22 Joining tables

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Joins

The information we need for a given analysis may not be just in one table. For example, when forecasting elections we used the function `left_join` to combine the information from two tables.

Here we use a simpler example to illustrate the general challenge of combining tables. Suppose we want to explore the relationship between population size for US states and electoral votes.

Joins

We have the population size in this table:

```r
library(tidyverse)
library(dslabs)
data(murders)
head(murders)
```

and electoral votes in this one:

```r
data(polls_us_election_2016)
head(results_us_election_2016)
```

Joins

Just concatenating these two tables together will not work since the order of the states is not the same.

```
identical(results_us_election_2016$state, murders$state)
```

The *join* functions, described below, are designed to handle this challenge.

Joins

The join functions in the dplyr package make sure that the tables are combined so that matching rows are together. The general idea is that one needs to identify one or more columns that will serve to match the two tables. Then a new table with the combined information is returned.

Joins

Notice what happens if we join the two tables above by state using `left_join`:

```
tab <- left_join(murders, results_us_election_2016, by = "stat
  select(-others) %>% rename(ev = electoral_votes)
head(tab)
```

Joins

The data has been successfully joined and we can now, for example, make a plot to explore the relationship:

```r
library(ggrepel)
tab %>% ggplot(aes(population/10^6, ev, label = abb)) +
  geom_point() +
  geom_text_repel() +
  scale_x_continuous(trans = "log2") +
  scale_y_continuous(trans = "log2") +
  geom_smooth(method = "lm", se = FALSE)
```

Joins

We see the relationship is close to linear with about 2 electoral votes for every million persons, but with very small states getting higher ratios.

In practice, it is not always the case that each row in one table has a matching row in the other. For this reason, we have several versions of join.

To illustrate this challenge, we will take subsets of the tables above.

Joins

We create the tables `tab1` and `tab2` so that they have some states in common but not all:

```r
tab_1 <- slice(murders, 1:6) %>% select(state, population)
tab_1

tab_2 <- results_us_election_2016 %>%
  filter(state%in%c("Alabama", "Alaska", "Arizona",
                    "California", "Connecticut", "Delaware"))
  select(state, electoral_votes) %>% rename(ev = electoral_vot
tab_2
```

We will use these two tables as examples in the next sections.

Left join

Suppose we want a table like `tab_1`, but adding electoral votes to whatever states we have available. For this, we use `left_join` with `tab_1` as the first argument. We specify which column to use to match with the by argument.

```r
left_join(tab_1, tab_2, by = "state")
```

Left join

Note that NAs are added to the two states not appearing in tab_2. Also, notice that this function, as well as all the other joins, can receive the first arguments through the pipe:

```
tab_1 %>% left_join(tab_2, by = "state")
```

Right join

If instead of a table with the same rows as first table, we want one with the same rows as second table, we can use `right_join`:

```r
tab_1 %>% right_join(tab_2, by = "state")
```

Now the NAs are in the column coming from `tab_1`.

Inner join

If we want to keep only the rows that have information in both tables, we use `inner_join`. You can think of this as an intersection:

```r
inner_join(tab_1, tab_2, by = "state")
```

Full join

If we want to keep all the rows and fill the missing parts with NAs, we can use `full_join`. You can think of this as a union:

```
full_join(tab_1, tab_2, by = "state")
```

Semi join

The `semi_join` function lets us keep the part of first table for which we have information in the second. It does not add the columns of the second:

```r
semi_join(tab_1, tab_2, by = "state")
```

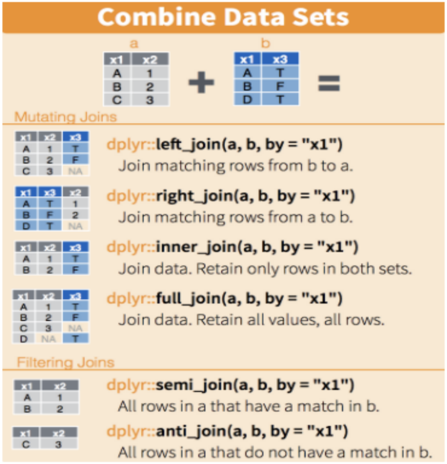
Anti join

The function `anti_join` is the opposite of `semi_join`. It keeps the elements of the first table for which there is no information in the second:

```r
anti_join(tab_1, tab_2, by = "state")
```

Joining

The following diagram summarizes the above joins:



Combine Data Sets

a

x1	x2
A	1
B	2
C	3

+

b

x1	x3
A	T
B	F
D	T

=

Mutating Joins

x1	x2	x3
A	1	T
B	2	F
C	3	NA

dplyr::**left_join(a, b, by = "x1")**
Join matching rows from b to a.

x1	x3	x2
A	T	1
B	F	2
D	T	NA

dplyr::**right_join(a, b, by = "x1")**
Join matching rows from a to b.

x1	x2	x3
A	1	T
B	2	F

dplyr::**inner_join(a, b, by = "x1")**
Join data. Retain only rows in both sets.

x1	x2	x3
A	1	T
B	2	F
C	3	NA
D	NA	T

dplyr::**full_join(a, b, by = "x1")**
Join data. Retain all values, all rows.

Filtering Joins

x1	x2
A	1
B	2

dplyr::**semi_join(a, b, by = "x1")**
All rows in a that have a match in b.

x1	x2
C	3

dplyr::**anti_join(a, b, by = "x1")**
All rows in a that do not have a match in b.

Binding

Unlike the join function, the binding functions do not try to match by a variable, but instead simply combine datasets. If the datasets don't match by the appropriate dimensions, one obtains an error.

Binding columns

The **dplyr** function *bind_cols* binds two objects by making them columns in a tibble. For example, we quickly want to make a data frame consisting of numbers we can use.

```
bind_cols(a = 1:3, b = 4:6)
```

This function requires that we assign names to the columns. Here we chose `a` and `b`.

Binding columns

Note that there is an R-base function `cbind` with the exact same functionality. An important difference is that `cbind` can create different types of objects, while `bind_cols` always produces a data frame.

Binding columns

For example, here we break up the tab data frame and then bind them back together:

```
tab_1 <- tab[, 1:3]
tab_2 <- tab[, 4:6]
tab_3 <- tab[, 7:8]
new_tab <- bind_cols(tab_1, tab_2, tab_3)
head(new_tab)
```

Binding by rows

The `bind_rows` function is similar to `bind_cols`, but binds rows instead of columns:

```r
tab_1 <- tab[1:2,]
tab_2 <- tab[3:4,]
bind_rows(tab_1, tab_2)
```

This is based on an R-base function `rbind`.

Set operators

Another set of commands useful for combining datasets are the set operators. When applied to vectors, these behave as their names suggest.

Examples are `intersect`, `union`, `setdiff`, and `setequal`. However, if the **tidyverse**, or more specifically **dplyr**, is loaded, these functions can be used on data frames as opposed to just on vectors.

Intersect

You can take intersections of vectors of any type, such as numeric:

```r
intersect(1:10, 6:15)
```

or characters:

```r
intersect(c("a","b","c"), c("b","c","d"))
```

The **dplyr** package includes an `intersect` function that can be applied to tables with the same column names.

Intersect

This function returns the rows in common between two tables. To make sure we use the **dplyr** version of `intersect` rather than the base package version, we can use `dplyr::intersect` like this:

```
tab_1 <- tab[1:5,]
tab_2 <- tab[3:7,]
dplyr::intersect(tab_1, tab_2)
```

Union

Similarly *union* takes the union of vectors. For example:

```r
union(1:10, 6:15)
union(c("a","b","c"), c("b","c","d"))
```

The **dplyr** package includes a version of `union` that combines all the rows of two tables with the same column names.

```r
tab_1 <- tab[1:5,]
tab_2 <- tab[3:7,]
dplyr::union(tab_1, tab_2)
```

setdiff

The set difference between a first and second argument can be obtained with `setdiff`. Unlike `intersect` and `union`, this function is not symmetric:

```
setdiff(1:10, 6:15)
```

As with the functions shown above, dplyr has a version for data frames:

```
tab_1 <- tab[1:5,]
tab_2 <- tab[3:7,]
dplyr::setdiff(tab_1, tab_2)
```

setequal

Finally, the function `setequal` tells us if two sets are the same, regardless of order. So notice that:

```
setequal(1:5, 1:6)
#> [1] FALSE
```

but:

```
setequal(1:5, 5:1)
#> [1] TRUE
```

setequal

When applied to data frames that are not equal, regardless of order, the dplyr version provides a useful message letting us know how the sets are different:

```
dplyr::setequal(tab_1, tab_2)
```

Exercises

1. Install and load the **Lahman** library. This database includes data related to baseball teams. It includes summary statistics about how the players performed on offense and defense for several years. It also includes personal information about the players.

The `Batting` data frame contains the offensive statistics for all players for many years. You can see, for example, the top 10 hitters by running this code:

```r
library(Lahman)

top <- Batting %>%
  filter(yearID == 2016) %>%
  arrange(desc(HR)) %>%
  slice(1:10)

top %>% as_tibble()
```

Exercises

But who are these players? We see an ID, but not the names. The player names are in this table

```
Master %>% as_tibble()
```

We can see column names `nameFirst` and `nameLast`. Use the `left_join` function to create a table of the top home run hitters. The table should have `playerID`, first name, last name, and number of home runs (HR). Rewrite the object `top` with this new table.

Exercises

2. Now use the `Salaries` data frame to add each player's salary to the table you created in exercise 1. Note that salaries are different every year so make sure to filter for the year 2016, then use `right_join`. This time show first name, last name, team, HR, and salary.

Exercises

3. In a previous exercise, we created a tidy version of the co2 dataset:

```
co2_wide <- data.frame(matrix(co2, ncol = 12, byrow = TRUE)) %
  setNames(1:12) %>%
  mutate(year = 1959:1997) %>%
  pivot_longer(-year, names_to = "month", values_to = "co2") %
  mutate(month = as.numeric(month))
```

We want to see if the monthly trend is changing so we are going to remove the year effects and then plot the results. We will first compute the year averages. Use the `group_by` and `summarize` to compute the average co2 for each year. Save in an object called `yearly_avg`.

Exercises

4. Now use the `left_join` function to add the yearly average to the `co2_wide` dataset. Then compute the residuals: observed co2 measure - yearly average.

5. Make a plot of the seasonal trends by year but only after removing the year effect.