

Lab 02: Data and Reproducibility

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! Due date

This lab is due on **Monday, September 22 at 11:59pm**. To be considered on time, the following must be done by the due date:

- Final `.pdf` file submitted on Gradescope

Introduction

The main goal is to learn data processing using tidyverse and introduce you to version control using Github.

Learning goals

By the end of the lab, you will learn:

1. Tidyverse basics
2. Data wrangling with dplyr
3. Data tidying with tidyr

The tidyverse

A whole “universe” of functions within R

- The most powerful, intuitive, and popular approach to data cleaning, wrangling, and visualization in R

Advantages:

- Consistent philosophy and syntax
- “Verb” based approach makes it more familiar to users of Stata/SAS/SPSS
- Serves as the front-end for many other big data and ML tools

Tidying Data

The two most important properties of tidy data are:

1. Each column is a unique variable.
2. Each row is a single observation.

[Image is from “[R for Data Science](#)” by Hadley Wickham & Garrett Grolemund, used under [CC BY-NC-ND 3.0](#)]

Tidy data is easier to work with, because you have a consistent way of referring to variables and observations. It then becomes easy to manipulate, visualize, and model.

Wide vs. Long Formats

Both of these data sets display information on heart rate observed in individuals across 3 different time periods:

	name	time1	time2	time3
1	Wilbur	67	56	70
2	Petunia	80	90	67
3	Gregory	64	50	101

	name	time	heartrate
1	Wilbur	1	67
2	Petunia	1	80
3	Gregory	1	64
4	Wilbur	2	56
5	Petunia	2	90
6	Gregory	2	50
7	Wilbur	3	70
8	Petunia	3	67
9	Gregory	3	10

Which dataframe is in *tidy* format?

Wide data:

- Row = patient. Columns = repeated observations over time.
- Often easier to take in at a glance (as in a spreadsheet).

Long data:

- Row = one observation. Columns = ID variables + observed variable.
- Usually easier to clean, merge with other data, and avoid errors.

Tidy data is more likely to be **long**.

- Most R packages have been written assuming your data is in long format.

“Tidy datasets are all alike but every messy dataset is messy in its own way.”

– Hadley Wickham

Tidyverse packages

We need to install and load a couple of packages. Run these preliminaries:

```
# load and install package if necessary
if (!require("pacman")) install.packages("pacman")
pacman::p_load(
  tidyverse,
  nycflights13
)
```

We see that we have actually loaded a number of packages (which could also be loaded individually): **ggplot2**, **tibble**, **dplyr**, etc. - We can also see information about the package versions and some [namespace conflicts](#).

The tidyverse actually comes with a lot more packages than those that are just loaded automatically.

```
tidyverse_packages()
```

```
[1] "broom"          "conflicted"    "cli"           "dbplyr"
[5] "dplyr"          "dtplyr"        "forcats"       "ggplot2"
[9] "googledrive"    "googlesheets4" "haven"         "hms"
[13] "httr"           "jsonlite"      "lubridate"     "magrittr"
[17] "modelr"         "pillar"        "purrr"         "ragg"
[21] "readr"          "readxl"        "reprex"        "rlang"
[25] "rstudioapi"     "rvest"         "stringr"       "tibble"
[29] "tidyr"          "xml2"          "tidyverse"
```

All of these are super useful

- **lubridate** helps us work with dates
- **rvest** is for webscraping

This labs will focus on two that are automatically loaded: **dplyr** and **tidyr**.

Pipes: |> or %>%

Pipes take the **output** of one function and feed it into the **first argument** of the next (which you then skip).

`dataframe |> filter(condition)` is equivalent to `filter(dataframe, condition)`.

Note: |> on these slides is generated by the two characters | >, without the space.

Older version of the pipe: %>% * From the **magrittr** package loaded with the tidyverse *
Works identically to |> in most situations.

Keyboard shortcut: Ctl/Cmd + Shift + M

- Have to turn on a setting in RStudio options to make |> the default

Pipes can dramatically improve the experience of reading and writing code. Compare:

```
## These next two lines of code do exactly the same thing.
```

```
mpg |> filter(manufacturer=="audi") |>  
  group_by(model) |>  
  summarize(hwy_mean = mean(hwy))
```

```
# A tibble: 3 x 2  
  model      hwy_mean  
  <chr>      <dbl>  
1 a4         28.3  
2 a4 quattro  25.8  
3 a6 quattro  24
```

```
summarize(group_by(filter(mpg, manufacturer=="audi"), model), hwy_mean = mean(hwy))
```

```
# A tibble: 3 x 2  
  model      hwy_mean  
  <chr>      <dbl>  
1 a4         28.3
```

```
2 a4 quattro      25.8
3 a6 quattro      24
```

The first line reads from left to right, exactly how you think about the operations.

The second line totally inverts this logical order (the final operation comes first!)

Best practice is to put each function on its own line and indent. Look how much more readable this is:

```
mpg |>
  filter(manufacturer == "audi") |>
  group_by(model) |>
  summarize(hwy_mean = mean(hwy))
```

```
# A tibble: 3 x 2
  model      hwy_mean
  <chr>      <dbl>
1 a4         28.3
2 a4 quattro  25.8
3 a6 quattro  24
```

Vertical space costs nothing and makes for much more readable/writable code than cramming things horizontally.

All together, this multi-line line of code is called a **pipeline**.

Key dplyr verbs

There are five key dplyr verbs that you need to learn.

1. **filter**: Filter (i.e. subset) rows based on their values.
2. **arrange**: Arrange (i.e. reorder) rows based on their values.
3. **select**: Select (i.e. subset) columns by their names:
4. **mutate**: Create new columns.
5. **summarize**: Collapse multiple rows into a single summary value.

Let's practice these functions together using the **starwars** data frame that comes pre-packaged with dplyr.

Exercise 1: dplyr::filter

We can chain multiple filter commands with the pipe (`|>`), or just separate them within a single filter command using commas.

```
starwars |>
  filter(
    species == "Human",
    height >= 190
  )
```

```
# A tibble: 4 x 14
  name      height  mass hair_color skin_color eye_color birth_year sex  gender
  <chr>      <int> <dbl> <chr>      <chr>      <chr>      <dbl> <chr> <chr>
1 Darth Va~    202   136 none       white      yellow      41.9 male  mascu~
2 Qui-Gon ~    193    89 brown      fair       blue        92  male  mascu~
3 Dooku        193    80 white      fair       brown      102  male  mascu~
4 Bail Pre~    191   NA black      tan        brown       67  male  mascu~
# i 5 more variables: homeworld <chr>, species <chr>, films <list>,
#   vehicles <list>, starships <list>
```

Regular expressions work well too.

```
starwars |>
  filter(str_detect(name, "Skywalker"))
```

```
# A tibble: 3 x 14
  name      height  mass hair_color skin_color eye_color birth_year sex  gender
  <chr>      <int> <dbl> <chr>      <chr>      <chr>      <dbl> <chr> <chr>
1 Luke Sky~    172    77 blond      fair       blue        19  male  mascu~
2 Anakin S~    188    84 blond      fair       blue      41.9 male  mascu~
3 Shmi Sky~    163   NA black      fair       brown       72  fema~ femin~
# i 5 more variables: homeworld <chr>, species <chr>, films <list>,
#   vehicles <list>, starships <list>
```

A very common filter use case is identifying (or removing) missing data cases.

```
starwars |>
  filter(is.na(height))
```

```
# A tibble: 6 x 14
  name      height  mass hair_color skin_color eye_color birth_year sex  gender
  <chr>      <int> <dbl> <chr>      <chr>      <chr>      <dbl> <chr> <chr>
1 Arvel Cr~    NA     NA brown      fair        brown         NA male  mascu~
2 Finn         NA     NA black     dark        dark         NA male  mascu~
3 Rey          NA     NA brown     light       hazel         NA fema~ femin~
4 Poe Dame~    NA     NA brown     light       brown         NA male  mascu~
5 BB8          NA     NA none      none        black         NA none  mascu~
6 Captain ~    NA     NA none      none        unknown       NA fema~ femin~
# i 5 more variables: homeworld <chr>, species <chr>, films <list>,
#   vehicles <list>, starships <list>
```

To remove missing observations, simply use negation: `filter(!is.na(height))`.
Try this yourself.

```
clean_starwars<-starwars |>
  filter(is.na(height))
clean_starwars
```

```
# A tibble: 6 x 14
  name      height  mass hair_color skin_color eye_color birth_year sex  gender
  <chr>      <int> <dbl> <chr>      <chr>      <chr>      <dbl> <chr> <chr>
1 Arvel Cr~    NA     NA brown      fair        brown         NA male  mascu~
2 Finn         NA     NA black     dark        dark         NA male  mascu~
3 Rey          NA     NA brown     light       hazel         NA fema~ femin~
4 Poe Dame~    NA     NA brown     light       brown         NA male  mascu~
5 BB8          NA     NA none      none        black         NA none  mascu~
6 Captain ~    NA     NA none      none        unknown       NA fema~ femin~
# i 5 more variables: homeworld <chr>, species <chr>, films <list>,
#   vehicles <list>, starships <list>
```

Exercise 2: dplyr::arrange

`arrange` sorts your data frame by a particular column (numerically, or alphabetically)

```
starwars |>
  arrange(birth_year)
```

```
# A tibble: 87 x 14
  name      height  mass hair_color skin_color eye_color birth_year sex  gender
```

```

      <chr>      <int> <dbl> <chr>      <chr>      <chr>      <dbl> <chr> <chr>
1 Wicket ~      88  20   brown      brown      brown          8   male  mascu~
2 IG-88         200 140   none       metal       red           15   none  mascu~
3 Luke Sk~     172  77   blond      fair        blue          19   male  mascu~
4 Leia Or~     150  49   brown      light       brown          19   fema~  femin~
5 Wedge A~     170  77   brown      fair        hazel          21   male  mascu~
6 Plo Koon     188  80   none       orange      black          22   male  mascu~
7 Biggs D~     183  84   black      light       brown          24   male  mascu~
8 Han Solo     180  80   brown      fair        brown          29   male  mascu~
9 Lando C~     177  79   black      dark        brown          31   male  mascu~
10 Boba Fe~    183  78.2 black      fair        brown          31.5 male  mascu~
# i 77 more rows
# i 5 more variables: homeworld <chr>, species <chr>, films <list>,
#   vehicles <list>, starships <list>

```

We can also arrange items in descending order using `arrange(desc())`.

```

starwars |>
  arrange(desc(birth_year))

```

```

# A tibble: 87 x 14
   name      height  mass hair_color skin_color eye_color birth_year sex  gender
   <chr>      <int> <dbl> <chr>      <chr>      <chr>      <dbl> <chr> <chr>
1 Yoda         66    17 white      green      brown        896 male  mascu~
2 Jabba D~    175  1358 <NA>      green-tan~ orange        600 herm~  mascu~
3 Chewbac~    228   112 brown      unknown    blue         200 male  mascu~
4 C-3PO       167    75 <NA>      gold       yellow        112 none  mascu~
5 Dooku       193    80 white      fair       brown        102 male  mascu~
6 Qui-Gon~    193    89 brown      fair       blue          92 male  mascu~
7 Ki-Adi-~    198    82 white      pale       yellow        92 male  mascu~
8 Finis V~    170    NA blond     fair       blue          91 male  mascu~
9 Palpati~    170    75 grey      pale       yellow        82 male  mascu~
10 Cliegg ~    183    NA brown     fair       blue          82 male  mascu~
# i 77 more rows
# i 5 more variables: homeworld <chr>, species <chr>, films <list>,
#   vehicles <list>, starships <list>

```

Exercise 3: `dplyr::select`

Use commas to select multiple columns out of a data frame. (You can also use “first:last” for consecutive columns). Deselect a column with “-”.


```
starwars |>
  select(name:skin_color, species, -height)
```

```
# A tibble: 87 x 5
  name          mass hair_color skin_color species
  <chr>         <dbl> <chr>      <chr>      <chr>
1 Luke Skywalker 77 blond     fair       Human
2 C-3PO          75 <NA>       gold       Droid
3 R2-D2          32 <NA>       white, blue Droid
4 Darth Vader    136 none      white      Human
5 Leia Organa    49 brown     light      Human
6 Owen Lars     120 brown, grey light      Human
7 Beru Whitesun Lars 75 brown     light      Human
8 R5-D4          32 <NA>       white, red Droid
9 Biggs Darklighter 84 black     light      Human
10 Obi-Wan Kenobi 77 auburn, white fair       Human
# i 77 more rows
```

You can also rename some (or all) of your selected variables in place.

```
starwars |>
  select(alias=name, planet=homeworld)
```

```
# A tibble: 87 x 2
  alias          planet
  <chr>         <chr>
1 Luke Skywalker Tatooine
2 C-3PO          Tatooine
3 R2-D2          Naboo
4 Darth Vader    Tatooine
5 Leia Organa    Alderaan
6 Owen Lars     Tatooine
7 Beru Whitesun Lars Tatooine
8 R5-D4          Tatooine
9 Biggs Darklighter Tatooine
10 Obi-Wan Kenobi Stewjon
# i 77 more rows
```

If you just want to rename columns without subsetting them, you can use `rename`. Try this!

```
starwars_rename<-starwars |>
  rename(alias=name)
names(starwars_rename)
```

```
[1] "alias"      "height"     "mass"       "hair_color" "skin_color"
[6] "eye_color"  "birth_year" "sex"        "gender"     "homeworld"
[11] "species"   "films"      "vehicles"   "starships"
```

The `select(contains(PATTERN))` option provides a nice shortcut in relevant cases.

```
starwars |>
  select(name, contains("color"))
```

```
# A tibble: 87 x 4
  name          hair_color skin_color eye_color
  <chr>         <chr>      <chr>    <chr>
1 Luke Skywalker blond      fair     blue
2 C-3PO         <NA>       gold     yellow
3 R2-D2         <NA>       white, blue red
4 Darth Vader   none       white     yellow
5 Leia Organa   brown     light     brown
6 Owen Lars     brown, grey light     blue
7 Beru Whitesun Lars brown     light     blue
8 R5-D4         <NA>       white, red red
9 Biggs Darklighter black     light     brown
10 Obi-Wan Kenobi auburn, white fair     blue-gray
# i 77 more rows
```

Some other selection helpers: `starts_with()`, `ends_with()`, `all_of(c("name1", "name2"))`, `matches()`.

Exercise 4: `dplyr::mutate`

You can create new columns from scratch, or (more commonly) as transformations of existing columns.

```
starwars |>
  select(name, birth_year) |>
  mutate(dog_years = birth_year * 7) |>
  mutate(comment = paste0(name, " is ", dog_years, " in dog years."))
```

A tibble: 87 x 4

	name	birth_year	dog_years	comment
	<chr>	<dbl>	<dbl>	<chr>
1	Luke Skywalker	19	133	Luke Skywalker is 133 in dog years.
2	C-3P0	112	784	C-3P0 is 784 in dog years.
3	R2-D2	33	231	R2-D2 is 231 in dog years.
4	Darth Vader	41.9	293.	Darth Vader is 293.3 in dog years.
5	Leia Organa	19	133	Leia Organa is 133 in dog years.
6	Owen Lars	52	364	Owen Lars is 364 in dog years.
7	Beru Whitesun Lars	47	329	Beru Whitesun Lars is 329 in dog year~
8	R5-D4	NA	NA	R5-D4 is NA in dog years.
9	Biggs Darklighter	24	168	Biggs Darklighter is 168 in dog year~
10	Obi-Wan Kenobi	57	399	Obi-Wan Kenobi is 399 in dog years.

i 77 more rows

Note: mutate is order aware. So you can chain multiple mutates in a single call.

```
starwars |>
  select(name, birth_year) |>
  mutate(
    dog_years = birth_year * 7,      # Separate with a comma
    comment = paste0(name, " is ", dog_years, " in dog years.")
  )
```

A tibble: 87 x 4

	name	birth_year	dog_years	comment
	<chr>	<dbl>	<dbl>	<chr>
1	Luke Skywalker	19	133	Luke Skywalker is 133 in dog years.
2	C-3P0	112	784	C-3P0 is 784 in dog years.
3	R2-D2	33	231	R2-D2 is 231 in dog years.
4	Darth Vader	41.9	293.	Darth Vader is 293.3 in dog years.
5	Leia Organa	19	133	Leia Organa is 133 in dog years.
6	Owen Lars	52	364	Owen Lars is 364 in dog years.
7	Beru Whitesun Lars	47	329	Beru Whitesun Lars is 329 in dog year~
8	R5-D4	NA	NA	R5-D4 is NA in dog years.
9	Biggs Darklighter	24	168	Biggs Darklighter is 168 in dog year~
10	Obi-Wan Kenobi	57	399	Obi-Wan Kenobi is 399 in dog years.

i 77 more rows

Boolean, logical and conditional operators all work well with `mutate` too.

```
starwars |>
  select(name, height) |>
  filter(name %in% c("Luke Skywalker", "Anakin Skywalker")) |>
  mutate(tall1 = height > 180) |>
  mutate(tall2 = if_else(height > 180, "Tall", "Short"))
```

```
# A tibble: 2 x 4
  name          height tall1 tall2
<chr>          <int> <lgl> <chr>
1 Luke Skywalker    172 FALSE Short
2 Anakin Skywalker    188 TRUE  Tall
```

Lastly, combining `mutate` with `across` allows you to easily perform the same operation on a subset of variables.

```
starwars |>
  select(name:eye_color) |>
  mutate(across(where(is.character), toupper))
```

```
# A tibble: 87 x 6
  name          height mass hair_color skin_color eye_color
<chr>          <int> <dbl> <chr>      <chr>      <chr>
1 LUKE SKYWALKER    172    77 BLOND      FAIR        BLUE
2 C-3PO            167    75 <NA>      GOLD        YELLOW
3 R2-D2             96    32 <NA>      WHITE, BLUE RED
4 DARTH VADER      202   136 NONE       WHITE        YELLOW
5 LEIA ORGANA      150    49 BROWN      LIGHT        BROWN
6 OWEN LARS        178   120 BROWN, GREY LIGHT        BLUE
7 BERU WHITESUN LARS 165    75 BROWN      LIGHT        BLUE
8 R5-D4             97    32 <NA>      WHITE, RED  RED
9 BIGGS DARKLIGHTER 183    84 BLACK      LIGHT        BROWN
10 OBI-WAN KENOBI   182    77 AUBURN, WHITE FAIR        BLUE-GRAY
# i 77 more rows
```

Exercise 5: `dplyr::summarize`

Particularly useful in combination with the `group_by` command.

```
starwars |>
  group_by(species) |>
  summarize(mean_height = mean(height))
```

```
# A tibble: 38 x 2
  species    mean_height
  <chr>         <dbl>
1 Aleena         79
2 Besalisk      198
3 Cerean        198
4 Chagrian      196
5 Clawdite      168
6 Droid         NA
7 Dug          112
8 Ewok          88
9 Geonosian     183
10 Gungan      209.
# i 28 more rows
```

Notice that some of these summarized values are missing. If we want to ignore missing values, use `na.rm = T`:

```
## Much better
starwars |>
  group_by(species) |>
  summarize(mean_height = mean(height, na.rm = T))
```

```
# A tibble: 38 x 2
  species    mean_height
  <chr>         <dbl>
1 Aleena         79
2 Besalisk      198
3 Cerean        198
4 Chagrian      196
5 Clawdite      168
6 Droid        131.
7 Dug          112
8 Ewok          88
9 Geonosian     183
10 Gungan      209.
# i 28 more rows
```

The same `across`-based workflow that we saw with `mutate` a few slides back also works with `summarize`.

```
starwars |>
  group_by(species) |>
  summarize(across(where(is.numeric), mean))
```

```
# A tibble: 38 x 4
  species    height  mass birth_year
  <chr>      <dbl> <dbl>      <dbl>
1 Aleena      79     15         NA
2 Besalisk   198    102         NA
3 Cerean     198     82         92
4 Chagrian   196     NA         NA
5 Clawdite   168     55         NA
6 Droid       NA     NA         NA
7 Dug       112     40         NA
8 Ewok        88     20          8
9 Geonosian  183     80         NA
10 Gungan   209.     NA         NA
# i 28 more rows
```

The same `across`-based workflow that we saw with `mutate` a few slides back also works with `summarize`. Though to add arguments, we have to use an **anonymous function**:

```
starwars |>
  group_by(species) |>
  summarize(across(where(is.numeric), ~ mean(.x, na.rm=T)))
```

```
# A tibble: 38 x 4
  species    height  mass birth_year
  <chr>      <dbl> <dbl>      <dbl>
1 Aleena      79     15        NaN
2 Besalisk   198    102        NaN
3 Cerean     198     82         92
4 Chagrian   196    NaN        NaN
5 Clawdite   168     55        NaN
6 Droid     131.    69.8     53.3
7 Dug       112     40        NaN
8 Ewok        88     20          8
9 Geonosian  183     80        NaN
10 Gungan   209.    74         52
# i 28 more rows
```

Other dplyr goodies

`ungroup`: For ungrouping after using `group_by`. - Use after doing your grouped `summarize` or `mutate` operation, or everything else you do will be super slow.

`slice`: Subset rows by position rather than filtering by values. - E.g. `starwars |> slice(1:10)`

`pull`: Extract a column from a data frame as a vector or scalar. - E.g. `starwars |> filter(sex=="female") |> pull(height)`

`distinct` and `count`: List unique values, with or without their number of appearances. - E.g. `starwars |> distinct(species)`, or `starwars |> count(species)` - `count` is equivalent to `group_by` and `summarize` with `n()`:

```
starwars |> group_by(species) |> summarize(n = n())
```

```
# A tibble: 38 x 2
  species      n
  <chr>    <int>
1 Aleena      1
2 Besalisk    1
3 Cerean      1
4 Chagrian    1
5 Clawdite    1
6 Droid        6
7 Dug         1
8 Ewok         1
9 Geonosian   1
10 Gungan     3
# i 28 more rows
```

Challenge 1

List the most common eye colors among female Star Wars characters in descending order of frequency.

As usual, there are multiple solutions.

```
starwars |>
  filter(sex == "female") |>
  count(eye_color) |>
  arrange(desc(n))
```

```
# A tibble: 6 x 2
  eye_color      n
  <chr>        <int>
1 blue          6
2 brown         4
3 black         2
4 hazel         2
5 unknown       1
6 yellow        1
```

```
starwars |>
  filter(sex == "female") |>
  group_by(eye_color) |>
  summarize(n = n()) |>
  arrange(desc(n))
```

```
# A tibble: 6 x 2
  eye_color      n
  <chr>        <int>
1 blue          6
2 brown         4
3 black         2
4 hazel         2
5 unknown       1
6 yellow        1
```

Explain what each line in the codes do:

Answer:

For the first chunk:

starwars → loads the dataset of Star Wars characters.

filter(sex == "female") → keeps only female characters.

`count(eye_color)` → counts how many females have each eye color.

`arrange(desc(n))` → sorts the counts from most to least common.

For the second chunk:

`starwars` → starts with the Star Wars dataset.

`filter(sex == "female")` → keeps only female characters.

`group_by(eye_color)` → groups the data by eye color.

`summarize(n = n())` → counts rows in each group (like `count()`).

`arrange(desc(n))` → orders counts from largest to smallest.

Storing results in memory

So far we haven't been saving the dataframes that result from our code in memory. Usually, we will want to use them for the next task. Create a new object each time you write a pipeline.

```
women = starwars |> filter(sex == "female")
brown_eyed_women = women |> filter(eye_color == "brown")
```

Resist the temptation to use the same object name. This is called **clobbering** since it overwrites the previous version. It ruins your ability to easily go back to previous steps.

```
# DON'T do this
starwars = starwars |> filter(sex == "female")
```

By keeping multiple copies of very similar dataframes, will you waste your computer's memory? Usually, no – R is smart and stores only the changes between objects.

Key tidyr verbs

1. `pivot_longer`: Pivot wide data into long format.
2. `pivot_wider`: Pivot long data into wide format.
3. `separate`: Separate (i.e. split) one column into multiple columns.
4. `unite`: Unite (i.e. combine) multiple columns into one.

Which of `pivot_longer` vs `pivot_wider` produces “tidy” data?

‘`pivot_longer`’ produces “tidy” data

Exercise 6: tidyr::pivot_longer

```
stocks = data.frame( ## Could use "tibble" instead of "data.frame" if you prefer
  time = as.Date('2009-01-01') + 0:1,
  X = rnorm(2, 10, 1),
  Y = rnorm(2, 10, 2),
  Z = rnorm(2, 10, 5)
)
stocks
```

	time	X	Y	Z
1	2009-01-01	10.36194	10.05057	11.63083
2	2009-01-02	10.59210	11.94640	12.60574

```
tidy_stocks = stocks |>
  pivot_longer(cols=X:Z, names_to="stock", values_to="price")
tidy_stocks
```

```
# A tibble: 6 x 3
  time      stock price
  <date>    <chr> <dbl>
1 2009-01-01 X      10.4
2 2009-01-01 Y      10.1
3 2009-01-01 Z      11.6
4 2009-01-02 X      10.6
5 2009-01-02 Y      11.9
6 2009-01-02 Z      12.6
```

Exercise 7: tidyr::pivot_wider

Now we can use pivot_wider to go back to the original dataframe:

```
tidy_stocks |> pivot_wider(names_from=stock, values_from=price)
```

```
# A tibble: 2 x 4
  time      X      Y      Z
  <date> <dbl> <dbl> <dbl>
1 2009-01-01 10.4 10.1 11.6
2 2009-01-02 10.6 11.9 12.6
```

Or, we can put it into a new (“transposed”) format, in which the observations are stocks and the columns are dates:

```
tidy_stocks |> pivot_wider(names_from=time, values_from=price)
```

```
# A tibble: 3 x 3
  stock `2009-01-01` `2009-01-02`
  <chr>      <dbl>      <dbl>
1 X          10.4        10.6
2 Y          10.1        11.9
3 Z          11.6        12.6
```

Exercise 8: tidyr::separate

`separate` helps when you have more than one value in a single column:

```
economists = data.frame(name = c("Adam_Smith", "Paul_Samuelson", "Milton_Friedman"))
economists
```

```
      name
1 Adam_Smith
2 Paul_Samuelson
3 Milton_Friedman
```

```
economists |> separate(name, c("first_name", "last_name"))
```

```
first_name last_name
1      Adam      Smith
2      Paul Samuelson
3     Milton  Friedman
```

—

This command is pretty smart. But to avoid ambiguity, you can also specify the separation character with the `sep` argument:

```
economists |> separate(name, c("first_name", "last_name"), sep = "_")
```

```
first_name last_name
1      Adam      Smith
2      Paul Samuelson
3     Milton  Friedman
```

Exercise 9: tidyr::separate

Related is `separate_rows`, for splitting cells with multiple values into multiple rows:

```
jobs = data.frame(  
  name = c("Joe", "Jill"),  
  occupation = c("President", "First Lady, Professor, Grandmother")  
)  
jobs
```

	name	occupation
1	Joe	President
2	Jill	First Lady, Professor, Grandmother

```
# Now split out Jill's various occupations into different rows  
jobs |> separate_rows(occupation)
```

```
# A tibble: 5 x 2  
  name occupation  
  <chr> <chr>  
1 Joe   President  
2 Jill  First  
3 Jill  Lady  
4 Jill  Professor  
5 Jill  Grandmother
```

Related is `separate_rows`, for splitting cells with multiple values into multiple rows:

```
jobs = data.frame(  
  name = c("Joe", "Jill"),  
  occupation = c("President", "First Lady, Professor, Grandmother")  
)  
jobs
```

	name	occupation
1	Joe	President
2	Jill	First Lady, Professor, Grandmother

```
# Now split out Jill's various occupations into different rows  
jobs |> separate_rows(occupation, sep = ", ")
```

```
# A tibble: 4 x 2
  name occupation
  <chr> <chr>
1 Joe   President
2 Jill  First Lady
3 Jill  Professor
4 Jill  Grandmother
```

Exercise 10: tidyr::unite

```
gdp = data.frame(
  yr = rep(2016, times = 4),
  mnth = rep(1, times = 4),
  dy = 1:4,
  gdp = rnorm(4, mean = 100, sd = 2)
)
gdp
```

```
   yr mnth dy      gdp
1 2016    1  1 99.02857
2 2016    1  2 100.86480
3 2016    1  3 100.78705
4 2016    1  4 100.04100
```

```
## Combine "yr", "mnth", and "dy" into one "date" column
gdp |> unite(date, c("yr", "mnth", "dy"), sep = "-")
```

```
   date      gdp
1 2016-1-1 99.02857
2 2016-1-2 100.86480
3 2016-1-3 100.78705
4 2016-1-4 100.04100
```

```
gdp_u <- gdp |> unite(date, c("yr", "mnth", "dy"), sep = "-")
```

Note that `unite` will automatically create a character variable.

If you want to convert it to something else (e.g. date or numeric) then you will need to modify it using `mutate`. This example uses the [lubridate](#) package's super helpful date conversion functions.

```
library(lubridate)
gdp_u |> mutate(date = ymd(date))
```

	date	gdp
1	2016-01-01	99.02857
2	2016-01-02	100.86480
3	2016-01-03	100.78705
4	2016-01-04	100.04100

Challenge 2

Using `nycflights13`, create a table of average arrival delay (in minutes) by day (in rows) and carrier (in columns).

Hint: Recall that you can tabulate summary statistics using `group_by` and `summarize`:

```
flights |>
  group_by(carrier) |>
  summarize(avg_late = mean(arr_delay, na.rm=T))
```

```
# A tibble: 16 x 2
  carrier avg_late
  <chr>      <dbl>
1 9E         7.38
2 AA         0.364
3 AS        -9.93
4 B6         9.46
5 DL         1.64
6 EV        15.8
7 F9        21.9
8 FL        20.1
9 HA        -6.92
10 MQ        10.8
11 OO        11.9
12 UA         3.56
13 US         2.13
14 VX         1.76
15 WN         9.65
16 YV        15.6
```

Solution:

```
delay_long = flights |>
  group_by(carrier, day) |>
  summarize(avg_late = mean(arr_delay, na.rm=T))
delay_wide = delay_long |>
  pivot_wider(names_from=carrier, values_from=avg_late)
head(delay_wide, 4)
```

```
# A tibble: 4 x 17
  day `9E`   AA   AS   B6   DL   EV   F9   FL   HA   MQ   OO
  <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1     1  7.21 -1.23  -5.96 11.9    0.866 21.3  21.7  22.7 -15.4 12.9  NA
2     2  7.35 -0.905 -13.7  9.90    3.05 18.0   7.71  20.9 -16.1  9.04 NaN
3     3  5.80 -3.09 -20.8  5.26   -0.204 15.3  18.0  19.6 -16.8 13.7  0.5
4     4 -2.11 -5.80 -22.3 -0.0939 -6.24   3.87 14.5   4.38 -15.2  3.82 -12
# i 5 more variables: UA <dbl>, US <dbl>, VX <dbl>, WN <dbl>, YV <dbl>
```

Explain what each line in the codes do:

Answer:

In the first chunk:

`flights` → loads the dataset with all info from NYC flights in 2013.

`group_by(carrier)` → groups rows by airline carrier (e.g., UA, AA, DL).

`summarize(avg_late = mean(arr_delay, na.rm = TRUE))` → for each carrier, calculates the average arrival delay.

`arr_delay` = arrival delay (minutes).

`na.rm = TRUE` removes missing values from the calculation.

In the second chunk:

`delay_long`: groups flights by carrier and day, then computes the average arrival delay in the long format: one row per carrier-day.

`delay_wide`: pivots to wide format, with carriers as columns and their average delays as values.

`head(delay_wide, 4)`: shows the first 4 rows of the wide table

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Grading

Component	Points
Replicating Ex 1-10	85
Challenge	5
Creating Github Account	5
Workflow & formatting	5

The “Workflow & formatting” grade is to assess the reproducible workflow and document format.