",...
## $ homeworld  <chr> "Umbara", "Chandrila", NA, "Naboo", NA, NA, "Iktotc...
## $ species    <chr> NA, "Human", "Human", "Gungan", "Human", "Droid", "...
```

Reordering rows

We'll also re-order this data frame's rows using `dplyr::arrange()` to show that it does indeed contain duplicates. Have a look at the result with `View(sw_dup)`.

```
sw_dup <-
    sw_dup %>%
    # Sort rows by homeworld, then species, then name.
    arrange(homeworld, species, name) %>%
    glimpse()
```

```
## Observations: 100
## Variables: 10
## $ name       <chr> "Bail Prestor Organa", "Leia Organa", "Leia Organa"...
## $ height     <int> 191, 150, 150, 150, 150, 188, 175, 180, 180, 180, 1...
## $ mass       <dbl> NA, 49, 49, 49, 49, 79, 79, 110, 110, 110, 82, 82, ...
## $ hair_color <chr> "black", "brown", "brown", "brown", "brown", "brown...
## $ skin_color <chr> "tan", "light", "light", "light", "light", "light",...
## $ eye_color  <chr> "brown", "brown", "brown", "brown", "brown", "brown...
## $ birth_year <dbl> 67, 19, 19, 19, 19, NA, 37, NA, NA, NA, 92, 92, 92,...
## $ gender     <chr> "male", "female", "female", "female", "female", "ma...
## $ homeworld  <chr> "Alderaan", "Alderaan", "Alderaan", "Alderaan", "Al...
## $ species    <chr> "Human", "Human", "Human", "Human", "Human", "Human...
```

The default sorting order of `arrange()` is A-Z for Character columns and in increasing order for Numeric and Factor columns. To sort in the opposite direction, use `desc()`:

```
sw_dup %>%
    arrange(mass) %>%  # Increasing quantity of mass
    glimpse()
```

```
## Observations: 100
## Variables: 10
## $ name       <chr> "Yoda", "Yoda", "Wicket Systri Warrick", "Wicket Sy...
## $ height     <int> 66, 66, 88, 88, 96, 97, 112, 112, 165, 165, 94, 193...
## $ mass       <dbl> 17.0, 17.0, 20.0, 20.0, 32.0, 32.0, 40.0, 40.0, 45....
## $ hair_color <chr> "white", "white", "brown", "brown", NA, NA, "none",...
## $ skin_color <chr> "green", "green", "brown", "brown", "white, blue", ...
## $ eye_color  <chr> "brown", "brown", "brown", "brown", "red", "red", "...
## $ birth_year <dbl> 896, 896, 8, 8, 33, NA, NA, NA, 46, 46, NA, NA, NA,...
## $ gender     <chr> "male", "male", "male", "male", NA, NA, "male", "ma...
## $ homeworld  <chr> NA, NA, "Endor", "Endor", "Naboo", "Tatooine", "Mal...
## $ species    <chr> "Yoda's species", "Yoda's species", "Ewok", "Ewok",...
```

```
sw_dup %>%
    arrange(desc(mass)) %>%  # Decreasing mass
    glimpse()
```

```
## Observations: 100
## Variables: 10
## $ name       <chr> "IG-88", "Tarfful", "Bossk", "Jek Tono Porkins", "J...
## $ height     <int> 200, 234, 190, 180, 180, 180, 198, 198, 193, 196, 1...
## $ mass       <dbl> 140, 136, 113, 110, 110, 110, 102, 102, 89, 87, 87,...
## $ hair_color <chr> "none", "brown", "none", "brown", "brown", "brown",...
## $ skin_color <chr> "metal", "brown", "green", "fair", "fair", "fair", ...
## $ eye_color  <chr> "red", "blue", "red", "blue", "blue", "blue", "yell...
```

```
## $ birth_year <dbl> 15, NA, 53, NA, NA, NA, NA, NA, 92, NA, NA, NA, NA,...
## $ gender     <chr> "none", "male", "male", "male", "male", "male", "ma...
## $ homeworld  <chr> NA, "Kashyyyk", "Trandosha", "Bestine IV", "Bestine...
## $ species    <chr> "Droid", "Wookiee", "Trandoshan", "Human", "Human",...
```

Removing duplicate rows

Use `dplyr::distinct()` to remove duplicate rows. By default, it will remove a row if every one of its values is identical to a previous row's values (i.e. it keeps the first instance of a duplicated row and discards the other copies).

```
sw_dup %>%
    distinct() %>%
    glimpse() %>%
    anyDuplicated()  # Returns 0 if there are no duplicate rows.
```

```
## Observations: 57
## Variables: 10
## $ name       <chr> "Bail Prestor Organa", "Leia Organa", "Raymus Antil...
## $ height     <int> 191, 150, 188, 175, 180, 198, 196, 150, 180, 170, 1...
## $ mass       <dbl> NA, 49.0, 79.0, 79.0, 110.0, 82.0, NA, NA, 80.0, 77...
## $ hair_color <chr> "black", "brown", "brown", "none", "brown", "white"...
## $ skin_color <chr> "tan", "light", "light", "light", "fair", "pale", "...
## $ eye_color  <chr> "brown", "brown", "brown", "blue", "blue", "yellow"...
## $ birth_year <dbl> 67, 19, NA, 37, NA, 92, NA, 48, 29, 21, NA, NA, 54,...
## $ gender     <chr> "male", "female", "male", "male", "male", "male", "...
## $ homeworld  <chr> "Alderaan", "Alderaan", "Alderaan", "Bespin", "Best...
## $ species    <chr> "Human", "Human", "Human", "Human", "Human", "Cerea...
```

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

You can also choose the columns that are compared for duplication. By default it only returns the columns that were chosen; to return all of the columns, use the argument `.keep_all = TRUE`.

```
sw_dup %>%
    distinct(species, homeworld) %>%  # Only check 'species' and 'homeworld'
    glimpse() %>%
    anyDuplicated()
```

```
## Observations: 42
## Variables: 2
## $ species   <chr> "Human", "Human", "Human", "Cerean", "Chagrian", "Hu...
## $ homeworld <chr> "Alderaan", "Bespin", "Bestine IV", "Cerea", "Champa...
```

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

```
sw_dup %>%
    distinct(species, homeworld, .keep_all = TRUE) %>%  # Keep all columns
    glimpse() %>%
    anyDuplicated()
```

```
## Observations: 42
## Variables: 10
## $ name       <chr> "Bail Prestor Organa", "Lobot", "Jek Tono Porkins",...
## $ height     <int> 191, 175, 180, 198, 196, 150, 180, 167, 184, 175, 1...
## $ mass       <dbl> NA, 79.0, 110.0, 82.0, NA, NA, 80.0, NA, 50.0, 80.0...
## $ hair_color <chr> "black", "none", "brown", "white", "none", "auburn"...
## $ skin_color <chr> "tan", "light", "fair", "pale", "blue", "fair", "fa...
## $ eye_color  <chr> "brown", "blue", "blue", "yellow", "blue", "blue", ...
## $ birth_year <dbl> 67, 37, NA, 92, NA, 48, 29, NA, NA, 54, 22, 8, NA, ...
## $ gender     <chr> "male", "male", "male", "male", "male", "female", "...
## $ homeworld  <chr> "Alderaan", "Bespin", "Bestine IV", "Cerea", "Champ...
## $ species    <chr> "Human", "Human", "Human", "Cerean", "Chagrian", "H...

## [1] 0
```

Removing rows with NAs

Use `tidyr::drop_na()` to remove any row that contains an `NA`.

```
sw_dup %>%
    drop_na() %>%
    glimpse() %>%
    anyNA()  # Returns FALSE if there are no NAs in the data frame
```

```
## Observations: 30
## Variables: 10
## $ name       <chr> "Leia Organa", "Leia Organa", "Leia Organa", "Leia ...
## $ height     <int> 150, 150, 150, 150, 175, 198, 198, 198, 180, 170, 1...
## $ mass       <dbl> 49.0, 49.0, 49.0, 49.0, 79.0, 82.0, 82.0, 82.0, 80....
## $ hair_color <chr> "brown", "brown", "brown", "brown", "none", "white"...
## $ skin_color <chr> "light", "light", "light", "light", "light", "pale"...
## $ eye_color  <chr> "brown", "brown", "brown", "brown", "blue", "yellow...
## $ birth_year <dbl> 19, 19, 19, 19, 37, 92, 92, 92, 29, 21, 21, 54, 54,...
## $ gender     <chr> "female", "female", "female", "female", "male", "ma...
## $ homeworld  <chr> "Alderaan", "Alderaan", "Alderaan", "Alderaan", "Be...
## $ species    <chr> "Human", "Human", "Human", "Human", "Human", "Cerea...

## [1] FALSE
```

Instead of looking for `NA`s inside every column, you can choose only some columns. `NA`s that occur outside the chosen columns will be ignored.

```
sw_dup %>%
    drop_na(gender:species) %>%
    glimpse() %>%
    anyNA()  # Returns TRUE because there are still NAs, e.g. in birth_year.
```

```
## Observations: 81
## Variables: 10
## $ name       <chr> "Bail Prestor Organa", "Leia Organa", "Leia Organa"...
```

```
## $ height     <int> 191, 150, 150, 150, 150, 188, 175, 180, 180, 180, 1...
## $ mass       <dbl> NA, 49, 49, 49, 49, 79, 79, 110, 110, 110, 82, 82, ...
## $ hair_color <chr> "black", "brown", "brown", "brown", "brown", "brown...
## $ skin_color <chr> "tan", "light", "light", "light", "light", "light",...
## $ eye_color  <chr> "brown", "brown", "brown", "brown", "brown", "brown...
## $ birth_year <dbl> 67, 19, 19, 19, 19, NA, 37, NA, NA, NA, 92, 92, 92,...
## $ gender     <chr> "male", "female", "female", "female", "female", "ma...
## $ homeworld  <chr> "Alderaan", "Alderaan", "Alderaan", "Alderaan", "Al...
## $ species    <chr> "Human", "Human", "Human", "Human", "Human", "Human...
```

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

Choosing rows by value

One of the most important verbs in `dplyr` is `dplyr::filter()`, which is used to subset a data frame to return the rows that you're interested in.

```
# Find all of the Humans whose homeworld was not Earth
sw_dup %>%
    #      filter() performs an AND search by default.
    #                          ↓
    filter(species == "Human", homeworld != "Earth") %>%
    distinct() %>%
    glimpse()
```

```
## Observations: 18
## Variables: 10
## $ name       <chr> "Bail Prestor Organa", "Leia Organa", "Raymus Antil...
## $ height     <int> 191, 150, 188, 175, 180, 150, 180, 170, 167, 188, 1...
## $ mass       <dbl> NA, 49, 79, 79, 110, NA, 80, 77, NA, 84, NA, 85, 45...
## $ hair_color <chr> "black", "brown", "brown", "none", "brown", "auburn...
## $ skin_color <chr> "tan", "light", "light", "light", "fair", "fair", "...
## $ eye_color  <chr> "brown", "brown", "brown", "blue", "blue", "blue", ...
## $ birth_year <dbl> 67, 19, NA, 37, NA, 48, 29, 21, NA, 72, NA, NA, 46,...
## $ gender     <chr> "male", "female", "male", "male", "male", "female",...
## $ homeworld  <chr> "Alderaan", "Alderaan", "Alderaan", "Bespin", "Best...
## $ species    <chr> "Human", "Human", "Human", "Human", "Human", "Human...
```

```
# Find everyone who is either a Droid OR whose homeworld is Tatooine
sw_dup %>%
    #        OR operator. For more info, read ?base::Logic
    #                          ↓
    filter(species == "Droid" | homeworld == "Tatooine") %>%
    distinct() %>%
    glimpse()
```

```
## Observations: 7
## Variables: 10
## $ name       <chr> "R2-D2", "R5-D4", "Beru Whitesun lars", "Cliegg Lar...
## $ height     <int> 96, 97, 165, 183, 163, NA, 200
## $ mass       <dbl> 32, 32, 75, NA, NA, NA, 140
```

```
## $ hair_color <chr> NA, NA, "brown", "brown", "black", "none", "none"
## $ skin_color <chr> "white, blue", "white, red", "light", "fair", "fair...
## $ eye_color  <chr> "red", "red", "blue", "blue", "brown", "black", "red"
## $ birth_year <dbl> 33, NA, 47, 82, 72, NA, 15
## $ gender     <chr> NA, NA, "female", "male", "female", "none", "none"
## $ homeworld  <chr> "Naboo", "Tatooine", "Tatooine", "Tatooine", "Tatoo...
## $ species    <chr> "Droid", "Droid", "Human", "Human", "Human", "Droid...
```

```
# Find every human who either has no recorded mass, or is taller than 180 cm
sw_dup %>%
    filter(species == "Human", (is.na(mass) | height > 180)) %>%
    distinct() %>%
    glimpse()
```

```
## Observations: 15
## Variables: 10
## $ name       <chr> "Bail Prestor Organa", "Raymus Antilles", "Mon Moth...
## $ height     <int> 191, 188, 150, 167, 188, 157, 185, 182, 183, 163, N...
## $ mass       <dbl> NA, 79, NA, NA, 84, NA, 85, 77, NA, NA, NA, NA, NA,...
## $ hair_color <chr> "black", "brown", "auburn", "white", "none", "brown...
## $ skin_color <chr> "tan", "light", "fair", "fair", "dark", "light", "d...
## $ eye_color  <chr> "brown", "brown", "blue", "blue", "brown", "brown",...
## $ birth_year <dbl> 67, NA, 48, NA, 72, NA, NA, 57, 82, 72, NA, NA, NA,...
## $ gender     <chr> "male", "male", "female", "female", "male", "female...
## $ homeworld  <chr> "Alderaan", "Alderaan", "Chandrila", "Coruscant", "...
## $ species    <chr> "Human", "Human", "Human", "Human", "Human", "Human...
```

```
# Find everyone who is 100-170 cm tall
sw_dup %>%
    filter(between(height, 100, 170)) %>%
    distinct() %>%
    glimpse()
```

```
## Observations: 14
## Variables: 10
## $ name       <chr> "Leia Organa", "Mon Mothma", "Wedge Antilles", "Joc...
## $ height     <int> 150, 150, 170, 167, 112, 170, 157, 165, 170, 165, 1...
## $ mass       <dbl> 49.0, NA, 77.0, NA, 40.0, 56.2, NA, 45.0, 75.0, 75....
## $ hair_color <chr> "brown", "auburn", "brown", "white", "none", "black...
## $ skin_color <chr> "light", "fair", "fair", "fair", "grey, red", "yell...
## $ eye_color  <chr> "brown", "blue", "hazel", "blue", "orange", "blue",...
## $ birth_year <dbl> 19, 48, 21, NA, NA, 58, NA, 46, 82, 47, 72, NA, NA, NA
## $ gender     <chr> "female", "female", "male", "female", "male", "fema...
## $ homeworld  <chr> "Alderaan", "Chandrila", "Corellia", "Coruscant", "...
## $ species    <chr> "Human", "Human", "Human", "Human", "Dug", "Miriala...
```

Chapter 11

Editing and creating columns

In this chapter, we will cover how to edit columns in a dataframe and how to calculate new ones.

Mutating columns by name

Creating new columns

The function `dplyr::mutate()` is used for column creation and editing. Its use is very similar to making a named vector in base R:

```
iris %>%
    mutate(new_column = "recycle_me") %>%
    glimpse()
```

```
## Observations: 150
## Variables: 6
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ new_column   <chr> "recycle_me", "recycle_me", "recycle_me", "recycl...
```

If you provide a vector of length 1 as your new column's contents (as we did above by providing a Character vector with only 1 element), then `mutate()` will automatically recycle it. In all other cases, the contents of the new column must be as long as the number of rows:

```
iris %>%
    # Repeat the names of the months as many times as there are rows
    mutate(new_column = rep_len(month.name, length.out = n())) %>%
    #                                                     ↑
    # n() is the group size -- in an ungrouped data frame it is number of rows
    glimpse()
```

```
## Observations: 150
```

```
## Variables: 6
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ new_column   <chr> "January", "February", "March", "April", "May", "...
```

Calculating with existing columns

To use the data frame's columns for calculations or logic, just use the columns' names. `dplyr` assumes that you are referring to columns that are located in the current data frame, so there is no need to refer to the columns with `$`:

```
iris %>%
    mutate(add_all = Sepal.Length + Sepal.Width + Petal.Length + Petal.Width) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 6
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ add_all      <dbl> 10.2, 9.5, 9.4, 9.4, 10.2, 11.4, 9.7, 10.1, 8.9, ...
```

But be careful! Look at what happens if, instead of manually adding the columns together, we tried to use `sum()`:

```
iris %>%
    mutate(sum_all = sum(Sepal.Length, Sepal.Width,
                         Petal.Length, Petal.Width)) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 6
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ sum_all      <dbl> 2078.7, 2078.7, 2078.7, 2078.7, 2078.7, 2078.7, 2...
```

Since `sum()` operates on entire vectors, it has grabbed **the entire contents of the columns** and added them together, and so the result is always `2078.7` in all rows. You will use this behaviour (calculating by whole columns) quite often, so it's something to be mindful of.

Editing an existing column

To edit an existing column, just name it as the target:

```
iris %>%
    mutate(Species = str_to_upper(Species)) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 5
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <chr> "SETOSA", "SETOSA", "SETOSA", "SETOSA", "SETOSA",...
```

Mutating multiple columns at a time

You can create and edit many columns together by putting them all in the same `mutate()` call. Each column is made one-after-the-other, so you can take the contents of a just-created column and do something else with it. For example, let's do three operations:

1. Find the median length of all petals in `iris`.
2. Flag each observation `TRUE` if its petal length is longer than the median length, otherwise flag it `FALSE`.
3. Convert `TRUE/FALSE` into `1/0` by using `as.numeric()`.

```
set.seed(123)

iris %>%
    mutate(median_petal_length = median(Petal.Length),
           has_long_petals     = Petal.Length > median_petal_length,
           has_long_petals     = as.numeric(has_long_petals)) %>%
    # Shuffle the rows so you can see both TRUE/1 and FALSE/0 values
    sample_frac(size = 1.00) %>%
    select(Petal.Length, median_petal_length, has_long_petals) %>%
    head()
```

```
##   Petal.Length median_petal_length has_long_petals
## 1          1.1                4.35              0
## 2          1.4                4.35              0
## 3          6.7                4.35              1
## 4          1.3                4.35              0
## 5          5.1                4.35              1
## 6          5.2                4.35              1
```

Programatically choosing columns

In Chapter @ref{choosing-and-renaming-columns} we had the option of using `select_if()` to choose columns based on, say, whether their names contained a particular string. We have the same options in two different versions: `mutate_if()` and `mutate_at()`.

mutate_if()

With `mutate_if()`, we can apply a function to all columns **whose contents** meet a particular condition. For example, we can find all of the columns that store numbers as Double and convert them to store those numbers as Integer:

```
iris %>%
    mutate_if(is.double, as.integer) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 5
## $ Sepal.Length <int> 5, 4, 4, 4, 5, 5, 4, 5, 4, 4, 5, 4, 4, 4, 5, 5, 5...
## $ Sepal.Width  <int> 3, 3, 3, 3, 3, 3, 3, 3, 2, 3, 3, 3, 3, 3, 4, 4, 3...
## $ Petal.Length <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1...
## $ Petal.Width  <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
```

You can also provide your own functions, or write anonymous functions with convenient `purrr`-style shorthand. Let's find any Factor columns, convert them to the Character data type, and then all-caps them:

```
iris %>%
    mutate_if(is.factor,
              ~ as.character(.) %>%  # A pipeline inside a pipeline!
                  str_to_upper()
              ) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 5
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <chr> "SETOSA", "SETOSA", "SETOSA", "SETOSA", "SETOSA",...
```

mutate_at()

With `mutate_at()`, we can apply a function to all columns **whose names** meet a particular condition. One common real-world situation is when you want to convert some measurement columns between units. In `iris`, the length and width measurements were performed in centimetres, and we can convert them to millimetres without disturbing any other columns that contain numbers:

```
iris %>%
    # Add a numeric column that will not be affected by the conversion
    mutate(sample_num = row_number()) %>%
    # Convert centimetres to millimetres
    mutate_at(vars(contains("Length"), contains("Width")), ~ . * 10) %>%
    # Rename the columns to show new units. For fun, we'll use a different
    # helper function that uses regular expressions instead of literal strings.
    rename_at(vars(matches("Length|Width")), ~ paste0(., "_mm")) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 6
## $ Sepal.Length_mm <dbl> 51, 49, 47, 46, 50, 54, 46, 50, 44, 49, 54, 48...
## $ Sepal.Width_mm  <dbl> 35, 30, 32, 31, 36, 39, 34, 34, 29, 31, 37, 34...
## $ Petal.Length_mm <dbl> 14, 14, 13, 15, 14, 17, 14, 15, 14, 15, 15, 16...
## $ Petal.Width_mm  <dbl> 2, 2, 2, 2, 2, 4, 3, 2, 2, 1, 2, 2, 1, 1, 2, 4...
## $ Species         <fct> setosa, setosa, setosa, setosa, setosa, setosa...
## $ sample_num      <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,...
```

In the above example, we wrapped our 'select helper' functions `contains()` and `matches()` in another function called `vars()`. You don't need to know much about this function, expect that it allows `mutate_at()` (and `summarise_at()`, in the next chapter) to recognise and use these helper functions to pick columns.

Replacing `NA` values

There are a few functions that let use replace `NA` values in a column quite effectively. For this demonstration, we will use the built-in dataset `starwars` because it has a nice mix of `NA` values.

11.0.1 Replace all `NA` in a column with one value

If you only want to replace the NAs with the same value, then you can use `tidyr::replace_na()`. This function takes a named list of columns where `NA` should be replaced, and what value it should be replaced with:

```
starwars %>%
    replace_na(list(hair_color = "UNKNOWN",
                    birth_year = 99999)) %>%
    glimpse()
```

```
## Observations: 87
## Variables: 13
## $ name       <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", ...
## $ height     <int> 172, 167, 96, 202, 150, 178, 165, 97, 183, 182, 188...
## $ mass       <dbl> 77.0, 75.0, 32.0, 136.0, 49.0, 120.0, 75.0, 32.0, 8...
## $ hair_color <chr> "blond", "UNKNOWN", "UNKNOWN", "none", "brown", "br...
## $ skin_color <chr> "fair", "gold", "white, blue", "white", "light", "l...
## $ eye_color  <chr> "blue", "yellow", "red", "yellow", "brown", "blue",...
## $ birth_year <dbl> 19.0, 112.0, 33.0, 41.9, 19.0, 52.0, 47.0, 99999.0,...
## $ gender     <chr> "male", NA, NA, "male", "female", "male", "female",...
## $ homeworld  <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Alder...
## $ species    <chr> "Human", "Droid", "Droid", "Human", "Human", "Human...
## $ films      <list> [<"Revenge of the Sith", "Return of the Jedi", "Th...
## $ vehicles   <list> [<"Snowspeeder", "Imperial Speeder Bike">, <>, <>,...
## $ starships  <list> [<"X-wing", "Imperial shuttle">, <>, <>, "TIE Adva...
```

Fill `NA` with the last good row (or next good row)

It's not strange to meet a table like the one below, where rather than copy-paste the same data across multiple rows, they decided to leave the cells empty instead:

```
## # A tibble: 9 x 4
##   site       species       sample_num bees_present
##   <chr>      <chr>              <dbl> <lgl>
## 1 Bilpin     A. longifolia          1 TRUE
## 2 <NA>       <NA>                   2 TRUE
## 3 <NA>       <NA>                   3 TRUE
## 4 <NA>       A. elongata            1 TRUE
## 5 <NA>       <NA>                   2 FALSE
## 6 <NA>       <NA>                   3 TRUE
## 7 Grose Vale A. terminalis          1 FALSE
## 8 <NA>       <NA>                   2 FALSE
## 9 <NA>       <NA>                   3 TRUE
```

You can use `tidyr::fill()` to fill these kinds of structural `NA`s. The default behaviour is to **fill down**, taking the last non-`NA` value and dragging it into the `NA` below it:

```
gap_data %>%  # The table above, which this manual built behind-the-scenes
    fill(site, species) %>%
    print()
```

```
## # A tibble: 9 x 4
##   site       species       sample_num bees_present
##   <chr>      <chr>              <dbl> <lgl>
## 1 Bilpin     A. longifolia          1 TRUE
## 2 Bilpin     A. longifolia          2 TRUE
## 3 Bilpin     A. longifolia          3 TRUE
## 4 Bilpin     A. elongata            1 TRUE
## 5 Bilpin     A. elongata            2 FALSE
## 6 Bilpin     A. elongata            3 TRUE
## 7 Grose Vale A. terminalis          1 FALSE
## 8 Grose Vale A. terminalis          2 FALSE
## 9 Grose Vale A. terminalis          3 TRUE
```

Recoding values

You will often want to replace some values in a column. For example, you may want to change the names of your sites, or convert words like `"yes"` and `"no"` into `TRUE` and `FALSE`. There are many ways to do this in R, but we will teach you the two most versatile ones. They are 1) using `dplyr::if_else()` to choose between two alternatives, and 2) using `dplyr::case_when()` to choose between multiple alternatives.

`if_else()`

We can use `if_else()` to make yes/no decisions about what values in a column to replace. For example, let's use the built-in dataset `warpbreaks` and label the wool types, named `"A"` and `"B"`, with the breed of sheep the yarn was sheared from:

```
set.seed(123)

warpbreaks %>%
    mutate(breed = if_else(wool == "A",
                           true  = "Merino",
```

```
                            false = "Corriedale")) %>%
    sample_frac(size = 1.0) %>%  # Shuffle the rows so you can see both labels
    glimpse()
```

```
## Observations: 54
## Variables: 4
## $ breaks  <dbl> 19, 18, 15, 12, 54, 28, 21, 42, 15, 28, 15, 26, 70, 24...
## $ wool    <fct> B, A, B, A, A, B, B, B, B, A, A, A, A, B, B, A, B, B, ...
## $ tension <fct> L, M, H, M, L, M, M, M, H, H, H, H, L, H, L, L, L, L, ...
## $ breed   <chr> "Corriedale", "Merino", "Corriedale", "Merino", "Merin...
```

You may be aware that base R includes a function called `ifelse()`. The difference between `ifelse()` and `dplyr::if_else()` is that `if_else()` checks that both your true/false cases are the same data type. This ensures that you always know what your new column's type is. Here is an example of the base `ifelse()` doing something unexpected because it does not type-check:

```
iris %>%
    # 'check' will be a Double, and TRUE will be silently coerced to '1.0'.
    # If you used if_else() instead, it would stop you by raising an error.
    mutate(check = ifelse(Sepal.Length > 5, TRUE, Sepal.Length)) %>%
    glimpse()
```

```
## Observations: 150
## Variables: 6
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, s...
## $ check        <dbl> 1.0, 4.9, 4.7, 4.6, 5.0, 1.0, 4.6, 5.0, 4.4, 4.9,...
```

case_when()

To do more complicated replacements with multiple conditions, use `case_when()`. Think of it as many nested `if_else()` calls. So instead of the clumsy nested `if_else()` version:

```
warpbreaks %>%
    #                       Each new if_else() runs if the first check is FALSE
    #                                                                  ↓
    mutate(tension = if_else(tension == "H", true = "High", false =
                             if_else(tension == "M", true = "Mid", false =
                                     if_else(tension == "L",
                                             true  = "Low",
                                             false = NA_character_)))) %>%
    glimpse()
```

We get the easy-to-read `case_when()` version:

```
set.seed(123)

warpbreaks %>%
```

```
    mutate(tension = case_when(tension == "H" ~ "High",
                               tension == "M" ~ "Medium",
                               tension == "L" ~ "Low",
                                         TRUE ~ NA_character_)) %>%
    sample_frac(size = 1.0) %>%  # Shuffle the rows so you can see both labels
    glimpse()
```

```
## Observations: 54
## Variables: 3
## $ breaks  <dbl> 19, 18, 15, 12, 54, 28, 21, 42, 15, 28, 15, 26, 70, 24...
## $ wool    <fct> B, A, B, A, A, B, B, B, B, A, A, A, A, B, B, A, B, B, ...
## $ tension <chr> "Low", "Medium", "High", "Medium", "Low", "Medium", "M...
```

Some things to note about how `case_when()` works:

1. The case is provided as a two-sided formula:
    - On the left, an expression or function that returns `TRUE` or `FALSE`,
    - Then a tilde (`~`),
    - Then the result to use if the expression is `TRUE`, which can also be an expression or function.
2. Each case is evaluated from top to bottom, and the first `TRUE` condition is accepted.
3. It is good practice to have a last case to determine what happens when none of the conditions returned `TRUE`. For this we just manually return TRUE in the last case by putting `TRUE` on the left side of the formula. In our example, if a row had tension recorded as something other than `H/M/L`, the value in that row would be set to `NA_character_`.

Chapter 12

Grouping and summarising

In this chapter, we will cover how to define groups within a data frame (say, grouping the replicates of each species) and how to perform per-group calculations.

An example of groups

Let's say that we have the built-in dataset `storms`:

```
glimpse(storms)
```

```
## Observations: 10,010
## Variables: 13
## $ name        <chr> "Amy", "Amy", "Amy", "Amy", "Amy", "Amy", "Amy", "...
## $ year        <dbl> 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 19...
## $ month       <dbl> 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 7,...
## $ day         <int> 27, 27, 27, 27, 28, 28, 28, 28, 29, 29, 29, 29, 30...
## $ hour        <dbl> 0, 6, 12, 18, 0, 6, 12, 18, 0, 6, 12, 18, 0, 6, 12...
## $ lat         <dbl> 27.5, 28.5, 29.5, 30.5, 31.5, 32.4, 33.3, 34.0, 34...
## $ long        <dbl> -79.0, -79.0, -79.0, -79.0, -78.8, -78.7, -78.0, -...
## $ status      <chr> "tropical depression", "tropical depression", "tro...
## $ category    <ord> -1, -1, -1, -1, -1, -1, -1, -1, 0, 0, 0, 0, 0, 0, ...
## $ wind        <int> 25, 25, 25, 25, 25, 25, 25, 30, 35, 40, 45, 50, 50...
## $ pressure    <int> 1013, 1013, 1013, 1013, 1012, 1012, 1011, 1006, 10...
## $ ts_diameter <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA...
## $ hu_diameter <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA...
```

And we want to count the number of hurricanes that were recorded in each month between the years 2005 and 2006:

```
storms %>%
    filter(status == "hurricane", between(year, 2005, 2006)) %>%
    distinct(name, year, month) %>%
    count(year, month)  # Counts the number of rows for each year and month
```

```
## # A tibble: 8 x 3
##    year month     n
```

```
##   <dbl> <dbl> <int>
## 1  2005     7     1
## 2  2005     8     1
## 3  2005     9     5
## 4  2005    10     4
## 5  2005    12     1
## 6  2006     8     1
## 7  2006     9     2
## 8  2006    10     1
```

This is the most basic example of what a data frame group is used for. Behind the scenes, the `dplyr::count()` function is taking `storms`, grouping its rows by year and month (e.g. "all hurricanes in December 2005"), and then counting the number of rows in each group. You can build your own groups to do any calculation in the same way.

Creating your own groups

In a regular ungrouped data frame, operations like `dplyr::mutate()` are performed across every row — or to put it another way, the entire data frame is a single group, and every row belongs to it.

When a data frame is grouped, those operations are now performed separately within each group. Think of it as splitting the data frame into smaller ones, running that operation on each smaller data frame, and then putting them back together at the end.

Groups are defined using the `dplyr::group_by()` function. You can look at the groups of a data frame with `dplyr::groups()`, and `dplyr::glimpse()` also shows you the groups and how many unique combinations there are.

```
grouped_sw <-
    starwars %>%
    group_by(species, homeworld)

groups(grouped_sw)
```

```
## [[1]]
## species
##
## [[2]]
## homeworld
```

Ungrouping a data frame

You can remove all groups with `dplyr::ungroup()`, which you should do when you have finished using them.

```
grouped_sw %>%
    ungroup() %>%
    groups()
```

```
## NULL
```

Reducing a grouped data frame

One of the most common reasons for using groups is to summarise a data frame, to combine rows in some way. For these tasks, we use `dplyr::summarise()`:

```
iris %>%
    group_by(Species) %>%
    # summarise() keeps only the grouping columns and the newly-created columns.
    summarise(avg_pet_len = mean(Petal.Length),
              med_pet_len = median(Petal.Length)) %>%
    glimpse()
```

```
## Observations: 3
## Variables: 3
## $ Species     <fct> setosa, versicolor, virginica
## $ avg_pet_len <dbl> 1.462, 4.260, 5.552
## $ med_pet_len <dbl> 1.50, 4.35, 5.55
```

This function also comes with scoped variants `summarise_at()`, `summarise_if()`, and `summarise_all()`. One of the benefits of `summarise_at()` is that not only can you choose multiple columns with *select helpers*, but you can also run multiple functions on those columns by putting them into a list:

```
iris %>%
    group_by(Species) %>%
    summarise_at(vars(ends_with("Length")),
                 list(~mean(.), ~median(.), ~min(.), ~max(.))) %>%
    #                    ↑
    #      A list of anonymous functions, which are also used as column names.
    glimpse()
```

```
## Observations: 3
## Variables: 9
## $ Species             <fct> setosa, versicolor, virginica
## $ Sepal.Length_mean   <dbl> 5.006, 5.936, 6.588
## $ Petal.Length_mean   <dbl> 1.462, 4.260, 5.552
## $ Sepal.Length_median <dbl> 5.0, 5.9, 6.5
## $ Petal.Length_median <dbl> 1.50, 4.35, 5.55
## $ Sepal.Length_min    <dbl> 4.3, 4.9, 4.9
## $ Petal.Length_min    <dbl> 1.0, 3.0, 4.5
## $ Sepal.Length_max    <dbl> 5.8, 7.0, 7.9
## $ Petal.Length_max    <dbl> 1.9, 5.1, 6.9
```

```
starwars %>%
    group_by(homeworld) %>%
    # For each homeworld, return the average of any numeric column.
    summarise_if(is.numeric, ~ mean(., na.rm = TRUE)) %>%
    drop_na() %>%
    glimpse()
```

```
## Observations: 23
## Variables: 4
```

```
## $ homeworld  <chr> "Alderaan", "Bespin", "Cerea", "Concord Dawn", "Cor...
## $ height     <dbl> 176.3333, 175.0000, 198.0000, 183.0000, 175.0000, 1...
## $ mass       <dbl> 64.00000, 79.00000, 82.00000, 79.00000, 78.50000, 5...
## $ birth_year <dbl> 43.00000, 37.00000, 92.00000, 66.00000, 25.00000, 9...
```

Groups are dropped with every summary

When you do a `summarise()` operation, what happens to the groups?

```
starwars %>%
    group_by(species, homeworld, hair_color) %>%
    summarise_if(is.numeric, ~ mean(., na.rm = TRUE)) %>%
    glimpse()
```

```
## Observations: 69
## Variables: 6
## Groups: species, homeworld [58]
## $ species    <chr> "Aleena", "Besalisk", "Cerean", "Chagrian", "Clawdi...
## $ homeworld  <chr> "Aleen Minor", "Ojom", "Cerea", "Champala", "Zolan"...
## $ hair_color <chr> "none", "none", "white", "none", "blonde", NA, NA, ...
## $ height     <dbl> 79.0000, 198.0000, 198.0000, 196.0000, 168.0000, 96...
## $ mass       <dbl> 15.0, 102.0, 82.0, NaN, 55.0, 32.0, 53.5, 140.0, 40...
## $ birth_year <dbl> NaN, NaN, 92.0, NaN, NaN, 33.0, 112.0, 15.0, NaN, 8...
```

Although we defined 3 groups, only 2 are shown by `glimpse()`. This is because all the replicate cases of `species × homeworld × hair_color` have been summarised into a single row each, and so `hair_color` is no longer meaningful as a grouping variable. If we ever needed to, we could run several `summarise()` calls in a row, each one progressively 'rolling-up' the table until no groups remained.

Reducing an ungrouped data frame

You can also use `summarise()` on an ungrouped data frame. It will combine every row and drop everything except the new values:

```
starwars %>%
    summarise_if(is.numeric, ~ mean(., na.rm = TRUE)) %>%
    glimpse()
```

```
## Observations: 1
## Variables: 3
## $ height     <dbl> 174.358
## $ mass       <dbl> 97.31186
## $ birth_year <dbl> 87.56512
```

Mutating within groups

If you do not want to remove rows with `summarise()`, then you can use `dplyr::mutate()` and its variants instead. Remember that for grouped data frames, operations like `mutate()` are applied separately to each group and not to the entire data frame as a whole. We can illustrate it with the built-in dataset `warpbreaks`:

```r
# Without groups.
# Every row of 'breaks' was averaged, so 'avg' is always the same result.
warpbreaks %>%
    mutate(avg = mean(breaks)) %>%
    distinct(wool, tension, avg) %>%  # Drop rows so that the pattern is obvious.
    head()
```

```
##   wool tension      avg
## 1    A       L 28.14815
## 2    A       M 28.14815
## 3    A       H 28.14815
## 4    B       L 28.14815
## 5    B       M 28.14815
## 6    B       H 28.14815
```

```r
# With groups.
# 'breaks' was averaged separately for every wool type and tension.
warpbreaks %>%
    group_by(wool, tension) %>%
    mutate(avg = mean(breaks)) %>%
    distinct(wool, tension, avg) %>%  # Drop rows so that the pattern is obvious.
    head()
```

```
## # A tibble: 6 x 3
## # Groups:   wool, tension [6]
##   wool  tension   avg
##   <fct> <fct>   <dbl>
## 1 A     L        44.6
## 2 A     M        24
## 3 A     H        24.6
## 4 B     L        28.2
## 5 B     M        28.8
## 6 B     H        18.8
```

Chapter 13

Graphing with ggplot2

In this chapter, we will visit `ggplot2` and learn how to build graphs by layering data and graphical elements together.

We strongly recommend that you find and use the `ggplot2` cheatsheet available at <https://www.rstudio.com/resources/cheatsheets/>. It includes information about many aspects of `ggplot2`, including previews of all the geometries available to you and what kinds of input data they need.

The 'grammar of graphics'

The graphing package `ggplot2` is based on a concept of graphics design laid out in a book called *The Grammar of Graphics* (Leland Wilkinson et al) and expanded on as the *Layered* Grammar of Graphics by Hadley Wickham.

The short version of these concepts is that a data graphic is built by layering 5 elements:

1. The **data set**, which has been cleaned and transformed as needed.
2. The data points are represented as **geometric objects** such as circles, squares, or lines.
3. These objects are positioned in a **coordinate system** and **scale**. For a typical graph, the coordinate system is Cartesian (X-Y axes on a 2D plane), but the axes themselves (the scales) can be discrete or continuous or logarithmic.
4. The geometric objects are modified by *mapping data variables* to **aesthetic properties**. For example, points from different groups can be plotted using different colours or shapes.
5. **Annotations** that label these elements.

Let us build a graphic by layering these elements. We will use the built-in dataset `mtcars` as the data set:

```
library(tidyverse)
library(ggplot2)

my_dataset <-
    mtcars %>%
    # In mtcars, the car model is used as the row name. We don't use row names
    # in 'tidy' data, so we need to put them into a column.
    tibble::rownames_to_column("car") %>%
    mutate_at(vars(car, cyl, vs:carb), as.factor) %>%
    glimpse()
```

```
## Observations: 32
## Variables: 12
## $ car  <fct> Mazda RX4, Mazda RX4 Wag, Datsun 710, Hornet 4 Drive, Hor...
## $ mpg  <dbl> 21.0, 21.0, 22.8, 21.4, 18.7, 18.1, 14.3, 24.4, 22.8, 19....
## $ cyl  <fct> 6, 6, 4, 6, 8, 6, 8, 4, 4, 6, 6, 8, 8, 8, 8, 8, 8, 4, 4, ...
## $ disp <dbl> 160.0, 160.0, 108.0, 258.0, 360.0, 225.0, 360.0, 146.7, 1...
## $ hp   <dbl> 110, 110, 93, 110, 175, 105, 245, 62, 95, 123, 123, 180, ...
## $ drat <dbl> 3.90, 3.90, 3.85, 3.08, 3.15, 2.76, 3.21, 3.69, 3.92, 3.9...
## $ wt   <dbl> 2.620, 2.875, 2.320, 3.215, 3.440, 3.460, 3.570, 3.190, 3...
## $ qsec <dbl> 16.46, 17.02, 18.61, 19.44, 17.02, 20.22, 15.84, 20.00, 2...
## $ vs   <fct> 0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, ...
## $ am   <fct> 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, ...
## $ gear <fct> 4, 4, 4, 3, 3, 3, 3, 4, 4, 4, 4, 3, 3, 3, 3, 3, 3, 4, 4, ...
## $ carb <fct> 4, 4, 1, 1, 2, 1, 4, 2, 2, 4, 4, 3, 3, 3, 4, 4, 4, 1, 2, ...
```

Now we can layer the graph. Note that `ggplot2` has its own pipeline, except that it uses the `+` operator instead of `%>%` (`ggplot2` was written first, so the pipeline concept in R was still being worked out).

```
my_ggplot <-
        # 1. Add the data set.
    ggplot(data = my_dataset) +
        # 2. Add the coordinate system and scales.
    coord_cartesian() +
    scale_x_continuous() +
    scale_y_continuous() +
        # 3. Add geometric objects. Here, we add dots to show each data point,
        #    and then add a smoothed line calculated with a linear model.

        # 4. Aesthetic properties are mapped in the aes() function. We map the x
        #    position to 'disp', the y position to 'wt', and the colour of the
        #    points to 'cyl'.
    geom_point(mapping  = aes(x = disp, y = wt,  colour = cyl)) +
        # To change an aesthetic without mapping it to data, set it outside aes().
        #                                                 ↓
    geom_smooth(mapping = aes(x = disp, y = wt), linetype = "dashed", method = "lm") +
        # 5. Add annotations. You can also annotate points in the graph.
    labs(x = "Displacement (cubic inches)",
         y = "Weight (1000 pounds)",
         title = "Relationship between a car's displacement and weight",
         subtitle = "Source: Motor Trend US, 1974") +
        # A large part of ggplots is that they are very customisable with
        # themes. We will use this minimal built-in theme.
    theme_minimal()

# Print the plot
my_ggplot
```

A `ggplot()` call need not be as complicated as this. The package has many sane defaults, such as Cartesian coordinates and auto-detection of scale types. For example, let's try a discrete scale on the X axis and a continuous scale on the Y axis:

```
ggplot(data = my_dataset, mapping = aes(x = cyl, y = mpg)) +
    #                               ↑
```

```
    # Aesthetics in the ggplot() call are used as the defaults for geoms.
    geom_violin() +
    geom_jitter(width = 0.025, height = 0, alpha = 0.25) +
    labs(x = "Number of cylinders",
         y = "Miles per gallon",
         title = "Mileage of cars by cylinder count",
         subtitle = "Source: Motor Trend US, 1974") +
    theme_minimal()
```

As you can see, layering different geoms together gives you a lot of flexibility in the type of graphic you can make. The 'ggplot2 cheatsheet at the start of this chapter shows you the geoms that are available to you and what kinds of data they accept.

Tidy data is incredibly important for ggplot2

Many issues that

Faceting a plot into sub-plots

Sometimes there are many dimensions of data that you would like to present in one plot, and they become muddled if they are visualised together:

```
yarn_plot <-
    ggplot(warpbreaks, aes(x = breaks, linetype = wool, colour = tension)) +
    geom_density(aes(y = stat(density)), size = 1) +
    theme_bw() +
    theme(legend.position = "top")

yarn_plot
```

In these cases, it is useful to break the plot into several smaller sub-plots. There are two functions that do this for you. First, `ggplot2::facet_grid()` lets you create a regular grid:

```
yarn_plot +
    facet_grid(wool ~ tension)
```

```
    #            ↑
    # Formula interface: Rows ~ Columns.
```

```
yarn_plot +
    facet_grid(. ~ tension)
```

```
    #          ↑
    # Use 'dot' to mean "no facetting"
```

If you do not want to create a regular grid, `ggplot2::facet_wrap()` creates each facet independently and stacks them next to each other to fill the plotting space.

```
yarn_plot +
    facet_wrap(wool ~ tension)
```

Making plots interactive with plotly

Finally, a great way to explore a new dataset is to make your ggplot interactive by wrapping it in plotly::ggplotly(). This means that you can hover over points and lines to get information about that data point, zoom or rescale the axes, and hide or isolate groups. This interactivity can't be shown in a PDF file, but a document knitted to an HTML page will preserve the interactive components and allow your collaborators to explore your graph.

```
library(plotly)

ggplotly(yarn_plot)
```

Chapter 14

Modelling

In this chapter, we will cover statistical modelling in the Tidyverse. This chapter will not teach you how to construct or evaluate models, but instead it will focus on how to do those things within the Tidyverse philosophy.

Modelling is generally unchanged

For the most part, you will be using Tidyverse packages to clean, reshape, and summarise your raw data before feeding the entire dataset into your modelling functions. This means that in general, you will do your modelling the same way as you always have:

```
fitted_model <-
    iris %>%
    lm(Sepal.Length ~ Petal.Length, data = .)

plot(Sepal.Length ~ Petal.Length, data = iris)
abline(fitted_model, col = "tomato")
```

The key changes in modelling are that it is now easier to extract model information (with the `broom` package) and fit models within groups. The package `parsnip` (still in development) provides a consistent and pipeline-friendly interface for several modelling packages. However, due to time constraints, we leave it to the student to explore this package if needed.

Extract model data

There are 3 kinds of information that you may want to get out of a fitted model, and so there are three different functions provided by `broom` to do it. They are:

1. *Add model information to an existing data frame with* `broom::augment()`.
   This includes predictions (fitted values), residuals, and standard errors.
2. *Create a new data frame of model summary information with* `broom::glance()`.
   These are R-squared, p-value, log-likelihood, AIC and BIC, and others.
3. *Create a new data frame of model components with* `tidy()`.
   This is the stuff you would use `summary()` to look at: variables and their associated estimates, test statistics, and p-value.

As an example, we will use the built-in dataset `mtcars` which contains two columns, `disp` (cubic inches of displacement, a measure of the car's volume) and `wt` (weight in thousands of pounds). Larger cars probably weigh more, so we will model that:

```
library(broom)

# Build the model
fitted_model <-
    mtcars %>%
    lm(disp ~ wt, data = .)


# Look at the model's goodness-of-fit
fitted_model %>%
    glance() %>%
    glimpse()
```

```
## Observations: 1
## Variables: 11
## $ r.squared     <dbl> 0.7885083
## $ adj.r.squared <dbl> 0.7814586
## $ sigma         <dbl> 57.93937
## $ statistic     <dbl> 111.8496
## $ p.value       <dbl> 1.22232e-11
## $ df            <int> 2
## $ logLik        <dbl> -174.2741
## $ AIC           <dbl> 354.5482
## $ BIC           <dbl> 358.9455
## $ deviance      <dbl> 100709.1
## $ df.residual   <int> 30
```

```
# Look at the model's summary
fitted_model %>%
    tidy()
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)    -131.      35.7     -3.67 9.33e- 4
## 2 wt              112.      10.6     10.6  1.22e-11
```

```
# Plot the residuals
fitted_model %>%
    augment() %>%                # Get the fitted values and residuals
    plot(.resid ~ wt, data = .)  # Plot the residuals
```

`broom` does not support mixed models. For those, use the package `broom.mixed` instead.

Running a model within each group

There may be some cases where you would like to run a model separately within each group. Perhaps you would like to run a model for each site individually, or perhaps you are running a bootstrap analysis with `rsample`. In these cases, the basic workflow is this:

1. Group the data frame with `dplyr::group_by()` into whatever strata you like.
2. Collapse the data frame using `tidyr::nest()`, which will create **a column of data frames**, each holding the raw data for that strata.
3. Use `dplyr::mutate()` and `purrr::map()` to create a new column that holds the model objects.

Nesting a data frame inside a data frame?

Yes, a data frame (specifically, a `tibble`, which is the Tidyverse's modern data frame type) can have a column that is typed as a List. In R, a List can hold any object:

```
tibble(my_list_col = list(1:5, rnorm(10), month.name, iris),
       strings = c("This", "column", "has", "strings"))
```

```
## # A tibble: 4 x 2
##   my_list_col        strings
##   <list>             <chr>
## 1 <int [5]>          This
## 2 <dbl [10]>         column
## 3 <chr [12]>         has
## 4 <df[,5] [150 x 5]> strings
```

The benefit of holding data frames and model objects inside a data frame is that your dataset stays together and can be subsetted as a single unit.

14.0.1 An example of nesting and modelling

We'll use the built-in dataset `mtcars` again. Imagine that we have data from 32 cars about how far they can travel on one gallon of fuel (miles per gallon, in the `mpg` column). We would like to use that information to predict how quickly the car can travel a quarter mile (the `qsec` column), but we would like to run the model separately for cars that have 4, 6, and 8 cylinders (the `cyl` column). First, we need to nest the data by `cyl`.

```
nested_mtcars <-
    mtcars %>%          # In mtcars...
    group_by(cyl) %>%   # Group the data by cylinder count...
    nest()              # And nest the data frames

nested_mtcars
```

```
## # A tibble: 3 x 2
##     cyl data
##   <dbl> <list>
## 1     6 <tibble [7 x 10]>
## 2     4 <tibble [11 x 10]>
## 3     8 <tibble [14 x 10]>
```

We now have a data frame with other data frames nested inside them. All of those new data frames are held in the column `data`, and they hold all of the rows where `cyl == 2`, `cyl == 4`, and `cyl == 8`. You can inspect them like this:

```
nested_mtcars$data[[2]] %>%  # The data for cyl == 4
    glimpse()
```

```
## Observations: 11
## Variables: 10
## $ mpg  <dbl> 22.8, 24.4, 22.8, 32.4, 30.4, 33.9, 21.5, 27.3, 26.0, 30....
## $ disp <dbl> 108.0, 146.7, 140.8, 78.7, 75.7, 71.1, 120.1, 79.0, 120.3...
## $ hp   <dbl> 93, 62, 95, 66, 52, 65, 97, 66, 91, 113, 109
## $ drat <dbl> 3.85, 3.69, 3.92, 4.08, 4.93, 4.22, 3.70, 4.08, 4.43, 3.7...
## $ wt   <dbl> 2.320, 3.190, 3.150, 2.200, 1.615, 1.835, 2.465, 1.935, 2...
## $ qsec <dbl> 18.61, 20.00, 22.90, 19.47, 18.52, 19.90, 20.01, 18.90, 1...
## $ vs   <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1
## $ am   <dbl> 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1
## $ gear <dbl> 4, 4, 4, 4, 4, 4, 3, 4, 5, 5, 4
## $ carb <dbl> 1, 2, 2, 1, 2, 1, 1, 1, 2, 2, 2
```

Now, we must fit the linear models and hold their results in a new column. Since we are creating a new column, we can use `dplyr::mutate()`. Since we want to *iterate* over the contents of a column and run a function on each element, we can use `purrr::map()`:

```
nested_mtcars <-
    nested_mtcars %>%  # Nested data frames are held in the 'data' column.
    mutate(model = map(data,                        # For every df in 'data'...
                       ~ lm(qsec ~ mpg, data = .))) # Fit this model to it.

nested_mtcars
```

```
## # A tibble: 3 x 3
##     cyl data              model
##   <dbl> <list>            <list>
## 1     6 <tibble [7 x 10]> <lm>
## 2     4 <tibble [11 x 10]> <lm>
## 3     8 <tibble [14 x 10]> <lm>
```

We've created a new column, `model`, that holds the `lm` object that `lm()` returns. To extract the fitted values from it, we can run `broom::augment()` on the `model` column in the exact same way:

```
nested_mtcars <-
    nested_mtcars %>%
    mutate(fitted = map(model, augment))

nested_mtcars
```

```
## # A tibble: 3 x 4
##     cyl data              model  fitted
##   <dbl> <list>            <list> <list>
## 1     6 <tibble [7 x 10]> <lm>   <tibble [7 x 9]>
## 2     4 <tibble [11 x 10]> <lm>   <tibble [11 x 9]>
## 3     8 <tibble [14 x 10]> <lm>   <tibble [14 x 9]>
```

To summarise, we have the groups we set (`cyl`), the data within each group (`data`), the linear model that was fitted to each group's data (`model`), and the fitted values and residuals that were generated by the model (`fitted`).

It time to actually do something with the model information, and we can do that by unnesting the data frame with `tidyr::unnest()`. Unnesting will expand the nested data frames into full rows:

```
modelled_mtcars <-
    nested_mtcars %>%
    unnest(fitted) %>%  # Expand the data frames in the 'fitted' column.
    glimpse()
```

```
## Observations: 32
## Variables: 10
## $ cyl        <dbl> 6, 6, 6, 6, 6, 6, 6, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, ...
## $ qsec       <dbl> 16.46, 17.02, 19.44, 20.22, 18.30, 18.90, 15.50, 18...
## $ mpg        <dbl> 21.0, 21.0, 21.4, 18.1, 19.2, 17.8, 19.7, 22.8, 24....
## $ .fitted    <dbl> 17.35903, 17.35903, 17.16235, 18.78491, 18.24406, 1...
## $ .se.fit    <dbl> 0.8782378, 0.8782378, 1.0180453, 1.0127659, 0.69202...
## $ .resid     <dbl> -0.89902637, -0.33902637, 2.27764706, 1.43509128, 0...
## $ .hat       <dbl> 0.26752310, 0.26752310, 0.35947712, 0.35575840, 0.1...
## $ .sigma     <dbl> 1.824292, 1.888034, 1.256631, 1.674727, 1.898148, 1...
## $ .cooksd    <dbl> 0.0698916515, 0.0099391078, 0.7882824181, 0.3061425...
## $ .std.resid <dbl> -0.61864851, -0.23329478, 1.67605247, 1.05298855, 0...
```

And now we can do stuff with it, like mutate it further or plot it.

```
library(ggplot2)

for_plotting <-
    modelled_mtcars %>%
    select(cyl:.fitted) %>%
    gather(data_source, qmile, qsec, .fitted) %>%
    mutate(data_source =
               if_else(data_source == "qsec", "Observed", "Modelled")) %>%
    glimpse()
```

```
## Observations: 64
## Variables: 4
## $ cyl         <dbl> 6, 6, 6, 6, 6, 6, 6, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4,...
## $ mpg         <dbl> 21.0, 21.0, 21.4, 18.1, 19.2, 17.8, 19.7, 22.8, 24...
## $ data_source <chr> "Observed", "Observed", "Observed", "Observed", "O...
## $ qmile       <dbl> 16.46, 17.02, 19.44, 20.22, 18.30, 18.90, 15.50, 1...
```

```
ggplot(data = for_plotting) +
    geom_point(aes(x = mpg, y = qmile, colour = data_source)) +
    facet_grid(cyl ~ .) +
    labs(x = "Miles per gallon", y = "Seconds to travel 1/4 mile") +
    theme_bw()
```

Chapter 15

Appendix

This document was last compiled on 27 June 2019.

Packages used in this manual

Package	Description	Version used in this manual
tidyverse	Installs core Tidyverse packages (partial list below).	1.2.1
→ broom	Turning model results into data frames.	0.5.1
→ dplyr	Manipulating, grouping, calculating on data frames.	0.8.1.9000
→ forcats	Convenience factors for factors.	0.4.0
→ ggplot2	Extensible graphing from tidy data.	3.1.0
→ haven	Convert SPSS/SAS/Stata files to data frames.	2.1.0
→ hms	Data class for time data.	0.4.2
→ lubridate	Maths with dates and times.	1.7.4
→ magrittr	Provides pipes (`%>%` and others).	1.5
→ modelr	Modelling inside a pipeline.	0.1.4
→ purrr	Iteration and functional programming.	0.3.2
→ readr	Read rectangular data (delimited text files, .CSV, etc.)	1.3.1
→ readxl	Read data from Excel (.XLS and .XLSX).	1.3.0
→ stringr	String matching/editing with regular expressions.	1.4.0
→ tibble	Modern update to base R's data frames.	2.1.3
→ tidyr	Reshaping data into tidy format.	0.8.3
here	Access project-root from anywhere.	0.1
janitor	Data frame convenience functions.	1.2.0
usethis	Used to download course materials for this workshop.	1.5.0
ViewPipeSteps	Show what each pipeline step does to the data.	0.1.0

Datasets used

'Wood Blocks' dataset is used with the permission of Jeff Powell and collaborators.

'Insect Light Trap' dataset is from the University of Copenhagen, in the Public Domain.
<https://www.kaggle.com/University-of-Copenhagen/insect-light-trap>

'Mongolia Livestock' dataset is from Robert Ritz, licensed under CC BY-SA 4.0.
<https://www.kaggle.com/robertritz/domesticated-animals-in-mongolia-19702017>