Data Wrangling II: Appending, joining, and reshaping data

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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.

Data

After you download and unzip the data for today's lesson, move the full folder, `sch_test`, into the `data` subdirectory. It should look something like this:

```
|__ data/
    |-- ...
    |__ sch_test/
        |-- all_schools.csv
        |-- all_schools_wide.csv
        |__ by_school/
            |-- bend_gate_1980.csv
            |-- bend_gate_1981.csv
            |...
            |-- spottsville_1985.csv
```

These fake data represent test scores across three subjects — math, reading, and science — across four schools over six years. Each school has a file for each year in the `by_school` subdirectory. The two files in `sch_test` directory, `all_schools.csv` and `all_schools_wide.csv`, combine the individual files but in different formats. We'll use these data sets to practice appending, joining, and reshaping.

Setup

As always, we begin by reading in the tidyverse library and assigning our paths to macros we can reuse below.

```r
## ---------------------------
## 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   1.1.0     ✔ 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()
```

As we did in the past lesson, we run this script assuming that our working directory is set to the `scripts` directory. Notice that we also include macros for our subdirectories within the `data` directory. Since they are nested, we can use the previous macros to set new macros.

```
## ---------------------------
## 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")  # use dat_dir
bys_dir <- file.path(sch_dir, "by_school") # use sch_dir
```

Appending data

Our first task is the most straightforward. When appending data, we simply add 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 appended. 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.

However, it's incumbent upon you as the researcher to understand your data. Just because you are able to append (R will try to make it work for you) doesn't mean you always should. What if the `score` column in our data weren't on the same scale? What if the test date mattered but isn't included in the file? What if the files actually represent scores from different grades or schools? It's possible that we can account for each of these issues as we clean our data, but it won't happen automatically — append with care!

Example

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

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

## read in data, storing in df_*, where * is a unique number
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, with the following columns in the same order: `school`, `year`, `math`, `read`, `science`:

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

```r
## show each
df_1
```

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

```r
df_2
```

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

```r
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 the dplyr library, we use the `bind_rows()` function to append the second and third data frames to the first.

```r
## 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 add to your data frame new columns (new variables) 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 uniquely identifies observations. It's this key 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

id	sch	year	score
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 of 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 within-year averages 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 all_schools 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 (math, reading, science) across all schools within each year and save the summary data frame in an object.
2. Join the new summary data frame to the original data frame.

1. Get summary

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

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

## show
df_sum
```

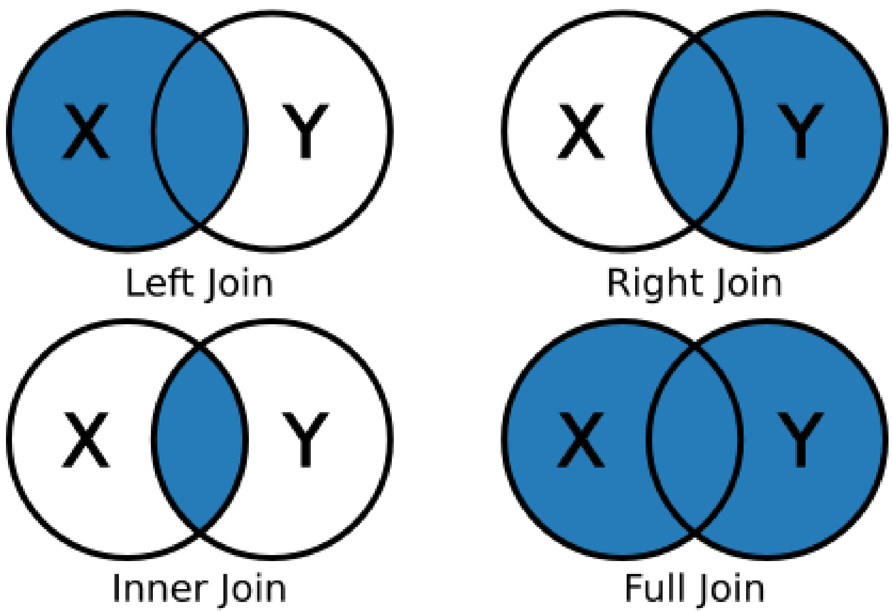
```
# A tibble: 6 x 4
   year math_m read_m science_m
  <dbl>  <dbl>  <dbl>     <dbl>
1  1980    507    295.      798.
2  1981    496.   293.      788.
3  1982    506    302.      802.
4  1983    500    293.      794.
5  1984    490    300.      792.
6  1985    500.   290.      794.
```

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 (particularly for those who already have experience with relational database structures). 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



For example, the result of a **left join** between data frame X and data frame Y will include all observations in X and those in Y that are also in X.

X

id	col_A	col_B
001	a	1
002	b	2
003	a	3

Y

id	col_C	col_D
001	T	9
002	T	9
004	F	9

XY (result of left join)

id	col_A	col_B	col_C	col_D
001	a	1	T	9
002	b	2	T	9
003	a	3	NA	NA

Observations in both X and Y (`001` and `002`, above), will have data for the columns that were separately in X and Y before. Those in X only (`003`), will have missing values in the new columns that came from Y because they didn't exist there. Observations in Y but not X (`004`) are dropped entirely.

Back to our example…

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.

```
## start with data frame...
df_joined <- df %>%
    ## pipe into left_join to join with df_sum using "year" as key
    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 use 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 that 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"`.

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

## wide to long
df_long <- df %>%
    ## cols: current test columns
    ## names_to: where "math", "read", and "science" will go
    ## values_to: where the values in cols will go
    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 %>%
    ## names_from: values in this column will become new column names
    ## values_from: values in this column will become values in new cols
    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 %>%
    ## NB: contains() looks for "19" in name: if there, it adds it to cols
    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 Why did we use "19" as our value in the contains() function? **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 %>%
    ## col: the column to split
    ## into: names of resulting splits
    ## sep: the split point --> left to "test", right to "year"
    separate(col = "test_year",
             into = c("test", "year"),
             sep = "_")
```

```r
## 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!