Data Wrangling II: Appending, joining, and reshaping data

EDH7916 | Spring 2020

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So far, we have only worked with single data files: we read in a file, wrangled our data, and, sometimes, outputted a new file. But very often, a key aspect of the data wrangling workflow is to combine more than one data set together. This may include **appending** new rows to an existing data frame in memory or **joining** two data sets together using a common key value found in both. Another key data manipulation task is to **reshape** our data, pivoting from wide to long form (or vice versa). We'll go through each individually below.

Setup

As always, we begin by reading in the {tidyverse} library and assigning our paths to macros we can reuse below. Notice that we have a new subdirectory in our `data` directory: `sch_test`, which has a subdirectory called `by_school`. These fake data represent test scores across three subjects — math, reading, and science — across four schools over six years. The two files in `sch_test` directory, `all_schools.csv` and `all_schools_wide.csv`, represent the same data, but in different formats. We'll use these data sets to practice appending, joining, and reshaping.

```
|__ data/
    |-- ...
    |__ sch_test/
        |-- all_schools.csv
        |-- all_schools_wide.csv
        |__ by_school/
            |-- bend_gate_1980.csv
            |-- bend_gate_1980.csv
            |...
            |-- spottsville_1985.csv
```

```
## ---------------------------
## libraries
## ---------------------------

library(tidyverse)
```

```
── Attaching packages ─────────────────────────────────────── tidyverse 1.3.0 ──

✔ ggplot2 3.3.0     ✔ purrr   0.3.4
✔ tibble  3.0.1     ✔ dplyr   0.8.5
✔ tidyr   1.0.2     ✔ stringr 1.4.0
✔ readr   1.3.1     ✔ forcats 0.5.0

── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
```

NB: As we did in the past lesson, we run this script assuming that our working directory is set to the `scripts` directory.

```
## --------------------------
## directory paths
## --------------------------

## assume we're running this script from the ./scripts subdirectory
dat_dir <- file.path("..", "data")
sch_dir <- file.path(dat_dir, "sch_test")
bys_dir <- file.path(sch_dir, "by_school")
```

Appending data

Our first task is the most straightforward. When appending data, we are simply adding similarly structured rows to an exiting data frame. What do I mean by similarly structured? Imagine you have a data frame that looks like this:

id	year	score
A	2020	98
B	2020	95
C	2020	85
D	2020	94

Now, assume you are given data that look like this:

id	year	score
E	2020	99
F	2020	90

These data are similarly structured: *same column names in the same order*. If we know that the data came from the same process (*e.g.*, **id**s represent students in the same classroom with each file representing a different test day), then we can safely append the second to the first:

id	year	score
A	2020	98
B	2020	95
C	2020	85
D	2020	94
E	*2020*	*99*
F	*2020*	*90*

Data that are the result of the *exact* same data collecting process across locations or time may be appendable. In education research, administrative data are often recorded each term or year, meaning you can build a panel data set by appending. The NCES IPEDS data files generally work like this, too.

> **Quick exercise** While appending data can be straightforward, it can also be *dangerous*. What do you think I mean by that? Think of some situations in which appending data frames may not

be a good idea.

Example

Let's practice with an example. First, we'll read in three data files from the `by_school` directory.

```
## ---------------------------
## input
## ---------------------------

## read in data
df_1 <- read_csv(file.path(bys_dir, "bend_gate_1980.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
  year = col_double(),
  math = col_double(),
  read = col_double(),
  science = col_double()
)
```

```
df_2 <- read_csv(file.path(bys_dir, "bend_gate_1981.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
  year = col_double(),
  math = col_double(),
  read = col_double(),
  science = col_double()
)
```

```
df_3 <- read_csv(file.path(bys_dir, "bend_gate_1982.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
  year = col_double(),
  math = col_double(),
  read = col_double(),
  science = col_double()
)
```

Looking at each, we can see that they are similarly structured.

```
## ---------------------------
## process
## ---------------------------

## show
df_1
```

```
# A tibble: 1 x 5
  school     year  math  read science
  <chr>     <dbl> <dbl> <dbl>   <dbl>
1 Bend Gate  1980   515   281     808
```

```
df_2
```

```
# A tibble: 1 x 5
  school     year  math  read science
  <chr>     <dbl> <dbl> <dbl>   <dbl>
1 Bend Gate  1981   503   312     814
```

```
df_3
```

```
# A tibble: 1 x 5
  school     year  math  read science
  <chr>     <dbl> <dbl> <dbl>   <dbl>
1 Bend Gate  1982   514   316     816
```

From tidyverse's {dplyr} library, we use `bind_rows()` to append the second and third first to the first.

```
## append files
df <- bind_rows(df_1, df_2, df_3)

## show
df
```

```
# A tibble: 3 x 5
  school     year  math  read science
  <chr>     <dbl> <dbl> <dbl>   <dbl>
1 Bend Gate  1980   515   281     808
2 Bend Gate  1981   503   312     814
3 Bend Gate  1982   514   316     816
```

That's it!

> **Quick exercise** Read in the rest of the files for Bend Gate and append them to the current data frame.

Joining data

More often than appending your data files, however, you will need to merge or join them. With a join, you are adding new columns (new variables) to your data frame that come from a second data frame. The key difference between joining and appending is that a join requires a *key*, that is, a variable or index common to each data frame that's used to line everything up.

For example, say you have these two data sets,

id	sch	year	score
A	1	2020	98
B	1	2020	95
C	2	2020	85
D	3	2020	94

sch	type
1	elementary
2	middle
3	high

and you want to add the school `type` to the first data set. You can do this because you have a common *key* between each set: `sch`. A pseudocode description on this join would be:

1. Add a column to the first data frame called `type`
2. Fill in each row of the new column with the `type` value that corresponds to the matching `sch` value in both data frames:
   - `sch == 1 --> elementary`
   - `sch == 2 --> middle`
   - `sch == 3 --> high`

The end result would then look like this:

id	sch	year	score	type
A	1	2020	98	elementary
B	1	2020	95	elementary
C	2	2020	85	middle
D	3	2020	94	high

Example

A common join task in education research involves adding group-level aggregate statistics to individual observations: for example, adding school-level average test scores to each student's row. With a panel data set (observations across time), we might want averages across all groups within each year added to each unit by time period row. Let's do the second, adding within-year across school average test scores to each school by year observation.

```
## ---------------------------
## input
## ---------------------------

## read in data
df <- read_csv(file.path(sch_dir, "all_schools.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
  year = col_double(),
  math = col_double(),
  read = col_double(),
  science = col_double()
)
```

Looking at the data, we see that it's similar to what we've seen above, with additional schools.

```
## show
df
```

```
# A tibble: 24 x 5
   school        year  math  read science
   <chr>        <dbl> <dbl> <dbl>   <dbl>
 1 Bend Gate     1980   515   281     808
 2 Bend Gate     1981   503   312     814
 3 Bend Gate     1982   514   316     816
 4 Bend Gate     1983   491   276     793
 5 Bend Gate     1984   502   310     788
 6 Bend Gate     1985   488   280     789
```

```
 7 East Heights  1980   501   318     782
 8 East Heights  1981   487   323     813
 9 East Heights  1982   496   294     818
10 East Heights  1983   497   306     795
# … with 14 more rows
```

Our task is two-fold:

1. Get the average of each test score within year and save in object.
2. Join the new summary data frame to the original data frame.

1. Get summary

```
## ---------------------------
## process
## ---------------------------

## get test score summary within year
df_sum <- df %>%
    group_by(year) %>%
    summarize(math_m = mean(math),
              read_m = mean(read),
              science_m = mean(science))

## show
df_sum
```

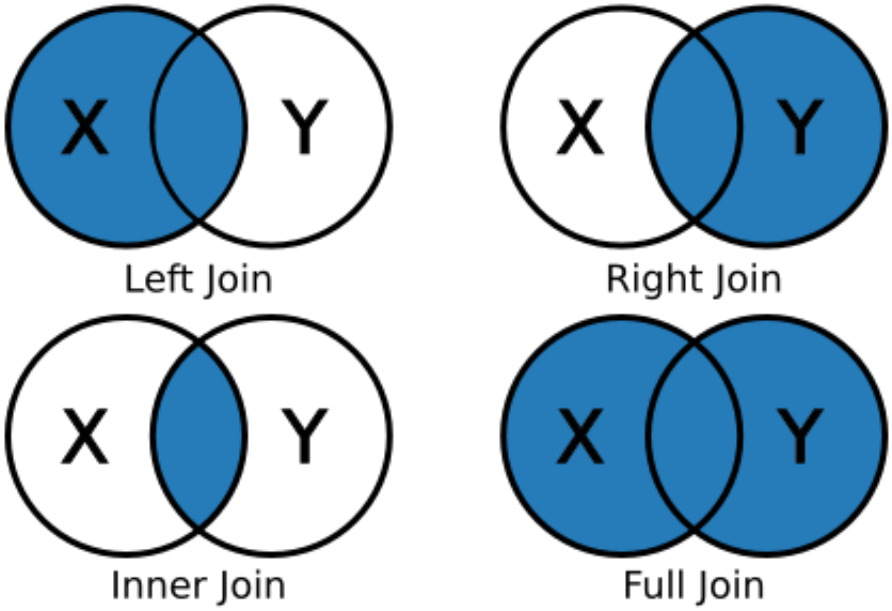
```
# A tibble: 6 x 4
   year math_m read_m science_m
  <dbl>  <dbl>  <dbl>     <dbl>
1  1980   507    295.      798.
2  1981   496.   293.      788.
3  1982   506    302.      802.
4  1983   500    293.      794.
5  1984   490    300.      792.
6  1985   500.   290.      794.
```

> **Quick exercise** Thinking ahead, why do you think we created new names for the summarized columns? Why the `_m` ending?

2. Join

While one can `merge` using base R, {dplyr} uses the SQL language of joins, which can be conceptually clearer. Here are the most common joins you will use:

- `left_join(x, y)`: keep all x, drop unmatched y
- `right_join(x, y)`: keep all y, drop unmatched x
- `inner_join(x, y)`: keep only matching
- `full_join(x, y)`: keep everything



Since we want to join a smaller aggregated data frame, `df_sum`, to the original data frame, `df`, we'll use a `left_join()`. The join functions will try to guess the joining variable (and tell you what it picked) if you don't supply one, but we'll specify one to be clear.

```
df_joined <- df %>%
    left_join(df_sum, by = "year")

## show
df_joined
```

```
# A tibble: 24 x 8
   school        year  math  read science math_m read_m science_m
   <chr>        <dbl> <dbl> <dbl>   <dbl>  <dbl>  <dbl>     <dbl>
 1 Bend Gate     1980   515   281     808   507    295.       798.
 2 Bend Gate     1981   503   312     814   496.   293.       788.
 3 Bend Gate     1982   514   316     816   506    302.       802.
 4 Bend Gate     1983   491   276     793   500    293.       794.
 5 Bend Gate     1984   502   310     788   490    300.       792.
 6 Bend Gate     1985   488   280     789   500.   290.       794.
 7 East Heights  1980   501   318     782   507    295.       798.
 8 East Heights  1981   487   323     813   496.   293.       788.
 9 East Heights  1982   496   294     818   506    302.       802.
10 East Heights  1983   497   306     795   500    293.       794.
# … with 14 more rows
```

> **Quick exercise** Look at the first 10 rows of `df_joined`. What do you notice about the new summary columns we added?

Reshaping data

Reshaping data is a common data wrangling task. Whether going from wide to long format or long to wide, it can be a painful process. But with a little practice, the ability to reshape data will become a powerful

tool in your toolbox.

Definitions

While there are various definitions of tabular data structure, the two you will most often come across are **wide** and **long**. Wide data are data structures in which all variable/values are columns. At the extreme end, every *id* will only have a single row:

id	math_score_2019	read_score_2019	math_score_2020	read_score_2020
A	93	88	92	98
B	99	92	97	95
C	89	88	84	85

Notice how each particular score (by year) has its own column? Compare this to long data in which each *observational unit* (id test score within a given year) will have a row:

id	year	test	score
A	2019	math	93
A	2019	read	88
A	2020	math	92
A	2020	read	98
B	2019	math	99
B	2019	read	92
B	2020	math	97
B	2020	read	95
C	2019	math	89
C	2019	read	88
C	2020	math	84
C	2020	read	85

The first wide and second long table present the same information in a different format. So why bother reshaping? The short answer is that you sometimes need one format and sometimes the other due to the demands of the analysis you want to run, the figure you want to plot, or the table you want to make.

NB: Data in the wild are often some combination of these two types: *wide-ish* or *long-ish*. For an example, see our `all_schools.csv` data below, which is wide in some variables (test), but long in others (year). The point of defining long vs wide is not to have a testable definition, but rather to have a framework for thinking about how your data are structured and if that structure will work for your data analysis needs.

Example: wide -> long

To start, we'll go back to the `all_schools.csv` file.

```
## ---------------------------
## input
## ---------------------------

## reading again just to be sure we have the original data
df <- read_csv(file.path(sch_dir, "all_schools.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
```

```
  year = col_double(),
  math = col_double(),
  read = col_double(),
  science = col_double()
)
```

Notice how the data are wide in **test**: each school has one row per year, but each test gets its own column. While this setup can be efficient for storage, it's not always the best for analysis or even just browsing. What we want is for the data to be long.

Instead of each test having its own column, we would like to make the data look like our long data example above, with each row representing a single *school*, *year*, *test*, *score*:

school	year	test	score
Bend Gate	1980	math	515
Bend Gate	1980	read	281
Bend Gate	1980	science	808
...	...	...	...

As with joins, you can reshape data frames using base R commands. But again, we'll tidyverse functions in the tidyr library. Specifically, we'll rely on the {tidyr} `pivot_longer()` and `pivot_wider()` commands.

`pivot_longer()`

The `pivot_longer()` function can take a number of arguments, but the core things it needs to know are:

- `data`: the name of the data frame you're reshaping (we can use `%>%` to pipe in the data name)
- `cols`: the names of the columns you want to pivot into values of a single new column (thereby making the data frame "longer")
- `names_to`: the name of the new column that will contain the names of the `cols` you just listed
- `values_to`: the name of the column where the values in the `cols` you listed will go

In our current situation, our `cols` to pivot are `"math"`, `"read"`, and `"science"`. Since they are test types, we'll call our `names_to` column `"test"` and our `values_to` column `"score"`.

```
## ---------------------------
## process
## ---------------------------

## wide to long
df_long <- df %>%
    pivot_longer(cols = c("math","read","science"),
                 names_to = "test",
                 values_to = "score")

## show
df_long
```

```
# A tibble: 72 x 4
   school     year test    score
   <chr>     <dbl> <chr>   <dbl>
 1 Bend Gate  1980 math      515
 2 Bend Gate  1980 read      281
 3 Bend Gate  1980 science   808
 4 Bend Gate  1981 math      503
 5 Bend Gate  1981 read      312
```

```
 6 Bend Gate  1981 science   814
 7 Bend Gate  1982 math      514
 8 Bend Gate  1982 read      316
 9 Bend Gate  1982 science   816
10 Bend Gate  1983 math      491
# … with 62 more rows
```

> **Quick (ocular test) exercise** How many rows did our initial data frame `df` have? How many unique tests did we have in each year? When reshaping from wide to long, how many rows should we expect our new data frame to have? Does our new data frame have that many rows?

Example: long –> wide

`pivot_wider()`

Now that we have our long data, let's reshape it back to wide format using `pivot_wider()`. In this case, we're doing just the opposite from before — here are the main arguments you need to attend to:

- `data`: the name of the data frame you're reshaping (we can use `%>%` to pipe in the data name)
- `names_from`: the name of the column that contains the values which will become new column names
- `values_from`: the name of the column that contains the values associated with the values in `names_from` column; these will go into the new columns.

```
## ---------------------------
## process
## ---------------------------

## long to wide
df_wide <- df_long %>%
    pivot_wider(names_from = "test",
                values_from = "score")

## show
df_wide
```

```
# A tibble: 24 x 5
   school        year  math  read science
   <chr>        <dbl> <dbl> <dbl>   <dbl>
 1 Bend Gate     1980   515   281     808
 2 Bend Gate     1981   503   312     814
 3 Bend Gate     1982   514   316     816
 4 Bend Gate     1983   491   276     793
 5 Bend Gate     1984   502   310     788
 6 Bend Gate     1985   488   280     789
 7 East Heights  1980   501   318     782
 8 East Heights  1981   487   323     813
 9 East Heights  1982   496   294     818
10 East Heights  1983   497   306     795
# … with 14 more rows
```

> **Quick exercise** In this case, our new wide data frame, `df_wide`, should be the same as our initial data frame. Is it? How can you tell?

Example: wide -> long with corrections

Unfortunately, it's not always so clear cut to reshape data. In this second example, we'll again reshape from wide to long, but we'll have to munge our data a bit after the reshape to make it analysis ready.

First, we'll read in a second file `all_schools_wide.csv`. This file contains the same information as before, but in a *very* wide format: each school has only one row and each test by year value gets its own column in the form `<test>_<year>`.

```
## ---------------------------
## input
## ---------------------------

## read in very wide test score data
df <- read_csv(file.path(sch_dir, "all_schools_wide.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
  math_1980 = col_double(),
  read_1980 = col_double(),
  science_1980 = col_double(),
  math_1981 = col_double(),
  read_1981 = col_double(),
  science_1981 = col_double(),
  math_1982 = col_double(),
  read_1982 = col_double(),
  science_1982 = col_double(),
  math_1983 = col_double(),
  read_1983 = col_double(),
  science_1983 = col_double(),
  math_1984 = col_double(),
  read_1984 = col_double(),
  science_1984 = col_double(),
  math_1985 = col_double(),
  read_1985 = col_double(),
  science_1985 = col_double()
)
```

```
## show
df
```

```
# A tibble: 4 x 19
  school math_1980 read_1980 science_1980 math_1981 read_1981 science_1981
  <chr>      <dbl>     <dbl>        <dbl>     <dbl>     <dbl>        <dbl>
1 Bend …       515       281          808       503       312          814
2 East …       501       318          782       487       323          813
3 Niaga…       514       292          787       499       268          762
4 Spott…       498       288          813       494       270          765
# … with 12 more variables: math_1982 <dbl>, read_1982 <dbl>,
#   science_1982 <dbl>, math_1983 <dbl>, read_1983 <dbl>, science_1983 <dbl>,
#   math_1984 <dbl>, read_1984 <dbl>, science_1984 <dbl>, math_1985 <dbl>,
#   read_1985 <dbl>, science_1985 <dbl>
```

Second, we can `pivot_longer()` as we did before using the following values for our key arguments:

- `data` : `df` (but piped in using `%>%`)
- `cols` : use special {tidyselect} helper function `contains()` to select all test by year columns

- names_to: test_year
- values_to: score

```
## ---------------------------
## process
## ---------------------------

## wide to long
df_long <- df %>%
    pivot_longer(cols = contains("19"),
                 names_to = "test_year",
                 values_to = "score")

## show
df_long
```

```
# A tibble: 72 x 3
   school    test_year    score
   <chr>     <chr>        <dbl>
 1 Bend Gate math_1980      515
 2 Bend Gate read_1980      281
 3 Bend Gate science_1980   808
 4 Bend Gate math_1981      503
 5 Bend Gate read_1981      312
 6 Bend Gate science_1981   814
 7 Bend Gate math_1982      514
 8 Bend Gate read_1982      316
 9 Bend Gate science_1982   816
10 Bend Gate math_1983      491
# … with 62 more rows
```

> **Quick exercise** What do you think `contains("19")` is doing? Why did we use "19" as our value? **HINT**: use the `names()` function to return a list of the original data frame (`df`) column names.

This mostly worked to get our data long, but now we have this weird combined `test_year` column. What we really want are two columns, one for the year and one for the test type. We can fix this using {tidyr} `separate()` function with the following arguments:

- `data`: our `df_long` object, piped in using `%>%`
- `col`: the column we want to split (`test_year`)
- `into`: the names of the new columns to create from `col` (`test` and `year`)
- `sep`: the name of the character that splits the values in `col`, so R knows how to fill each of the `into` columns (`"_"`)

```
## separate test_year into two columns, filling appropriately
df_long_fix <- df_long %>%
    separate(col = "test_year",
             into = c("test", "year"),
             sep = "_")

## show
df_long_fix
```

```
# A tibble: 72 x 4
```

```
   school    test    year  score
   <chr>     <chr>   <chr> <dbl>
 1 Bend Gate math    1980    515
 2 Bend Gate read    1980    281
 3 Bend Gate science 1980    808
 4 Bend Gate math    1981    503
 5 Bend Gate read    1981    312
 6 Bend Gate science 1981    814
 7 Bend Gate math    1982    514
 8 Bend Gate read    1982    316
 9 Bend Gate science 1982    816
10 Bend Gate math    1983    491
# … with 62 more rows
```

Quick exercise Redo the last few steps in a single combined chain using pipes. That is, start with `df` (which contains `all_schools_wide.csv`), reshape long, and fix so that you end up with four columns — all in a single piped chain.

Final note

Just as all data sets are unique, so too are the particular steps you may need to take to **append**, **join**, or **reshape** your data. Even experienced coders rarely get all the steps correct the first try. Be prepared to spend time getting to know your data and figuring out, through trial and error, how to wrangle it so that it meets your analytic needs. Code books, institutional/domain knowledge, and patience are your friends here!