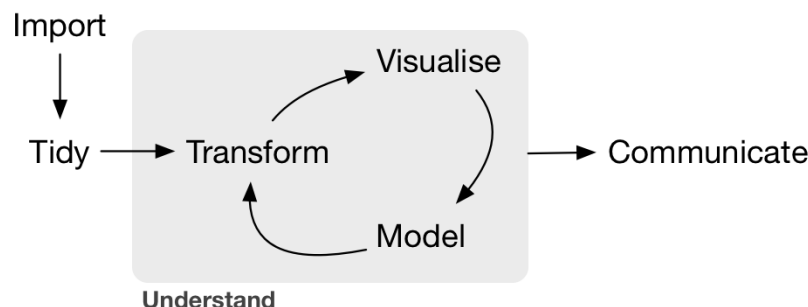


# Data Wrangling with `dplyr`

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Once data has been transformed into a **tidy** tabular format, an important part of “data wrangling” or “data munging” is data transformation.



We have learned about some functions in the R package `dplyr` that can transform and summarize tabular data with rows and columns. For example, when data is a tabular format, you have seen how we can use `dplyr` to `filter()` rows, `select()` columns and add new columns using `mutate()`. Now we will explore some more advanced `dplyr` functionality.

## Brief recap of `dplyr`

`dplyr` is a powerful R-package to transform and summarize tabular data with rows and columns.

The package contains a set of functions (or “verbs”) to perform common data manipulation operations such as filtering for rows, selecting specific columns, re-ordering rows, adding new columns and summarizing data. In addition, `dplyr` contains a useful function to perform another common task which is the “split-apply-combine” concept. We will discuss that in a little bit.

## Data

### mammals sleep

The `msleep` (mammals sleep) data set contains the sleeptimes and weights for a set of mammals and is available in the [data repository on GitHub](https://raw.githubusercontent.com/datasciencelabs/data/master/msleep_ggplot2.csv). This data set contains 83 rows and 11 variables.

To load the `msleep` data set

```
library(readr)
library(dplyr)
library(ggplot2)

msleep <- read_csv("https://raw.githubusercontent.com/datasciencelabs/data/master/msleep_ggplot2.csv")
msleep
```

```
## Source: local data frame [83 x 11]
##
##           name      genus  vore      order conservation
```

```
##           (chr)      (chr) (chr)      (chr)      (chr)
## 1          Cheetah    Acinonyx carni    Carnivora      lc
## 2          Owl monkey    Aotus  omni    Primates      NA
## 3      Mountain beaver Aplodontia herbi    Rodentia      nt
## 4 Greater short-tailed shrew    Blarina  omni Soricomorpha      lc
## 5              Cow          Bos herbi Artiodactyla domesticated
## 6      Three-toed sloth    Bradypus herbi    Pilosa      NA
## 7      Northern fur seal Callorhinus carni    Carnivora      vu
## 8          Vesper mouse    Calomys    NA    Rodentia      NA
## 9              Dog          Canis carni    Carnivora domesticated
## 10         Roe deer    Capreolus herbi Artiodactyla      lc
## ..           ...      ...      ...      ...      ...
## Variables not shown: sleep_total (dbl), sleep_rem (dbl), sleep_cycle
##      (dbl), awake (dbl), brainwt (dbl), bodywt (dbl)
```

The columns (in order) correspond to the following:

column name	Description
<code>name</code>	common name
<code>genus</code>	taxonomic rank
<code>vore</code>	carnivore, omnivore or herbivore?
<code>order</code>	taxonomic rank
<code>conservation</code>	the conservation status of the mammal
<code>sleep_total</code>	total amount of sleep, in hours
<code>sleep_rem</code>	rem sleep, in hours
<code>sleep_cycle</code>	length of sleep cycle, in hours
<code>awake</code>	amount of time spent awake, in hours
<code>brainwt</code>	brain weight in kilograms
<code>bodywt</code>	body weight in kilograms

## Important dplyr verbs to remember

dplyr verbs	Description
<code>select()</code>	select columns
<code>mutate()</code>	create new columns
<code>filter()</code>	filter rows
<code>arrange()</code>	re-order or arrange rows
<code>summarise()</code>	summarise values
<code>group_by()</code>	allows for group operations in the “split-apply-combine” concept

## dplyr verbs in action

### `select()` and `mutate()` columns; `filter()` rows

The two most basic functions are `select()` and `filter()` which selects columns and filters rows, respectively. The function `mutate()` can be used to create new columns. We have already seen examples of all of these in class.

For example, to select a range of columns by name, use the “:” (colon) operator

```
msleep %>% select(name:order)
```

```
## Source: local data frame [83 x 4]
##
##           name      genus vore      order
##           (chr)     (chr) (chr)    (chr)
## 1      Cheetah    Acinonyx carni   Carnivora
## 2      Owl monkey    Aotus  omni    Primates
## 3      Mountain beaver Aplodontia herbi   Rodentia
## 4 Greater short-tailed shrew Blarina  omni Soricomorpha
## 5      Cow        Bos  herbi Artiodactyla
## 6      Three-toed sloth Bradypus herbi   Pilosa
## 7      Northern fur seal Callorhinus carni   Carnivora
## 8      Vesper mouse   Calomys  NA     Rodentia
## 9      Dog          Canis  carni   Carnivora
## 10     Roe deer     Capreolus herbi Artiodactyla
## ..           ...      ...    ...      ...
```

To select all columns that start with the character string "sl", use the function `starts_with()`

```
msleep %>% select(starts_with("sl"))
```

```
## Source: local data frame [83 x 3]
##
##      sleep_total sleep_rem sleep_cycle
##      (dbl)      (dbl)      (dbl)
## 1      12.1        NA        NA
## 2      17.0        1.8        NA
## 3      14.4        2.4        NA
## 4      14.9        2.3    0.1333333
## 5       4.0        0.7    0.6666667
## 6      14.4        2.2    0.7666667
## 7       8.7        1.4    0.3833333
## 8       7.0        NA        NA
## 9      10.1        2.9    0.3333333
## 10     3.0        NA        NA
## ..           ...      ...      ...
```

Some additional options to select columns based on a specific criteria include

1. `ends_with()` = Select columns that end with a character string
2. `contains()` = Select columns that contain a character string
3. `matches()` = Select columns that match a regular expression
4. `one_of()` = Select columns names that are from a group of names

**Assessment** Select all columns except those from `genus` to `conservation` and filter the rows for mammals that sleep a total of more than 16 hours and have a body weight of greater than 1 kilogram

```
## Provide your code here
```

```
msleep %>%  
  select(-(genus:conservation)) %>%  
  filter(sleep_total >= 16, bodywt >= 1)
```

```
## Source: local data frame [3 x 7]
```

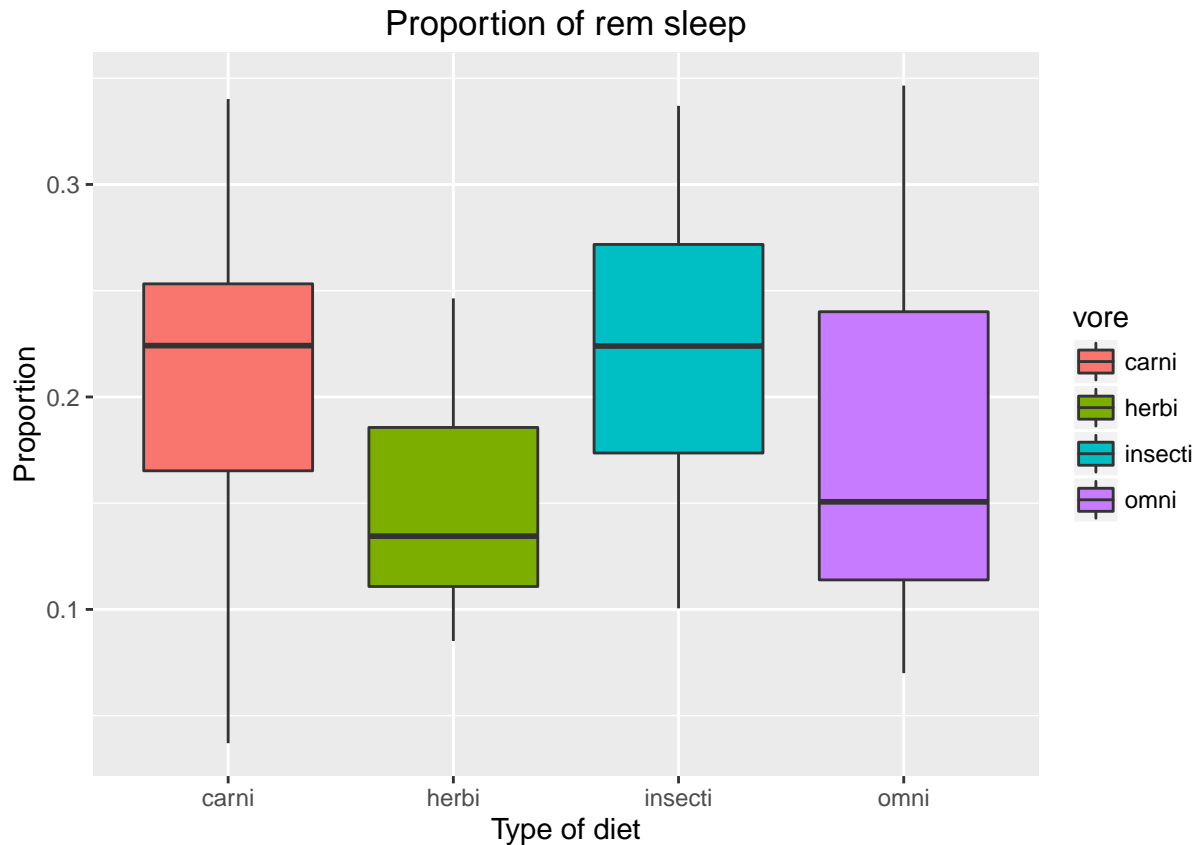
```
##  
##           name sleep_total sleep_rem sleep_cycle awake brainwt  
##           (chr)      (dbl)    (dbl)      (dbl) (dbl)  (dbl)  
## 1 Long-nosed armadillo      17.4      3.1  0.3833333  6.6  0.0108  
## 2 North American Opossum     18.0      4.9  0.3333333  6.0  0.0063  
## 3      Giant armadillo      18.1      6.1         NA   5.9  0.0810  
## Variables not shown: bodywt (dbl)
```

**Assessment** Create a new column called `rem_proportion` which is the ratio of rem sleep to total amount of sleep and create boxplots of the `rem_proportion` column split and colored by the `vore` column. Create labels for the x and y axis.

```
## Provide your code here
```

```
msleep %>%  
  mutate(rem_proportion = sleep_rem / sleep_total) %>%  
  ggplot(aes(x = vore, y = rem_proportion, fill = vore)) +  
    geom_boxplot() + xlab("Type of diet") +  
    ylab("Proportion") + labs(title = "Proportion of rem sleep")
```

```
## Warning: Removed 27 rows containing non-finite values (stat_boxplot).
```



**Assessment (optional)** Select all columns that start with the character string “sl” or ends with the character string “wt”, create a new column called `rem_proportion` which is the ratio of rem sleep to total amount of sleep, create a second column `bodywt_grams` which is the bodywt column in grams and filter for the rows 20 to 30 in the `msleep` data set by numerical position.

Hint: Look at the `slice()` help file to filter for rows by numerical position.

## Provide your code here

```
msleep %>%
  select(starts_with("sl"), ends_with("wt")) %>%
  mutate(rem_proportion = sleep_rem / sleep_total,
         bodywt_grams = bodywt * 1000) %>%
  slice(20:30)
```

## Source: local data frame [11 x 7]

```
##
##   sleep_total sleep_rem sleep_cycle brainwt  bodywt rem_proportion
##   (dbl)      (dbl)      (dbl)      (dbl)    (dbl)      (dbl)
## 1    18.0        4.9    0.3333333  0.0063    1.700    0.2722222
## 2     3.9         NA         NA    4.6030 2547.000         NA
## 3    19.7        3.9    0.1166667  0.0003    0.023    0.1979695
## 4     2.9        0.6    1.0000000  0.6550   521.000    0.2068966
## 5     3.1        0.4         NA    0.4190   187.000    0.1290323
## 6    10.1        3.5    0.2833333  0.0035    0.770    0.3465347
## 7    10.9        1.1         NA    0.1150   10.000    0.1009174
```

```
## 8      14.9      NA      NA      NA      0.071      NA
## 9      12.5      3.2  0.4166667  0.0256  3.300      0.2560000
## 10      9.8      1.1  0.5500000  0.0050  0.200      0.1122449
## 11      1.9      0.4      NA      NA  899.995      0.2105263
## Variables not shown: bodywt_grams (dbl)
```

## Arrange or re-order rows using `arrange()`

To arrange (or re-order) rows by a particular column such as the taxonomic order, list the name of the column you want to arrange the rows by

```
msleep %>%
  arrange(order)
```

```
## Source: local data frame [83 x 11]
##
##      name      genus vore      order conservation
##      (chr)      (chr) (chr)      (chr)      (chr)
## 1      Tenrec      Tenrec  omni  Afrosoricida      NA
## 2      Cow        Bos  herbi  Artiodactyla  domesticated
## 3      Roe deer    Capreolus  herbi  Artiodactyla      lc
## 4      Goat        Capri  herbi  Artiodactyla      lc
## 5      Giraffe      Giraffa  herbi  Artiodactyla      cd
## 6      Sheep        Ovis  herbi  Artiodactyla  domesticated
## 7      Pig          Sus   omni  Artiodactyla  domesticated
## 8      Cheetah      Acinonyx  carni  Carnivora      lc
## 9      Northern fur seal Callorhinus  carni  Carnivora      vu
## 10     Dog          Canis  carni  Carnivora  domesticated
## ..      ...      ...      ...      ...      ...
## Variables not shown: sleep_total (dbl), sleep_rem (dbl), sleep_cycle
##      (dbl), awake (dbl), brainwt (dbl), bodywt (dbl)
```

**Assessment** Select all columns names with the characters “sleep” and arrange the rows for the `sleep_rem` in a decreasing order.

Hint: look at the `?arrange` help file for the `desc()` option.

```
## Provide your code here
```

```
msleep %>%
  select(matches("sleep")) %>%
  arrange(desc(sleep_rem))
```

```
## Source: local data frame [83 x 3]
##
##      sleep_total sleep_rem sleep_cycle
##      (dbl)      (dbl)      (dbl)
## 1      19.4      6.6      NA
## 2      18.1      6.1      NA
## 3      18.0      4.9  0.3333333
## 4      19.7      3.9  0.1166667
## 5      10.1      3.5  0.2833333
```

```
## 6      13.8      3.4  0.2166667
## 7      12.5      3.2  0.4166667
## 8      17.4      3.1  0.3833333
## 9      14.3      3.1  0.2000000
## 10     15.9      3.0      NA
## ..      ...      ...      ...
```

**Assessment** Select three columns from `msleep` (`name`, `order`, `sleep_total`), arrange the rows in the `sleep_total` column in a descending order, and filter the rows for mammals that sleep for a total of 16 or more hours.

```
## Provide your code here
```

```
msleep %>%
  select(name, order, sleep_total) %>%
  arrange(order, desc(sleep_total)) %>%
  filter(sleep_total >= 16)
```

```
## Source: local data frame [8 x 3]
##
##           name           order sleep_total
##           (chr)          (chr)      (dbl)
## 1 Little brown bat    Chiroptera    19.9
## 2 Big brown bat      Chiroptera    19.7
## 3 Giant armadillo     Cingulata     18.1
## 4 Long-nosed armadillo Cingulata     17.4
## 5 Thick-tailed opossum Didelphimorphia 19.4
## 6 North American Opossum Didelphimorphia 18.0
## 7 Owl monkey          Primates      17.0
## 8 Arctic ground squirrel Rodentia     16.6
```

**Create summaries of the data frame using `summarise()`**

The `summarise()` function will create summary statistics for a given column in the data frame such as finding the mean. For example, to compute the average number of hours of sleep, apply the `mean()` function to the column `sleep_total` and call the summary value `avg_sleep`.

```
msleep %>%
  summarise(avg_sleep = mean(sleep_total))
```

```
## Source: local data frame [1 x 1]
##
##   avg_sleep
##   (dbl)
## 1  10.43373
```

There are many other summary statistics you could consider such `sd()`, `min()`, `max()`, `median()`, `sum()`, `n()` (returns the length of vector), `first()` (returns first value in vector), `last()` (returns last value in vector) and `n_distinct()` (number of distinct values in vector).

**Assessment** Summarize `sleep_total` column in the `msleep` data set with the average sleep, the minimum and maximum amount of sleep, and the total number of mammals.

```
## Provide your code here

msleep %>%
  summarise(avg_sleep = mean(sleep_total),
            min_sleep = min(sleep_total),
            max_sleep = max(sleep_total),
            total = n())
```

```
## Source: local data frame [1 x 4]
##
##   avg_sleep min_sleep max_sleep total
##   (dbl)      (dbl)      (dbl) (int)
## 1  10.43373      1.9      19.9    83
```

### Group operations using `group_by()`

The `group_by()` verb is an important function in `dplyr`. As we mentioned before it's related to concept of "split-apply-combine". We literally want to split the data frame by some variable (e.g. `vore`), apply a function to the individual data frames and then combine the output.

Say we wanted to calculate the standard deviation of the body and brain weights for each of factor in the `vore` column. First, we can look at the types of factors in the `vore` column

```
table(msleep$vore)
```

```
##
##   carni   herbi insecti   omni
##    19     32         5    20
```

Then, we could use `filter()` to filter for rows that contain "carni" in the `vore` column and summarize with the mean of the brain and body weights.

```
msleep %>%
  filter(vore == "carni") %>%
  summarize("bodywt_sd" = mean(bodywt),
            "brainwt_sd" = mean(brainwt, na.rm = TRUE))
```

```
## Source: local data frame [1 x 2]
##
##   bodywt_sd brainwt_sd
##   (dbl)      (dbl)
## 1  90.75111  0.07925556
```

We could repeat this for each factor in `vore`, which is a bit tedious. Instead, we could use this using the `group_by()` function.

Let's do that: split the `msleep` data frame by the `vore` column, then calculate the mean of body weight and brain weight for each individual data frame. (hint: We expect a set of summary statistics for each level in `vore`.)



```
msleep %>%
  group_by(vore) %>%
  summarize("bodywt_sd" = mean(bodywt),
            "brainwt_sd" = mean(brainwt, na.rm = TRUE))
```

```
## Source: local data frame [5 x 3]
##
##      vore bodywt_sd brainwt_sd
##      (chr)      (dbl)      (dbl)
## 1   carni  90.75111 0.07925556
## 2   herbi 366.87725 0.62159750
## 3 insecti  12.92160 0.02155000
## 4    omni  12.71800 0.14573118
## 5      NA   0.85800 0.00762600
```

**Assessment** Split the `msleep` data frame by the taxonomic order, then for each taxonomic order summarize the `sleep_total` with the average sleep, the minimum and maximum amount of sleep, and the total number of mammals in each order.

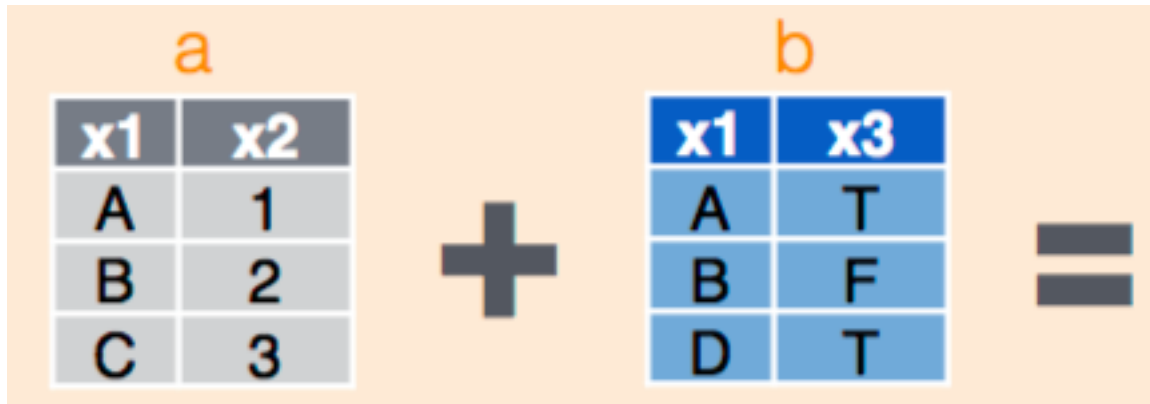
```
## Provide your code here
```

```
msleep %>%
  group_by(order) %>%
  summarise(avg_sleep = mean(sleep_total),
            min_sleep = min(sleep_total),
            max_sleep = max(sleep_total),
            total = n())
```

```
## Source: local data frame [19 x 5]
##
##      order avg_sleep min_sleep max_sleep total
##      (chr)      (dbl)      (dbl)      (dbl) (int)
## 1   Afrosoricida 15.600000      15.6      15.6      1
## 2   Artiodactyla  4.516667       1.9       9.1      6
## 3     Carnivora 10.116667       3.5     15.8     12
## 4     Cetacea  4.500000       2.7       5.6      3
## 5   Chiroptera 19.800000     19.7     19.9      2
## 6    Cingulata 17.750000     17.4     18.1      2
## 7 Didelphimorphia 18.700000     18.0     19.4      2
## 8   Diprotodontia 12.400000     11.1     13.7      2
## 9   Erinaceomorpha 10.200000     10.1     10.3      2
## 10   Hyracoidea  5.666667       5.3       6.3      3
## 11   Lagomorpha  8.400000       8.4       8.4      1
## 12   Monotremata  8.600000       8.6       8.6      1
## 13 Perissodactyla  3.466667       2.9       4.4      3
## 14     Pilosa 14.400000     14.4     14.4      1
## 15    Primates 10.500000       8.0     17.0     12
## 16   Proboscidea  3.600000       3.3       3.9      2
## 17    Rodentia 12.468182       7.0     16.6     22
## 18   Scandentia  8.900000       8.9       8.9      1
## 19   Soricomorpha 11.100000       8.4     14.9      5
```

## joining two data frames in dplyr

The last part of `dplyr` that we will discuss are a set of `dplyr` verbs that allow you to join two data sets. The following are cartoons extracted from [Data Wrangling with dplyr and tidyr Cheatsheet from RStudio](#) to illustrate the different ways to join data frames using `dplyr`.



Two types of functions to join together data frames

### 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.

## Data

For this section, we will work with two small data sets related to the 2016 Oscars Nominations. The two data sets are `oscars` and `movies`. The first data set contains information about the the name of the actor/actress, the name of the movie and the category for nomination. The second data set contains a list of movies and the length of the movie in minutes.

We will explore the `dplyr` verbs to join the two tables. First let's load the data.

```
library(readr)

oscars <- "
name,movie,category
Adam McKay,The Big Short,Best Director
Alejandro González Iñárritu,The Revenant,Best Director
Lenny Abrahamson,Room,Best Director
Tom McCarthy,Spotlight,Best Director
George Miller,Mad Max: Fury Road,Best Director
Bryan Cranston,Trumbo,Best Actor
Matt Damon,The Martian,Best Actor
Michael Fassbender,Steve Jobs,Best Actor
Leonardo DiCaprio,The Revenant,Best Actor
Eddie Redmayne,The Danish Girl,Best Actor
Cate Blanchett,Carol,Best Actress
Brie Larson,Room,Best Actress
Jennifer Lawrence,Joy,Best Actress
Charlotte Rampling,45 Years,Best Actress
Saoirse Ronan,Brooklyn,Best Actress
"

oscars <- read_csv(oscars, trim_ws = TRUE, skip = 1)
oscars
```

```
## Source: local data frame [15 x 3]
##
##           name           movie      category
##           (chr)          (chr)      (chr)
## 1      Adam McKay      The Big Short Best Director
## 2 Alejandro González Iñárritu The Revenant Best Director
## 3      Lenny Abrahamson      Room Best Director
## 4      Tom McCarthy      Spotlight Best Director
## 5      George Miller Mad Max: Fury Road Best Director
```

## 6	Bryan Cranston	Trumbo	Best Actor
## 7	Matt Damon	The Martian	Best Actor
## 8	Michael Fassbender	Steve Jobs	Best Actor
## 9	Leonardo DiCaprio	The Revenant	Best Actor
## 10	Eddie Redmayne	The Danish Girl	Best Actor
## 11	Cate Blanchett	Carol	Best Actress
## 12	Brie Larson	Room	Best Actress
## 13	Jennifer Lawrence	Joy	Best Actress
## 14	Charlotte Rampling	45 Years	Best Actress
## 15	Saoirse Ronan	Brooklyn	Best Actress

```

movies <- "
movie,length_mins
The Big Short,130
Star Wars: The Force Awakens,135
Brooklyn,111
Mad Max: Fury Road,120
Room,118
The Martian,144
The Revenant,156
Spotlight,128
"
movies <- read_csv(movies, trim_ws = TRUE, skip = 1)
movies

```

```

## Source: local data frame [8 x 2]
##
##           movie length_mins
##           (chr)      (int)
## 1           The Big Short      130
## 2 Star Wars: The Force Awakens 135
## 3           Brooklyn         111
## 4 Mad Max: Fury Road         120
## 5           Room            118
## 6           The Martian      144
## 7           The Revenant     156
## 8           Spotlight       128

```

`inner_join(x,y)`

This function joins all rows from x where there are matching values in y, and all columns from x and y. If there are multiple matches between x and y, all combination of the matches are returned.

```
inner_join(oscars, movies, by = "movie")
```

```

## Source: local data frame [9 x 4]
##
##           name           movie      category length_mins
##           (chr)      (chr)      (chr)      (int)
## 1           Adam McKay   The Big Short Best Director      130
## 2 Alejandro González Iñárritu The Revenant Best Director      156
## 3           Lenny Abrahamson Room Best Director      118

```

## 4	Tom McCarthy	Spotlight	Best Director	128
## 5	George Miller	Mad Max: Fury Road	Best Director	120
## 6	Matt Damon	The Martian	Best Actor	144
## 7	Leonardo DiCaprio	The Revenant	Best Actor	156
## 8	Brie Larson	Room	Best Actress	118
## 9	Saoirse Ronan	Brooklyn	Best Actress	111

`semi_join(x,y)`

This function returns all rows from x where there are matching values in y, keeping just columns from x. A semi join differs from an inner join because an inner join will return one row of x for each matching row of y, where a semi join will never duplicate rows of x.

```
semi_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [9 x 3]
##
##           name           movie      category
##           (chr)          (chr)      (chr)
## 1      Adam McKay      The Big Short Best Director
## 2    Saoirse Ronan      Brooklyn   Best Actress
## 3    George Miller Mad Max: Fury Road Best Director
## 4    Lenny Abrahamson      Room     Best Director
## 5      Brie Larson      Room     Best Actress
## 6      Matt Damon      The Martian Best Actor
## 7 Alejandro González Iñárritu The Revenant Best Director
## 8    Leonardo DiCaprio The Revenant Best Actor
## 9      Tom McCarthy      Spotlight Best Director
```

**Assessment** Try applying the `semi_join()` function with `x=movies` and `y=oscars`. What is the difference?

```
## Provide your code here
```

```
semi_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [7 x 2]
##
##           movie length_mins
##           (chr)      (int)
## 1    The Big Short      130
## 2    The Revenant      156
## 3      Room            118
## 4    Spotlight        128
## 5 Mad Max: Fury Road    120
## 6    The Martian      144
## 7    Brooklyn        111
```

**Assessment**

Using the `dplyr` join functions, combine the columns from the `oscars` and `movies` data sets and return all rows from the `oscars` data set and all columns in both the `oscars` and `movies` columns.

Hint: read the help file for `left_join()` or `right_join()`.

```
## Provide your code here
```

```
left_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [15 x 4]
##
##           name           movie      category
##       (chr)         (chr)      (chr)
## 1      Adam McKay      The Big Short Best Director
## 2 Alejandro González Iñárritu    The Revenant Best Director
## 3      Lenny Abrahamson          Room Best Director
## 4      Tom McCarthy      Spotlight Best Director
## 5      George Miller Mad Max: Fury Road Best Director
## 6      Bryan Cranston      Trumbo    Best Actor
## 7      Matt Damon       The Martian Best Actor
## 8      Michael Fassbender      Steve Jobs Best Actor
## 9      Leonardo DiCaprio    The Revenant Best Actor
## 10     Eddie Redmayne    The Danish Girl Best Actor
## 11     Cate Blanchett          Carol Best Actress
## 12     Brie Larson       Room Best Actress
## 13     Jennifer Lawrence          Joy Best Actress
## 14     Charlotte Rampling      45 Years Best Actress
## 15     Saoirse Ronan      Brooklyn Best Actress
## Variables not shown: length_mins (int)
```

```
## or
```

```
right_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [15 x 4]
##
##           movie length_mins           name
##       (chr)      (int)      (chr)
## 1      The Big Short      130      Adam McKay
## 2      The Revenant      156 Alejandro González Iñárritu
## 3          Room      118      Lenny Abrahamson
## 4      Spotlight      128      Tom McCarthy
## 5 Mad Max: Fury Road      120      George Miller
## 6      Trumbo      NA      Bryan Cranston
## 7      The Martian      144      Matt Damon
## 8      Steve Jobs      NA      Michael Fassbender
## 9      The Revenant      156      Leonardo DiCaprio
## 10     The Danish Girl      NA      Eddie Redmayne
## 11          Carol      NA      Cate Blanchett
## 12          Room      118      Brie Larson
## 13          Joy      NA      Jennifer Lawrence
## 14      45 Years      NA      Charlotte Rampling
## 15     Brooklyn      111      Saoirse Ronan
## Variables not shown: category (chr)
```

Why are there NAs?

## Assessment

Using the `dplyr` join functions, combine the columns from the `oscars` and `movies` data sets and return all rows from the `movies` data set and all columns in both the `oscars` and `movies` columns.

```
## Provide your code here
```

```
right_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [10 x 4]
```

```
##
```

	name (chr)	movie (chr)	category (chr)
## 1	Adam McKay	The Big Short	Best Director
## 2	NA	Star Wars: The Force Awakens	NA
## 3	Saoirse Ronan	Brooklyn	Best Actress
## 4	George Miller	Mad Max: Fury Road	Best Director
## 5	Lenny Abrahamson	Room	Best Director
## 6	Brie Larson	Room	Best Actress
## 7	Matt Damon	The Martian	Best Actor
## 8	Alejandro González Iñárritu	The Revenant	Best Director
## 9	Leonardo DiCaprio	The Revenant	Best Actor
## 10	Tom McCarthy	Spotlight	Best Director

```
## Variables not shown: length_mins (int)
```

```
## or
```

```
left_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [10 x 4]
```

```
##
```

	movie (chr)	length_mins (int)	name (chr)
## 1	The Big Short	130	Adam McKay
## 2	Star Wars: The Force Awakens	135	NA
## 3	Brooklyn	111	Saoirse Ronan
## 4	Mad Max: Fury Road	120	George Miller
## 5	Room	118	Lenny Abrahamson
## 6	Room	118	Brie Larson
## 7	The Martian	144	Matt Damon
## 8	The Revenant	156	Alejandro González Iñárritu
## 9	The Revenant	156	Leonardo DiCaprio
## 10	Spotlight	128	Tom McCarthy

```
## Variables not shown: category (chr)
```

```
full_join(x,y)
```

This function returns all rows and all columns from both `x` and `y`. When there are not matching values, it will return `NA` for the one missing.

```
full_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [16 x 4]
##
##           name                movie      category
##           (chr)              (chr)      (chr)
## 1           Adam McKay          The Big Short Best Director
## 2 Alejandro González Iñárritu    The Revenant Best Director
## 3           Lenny Abrahamson      Room Best Director
## 4           Tom McCarthy          Spotlight Best Director
## 5           George Miller         Mad Max: Fury Road Best Director
## 6           Bryan Cranston        Trumbo   Best Actor
## 7           Matt Damon            The Martian Best Actor
## 8           Michael Fassbender    Steve Jobs Best Actor
## 9           Leonardo DiCaprio     The Revenant Best Actor
## 10          Eddie Redmayne        The Danish Girl Best Actor
## 11          Cate Blanchett        Carol   Best Actress
## 12          Brie Larson           Room   Best Actress
## 13          Jennifer Lawrence     Joy    Best Actress
## 14          Charlotte Rampling    45 Years Best Actress
## 15          Saoirse Ronan         Brooklyn Best Actress
## 16                                     NA Star Wars: The Force Awakens NA
## Variables not shown: length_mins (int)
```

```
full_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [16 x 4]
##
##           movie length_mins      name
##           (chr)      (int)      (chr)
## 1           The Big Short      130      Adam McKay
## 2 Star Wars: The Force Awakens  135      NA
## 3           Brooklyn          111      Saoirse Ronan
## 4           Mad Max: Fury Road  120      George Miller
## 5           Room              118      Lenny Abrahamson
## 6           Room              118      Brie Larson
## 7           The Martian        144      Matt Damon
## 8           The Revenant        156 Alejandro González Iñárritu
## 9           The Revenant        156      Leonardo DiCaprio
## 10          Spotlight          128      Tom McCarthy
## 11          Trumbo             NA      Bryan Cranston
## 12          Steve Jobs          NA      Michael Fassbender
## 13          The Danish Girl      NA      Eddie Redmayne
## 14          Carol              NA      Cate Blanchett
## 15          Joy                NA      Jennifer Lawrence
## 16          45 Years            NA      Charlotte Rampling
## Variables not shown: category (chr)
```

## Assessment

Using the `dplyr` join functions, return all rows from `oscars` data set where there are not matching values in `movies`, only keeping the columns from the `oscars` data set.

Hint: Read the help file for `anti_join()`.



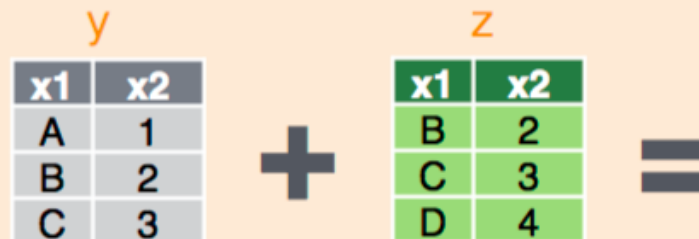
```
## Provide your code here
```

```
anti_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [6 x 3]
```

```
##           name           movie    category
##      (chr)      (chr)      (chr)
## 1 Charlotte Rampling    45 Years Best Actress
## 2  Jennifer Lawrence      Joy Best Actress
## 3   Cate Blanchett      Carol Best Actress
## 4  Eddie Redmayne The Danish Girl Best Actor
## 5 Michael Fassbender  Steve Jobs Best Actor
## 6   Bryan Cranston    Trumbo Best Actor
```

Other functions in dplyr to join together data frames



## Set Operations

x1	x2
B	2
C	3

**dplyr::intersect(y, z)**

Rows that appear in both y and z.

x1	x2
A	1
B	2
C	3
D	4

**dplyr::union(y, z)**

Rows that appear in either or both y and z.

x1	x2
A	1

**dplyr::setdiff(y, z)**

Rows that appear in y but not z.

## Binding

x1	x2
A	1
B	2
C	3
B	2
C	3
D	4

### **dplyr::bind\_rows(y, z)**

Append z to y as new rows.

x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4

### **dplyr::bind\_cols(y, z)**

Append z to y as new columns.

Caution: matches rows by position.

## Cheatsheets

- [Data Wrangling with dplyr and tidyr from RStudio](#)