

# Data transformation with dplyr

Day 2 - Introduction to Data Analysis with R

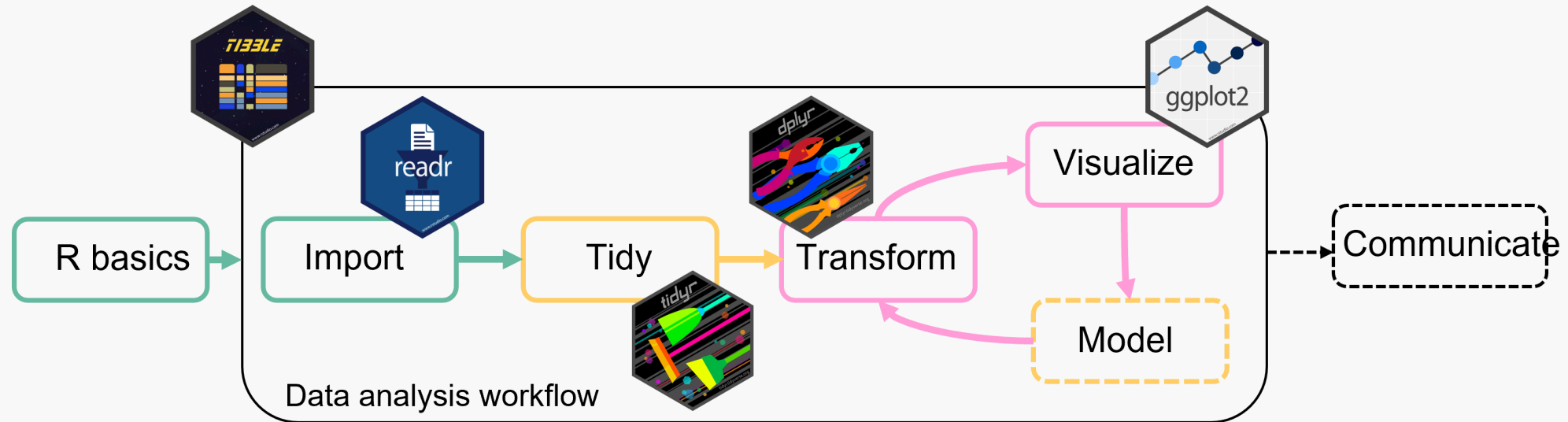
Selina Baldauf

Freie Universität Berlin - Theoretical Ecology

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# Data transformation

Data transformation is an important step in **understanding** the data and **preparing** it for further analysis.



We can use the tidyverse package **dp1yr** for this.

# Data transformation

With **dplyr** we can (among other things)

- **Filter** data to analyse only a part of it
- **Create** new variables
- **Summarize** data
- **Combine** multiple tables
- **Rename** variables
- **Reorder** observations or variables

To get started load the package **dplyr**:

```
library(dplyr)
# or
library(tidyverse)
```

# Dplyr basic vocabulary

All of the **dp1yr** functions work similarly:

- **First argument** is the data (a tibble)
- **Other arguments** specify what to do exactly
- **Return** a tibble

# The data

Data set **and\_vertebrates** with measurements of a trout and 2 salamander species in different forest sections.

- **year**: observation year
- **section**: CC (clear cut forest) or OG (old growth forest)
- **unittype**: channel classification (C = Cascade, P = Pool, ...)
- **species**: Species measured
- **length\_1\_mm**: body length [mm]
- **weight\_g**: body weight [g]



Coastal giant salamander (terrestrial form)  
Andrews Forest Program by Lina DiGregorio  
via CC-BY from  
<https://andrewsforest.oregonstate.edu>

References: [Kaylor, M.J. and D.R. Warren. \(2017\)](#) and  
[Gregory, S.V. and I. Arismendi. \(2020\)](#) as provided in the  
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# The data

Data set `and_vertebrates` with measurements of a trout and 2 salamander species in different forest sections.

```
library(literdatasampler)
vertebrates <- and_vertebrates |>
  select(year, section, unitttype, species, length_1_mm, weight_g) |>
  filter(species != "Cascade torrent salamander")
vertebrates
#> # A tibble: 32,191 × 6
#>   year section unitttype species      length_1_mm weight_g
#>   <dbl> <chr>    <chr>    <chr>          <dbl>      <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75
#> 2  1987 CC      R      Cutthroat trout      61      1.95
#> 3  1987 CC      R      Cutthroat trout      89      5.6
#> 4  1987 CC      R      Cutthroat trout      58      2.15
#> 5  1987 CC      R      Cutthroat trout      93      6.9
#> 6  1987 CC      R      Cutthroat trout      86      5.9
#> 7  1987 CC      R      Cutthroat trout     107     10.5
#> 8  1987 CC      R      Cutthroat trout     131     20.6
#> 9  1987 CC      R      Cutthroat trout     103      9.55
#> 10 1987 CC      R      Cutthroat trout     117     13
#> # i 32,181 more rows
```

# filter()

picks rows based on their value

# filter()

Filter only the trout species:

```
filter(vertebrates, species == "Cutthroat trout")
#> # A tibble: 20,433 × 6
#>   year section unittype species      length_1_mm weight_g
#>   <dbl> <chr>    <chr>    <chr>      <dbl>      <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75
#> 2  1987 CC      R      Cutthroat trout      61      1.95
#> 3  1987 CC      R      Cutthroat trout      89      5.6
#> 4  1987 CC      R      Cutthroat trout      58      2.15
#> 5  1987 CC      R      Cutthroat trout      93      6.9
#> 6  1987 CC      R      Cutthroat trout      86      5.9
#> 7  1987 CC      R      Cutthroat trout     107     10.5
#> 8  1987 CC      R      Cutthroat trout     131     20.6
#> 9  1987 CC      R      Cutthroat trout     103      9.55
#> 10 1987 CC      R      Cutthroat trout     117      13
#> # i 20,423 more rows
```

`filter()` goes through each row of the data and return only those rows where the value for `species` is "Cutthroat trout"



# filter()

You can also combine filters using logical operators (&, |, !):

```
filter(vertebrates, species == "Cutthroat trout" & year == 1987)
#> # A tibble: 603 × 6
#>   year section unittype species      length_1_mm weight_g
#>   <dbl> <chr>   <chr>   <chr>         <dbl>      <dbl>
#> 1  1987 CC      R      Cutthroat trout      58        1.75
#> 2  1987 CC      R      Cutthroat trout      61        1.95
#> 3  1987 CC      R      Cutthroat trout      89         5.6
#> 4  1987 CC      R      Cutthroat trout      58        2.15
#> 5  1987 CC      R      Cutthroat trout      93         6.9
#> 6  1987 CC      R      Cutthroat trout      86         5.9
#> 7  1987 CC      R      Cutthroat trout     107        10.5
#> 8  1987 CC      R      Cutthroat trout     131        20.6
#> 9  1987 CC      R      Cutthroat trout     103         9.55
#> 10 1987 CC      R      Cutthroat trout     117         13
#> # i 593 more rows
```

# filter() + %in%

Use the `%in%` operator to filter rows based on multiple values, e.g. unittypes

```
unittypes_select <- c("R", "C", "S")
filter(vertebrates, unittypes %in% unittypes_select)
#> # A tibble: 19,619 × 6
#>   year section unittypes species      length_1_mm weight_g
#>   <dbl> <chr>   <chr>   <chr>         <dbl>     <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75
#> 2  1987 CC      R      Cutthroat trout      61      1.95
#> 3  1987 CC      R      Cutthroat trout      89      5.6
#> 4  1987 CC      R      Cutthroat trout      58      2.15
#> 5  1987 CC      R      Cutthroat trout      93      6.9
#> 6  1987 CC      R      Cutthroat trout      86      5.9
#> 7  1987 CC      R      Cutthroat trout     107     10.5
#> 8  1987 CC      R      Cutthroat trout     131     20.6
#> 9  1987 CC      R      Cutthroat trout     103      9.55
#> 10 1987 CC      R      Cutthroat trout     117     13
#> # i 19,609 more rows
```

# filter() + is.na()

Filter only rows that don't have a value for the weight

```
filter(vertebrates, is.na(weight_g))
#> # A tibble: 13,259 × 6
#>   year section unittype species      length_1_mm weight_g
#>   <dbl> <chr>    <chr>    <chr>      <dbl>      <dbl>
#> 1  1993 CC      P      Cutthroat trout      93        NA
#> 2  1993 CC      P      Cutthroat trout     175        NA
#> 3  1993 CC      P      Cutthroat trout     104        NA
#> 4  1993 CC      P      Cutthroat trout      98        NA
#> 5  1993 CC      P      Cutthroat trout      97        NA
#> 6  1993 CC      P      Cutthroat trout     123        NA
#> 7  1993 CC      P      Cutthroat trout     149        NA
#> 8  1993 CC      P      Cutthroat trout     100        NA
#> 9  1993 CC      P      Cutthroat trout     118        NA
#> 10 1993 CC      P      Cutthroat trout     163        NA
#> # i 13,249 more rows
```

Or the opposite: filter only the rows that have a value for the weight

```
filter(vertebrates, !is.na(weight_g))
```

# filter() + between()

## Combine different filters:

Filter rows where the value for **year** is between 2000 and 2005

```
filter(vertebrates, between(year, 2000, 2005))
#> # A tibble: 6,662 × 6
#>   year section unittype species      length_1_mm weight_g
#>   <dbl> <chr>   <chr>   <chr>         <dbl>     <dbl>
#> 1  2000 CC      C      Cutthroat trout      84      NA
#> 2  2000 CC      C      Cutthroat trout     132      NA
#> 3  2000 CC      C      Cutthroat trout     105      NA
#> 4  2000 CC      C      Cutthroat trout      41      NA
#> 5  2000 CC      C      Cutthroat trout      42      NA
#> 6  2000 CC      C      Cutthroat trout      42      NA
#> 7  2000 CC      C      Cutthroat trout      41      NA
#> 8  2000 CC      C      Cutthroat trout      51      NA
#> 9  2000 CC      C      Cutthroat trout      45      NA
#> 10 2000 CC      C      Cutthroat trout      44      NA
#> # i 6,652 more rows
```

Or you could also do it like this:

```
filter(vertebrates, year >= 2000 & year <= 2005)
```

# Useful `filter()` helpers

These functions and operators help you filter your observations:

- relational operators `<`, `>`, `==`, ...
- logical operators `&`, `|`, `!`
- `%in%` to filter multiple values
- `is.na()` to filter missing values
- `between()` to filter values that are between an upper and lower boundary
- `near()` to compare floating points (use instead of `==` for doubles)

# select()

picks columns based on their names

# select()

Select the columns `species`, `length_1_mm`, and `year`

```
select(vertebrates, species, length_1_mm, year)
#> # A tibble: 32,191 × 3
#>   species      length_1_mm year
#>   <chr>          <dbl> <dbl>
#> 1 Cutthroat trout         58  1987
#> 2 Cutthroat trout         61  1987
#> 3 Cutthroat trout         89  1987
#> 4 Cutthroat trout         58  1987
#> 5 Cutthroat trout         93  1987
#> 6 Cutthroat trout         86  1987
#> 7 Cutthroat trout        107  1987
#> 8 Cutthroat trout        131  1987
#> 9 Cutthroat trout        103  1987
#> 10 Cutthroat trout        117  1987
#> # i 32,181 more rows
```

Remove variables using `-`

```
select(vertebrates, -species, -length_1_mm, -year)
```

# select() + starts\_with()

Select all columns that start with "s"

```
select(vertebrates, starts_with("s"))
```

```
#> # A tibble: 32,191 × 2  
#>   section species  
#>   <chr>    <chr>  
#> 1 CC      Cutthroat trout  
#> 2 CC      Cutthroat trout  
#> 3 CC      Cutthroat trout  
#> # i 32,188 more rows
```

You can use the same structure for `ends_with()` and `contains()`.

```
# this does not make sense for the example data  
# but combinations like this are helpful for research data  
select(vertebrates, starts_with("_location1"))  
  
select(vertebrates, contains("_id_"))
```



# Useful `select()` helpers

- `starts_with()` and `ends_with()`: variable names that start/end with a specific string
- `contains()`: variable names that contain a specific string
- `matches()`: variable names that match a regular expression
- `any_of()` and `all_of()`: variables that are contained in a character vector

# mutate()

Adds new columns to your data

# mutate()

New columns can be added based on values from other columns

```
mutate(vertebrates, weight_kg = weight_g/1000)
```

```
#> # A tibble: 32,191 × 7
#>   year section unittype species      length_1_mm weight_g weight_kg
#>   <dbl> <chr>    <chr>    <chr>          <dbl>    <dbl>    <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75    0.00175
#> 2  1987 CC      R      Cutthroat trout      61      1.95    0.00195
#> 3  1987 CC      R      Cutthroat trout      89      5.6     0.0056
#> # i 32,188 more rows
```

Add multiple new columns at once:

```
mutate(vertebrates,
  weight_kg = weight_g/1000,
  length_m = length_1_mm/1000)
```

# mutate() + case\_when()

Use `case_when` to add column values conditional on other columns.

`case_when()` can combine many cases into one.

```
mutate(vertebrates,
  type = case_when(
    species == "Cutthroat trout" ~ "Fish",          # case 1
    species == "Coastal giant salamander" ~ "Amphibian", # case 2
    .default = NA                                     # all other
  ))
#> # A tibble: 32,191 × 7
#>   year section unittype species      length_1_mm weight_g type
#>   <dbl> <chr>   <chr>   <chr>          <dbl>    <dbl> <chr>
#> 1  1987 CC      R      Cutthroat trout      58      1.75 Fish
#> 2  1987 CC      R      Cutthroat trout      61      1.95 Fish
#> 3  1987 CC      R      Cutthroat trout      89      5.6  Fish
#> 4  1987 CC      R      Cutthroat trout      58      2.15 Fish
#> 5  1987 CC      R      Cutthroat trout      93      6.9  Fish
#> 6  1987 CC      R      Cutthroat trout      86      5.9  Fish
#> 7  1987 CC      R      Cutthroat trout     107     10.5 Fish
#> 8  1987 CC      R      Cutthroat trout     131     20.6 Fish
#> 9  1987 CC      R      Cutthroat trout     103      9.55 Fish
#> 10 1987 CC      R      Cutthroat trout     117     13   Fish
#> # i 32,181 more rows
```

# summarize()

summarizes data

# summarize()

`summarize` will collapse the data to a single row

```
summarize(vertebrates,  
  mean_length = mean(length_1_mm, na.rm = TRUE),  
  mean_weight = mean(weight_g, na.rm = TRUE))  
#> # A tibble: 1 × 2  
#>   mean_length mean_weight  
#>   <dbl>      <dbl>  
#> 1      73.8        8.91
```

# summarize() by group

`summarize` is much more useful in combination with the grouping argument `.by`

- `summary` will be calculated **separately** for each group

```
# summarize the grouped data
summarize(vertebrates,
  mean_length = mean(length_1_mm, na.rm = TRUE),
  mean_weight = mean(weight_g, na.rm = TRUE),
  .by = species
)
#> # A tibble: 2 × 3
#>   species                mean_length mean_weight
#>   <chr>                  <dbl>         <dbl>
#> 1 Cutthroat trout        83.5           8.84
#> 2 Coastal giant salamander 57.0           9.03
```

- Combine variables if you want to summarize by more than one group (e.g. `.by = c(species, unittype)`)

# count()

Counts observations by group

```
# count rows grouped by year
count(vertebrates, year)
#> # A tibble: 33 × 2
#>   year     n
#>   <dbl> <int>
#> 1  1987   603
#> 2  1988   302
#> 3  1989   308
#> 4  1990   513
#> 5  1991   626
#> 6  1992   616
#> 7  1993   870
#> 8  1994   948
#> 9  1995   583
#> 10 1996   928
#> # i 23 more rows
```



# The pipe |>

Combine multiple data operations into one command

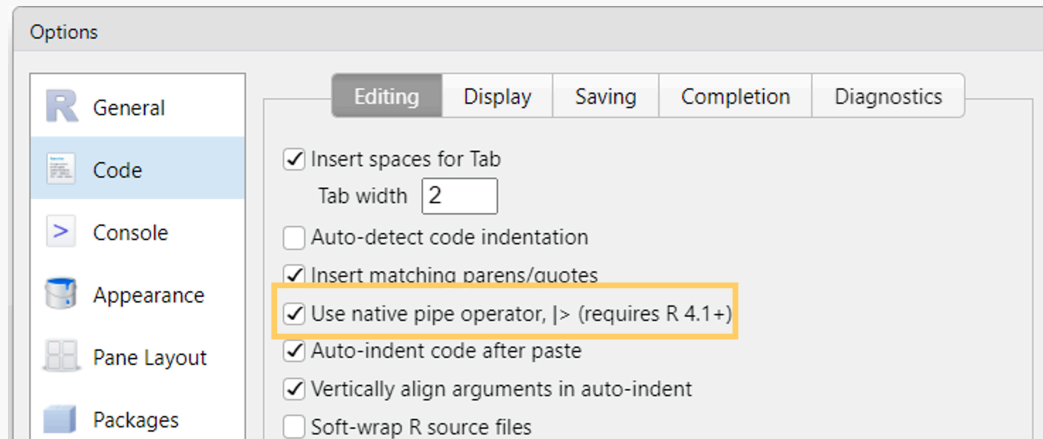
# The pipe |>

Data transformation often requires **multiple operations** in sequence.

The pipe operator |> helps to keep these operations clear and readable.

- You may also see %>% from the **magrittr** package

Turn on the native R pipe |> in **Tools -> Global Options -> Code**



# The pipe |>

Let's look at an example without pipe:

```
# 1: filter rows that have don't have NA in the unittype column
vertebrates_new <- filter(vertebrates, !is.na(unittype))

# 2: summarize mean values by year
vertebrates_new <- count(vertebrates_new, year, species, section)
```

How could we make this more efficient?

Use one **nested function** without intermediate results:

```
vertebrates_new <- count(
  filter(vertebrates, !is.na(unittype)),
  year, species, section
)
```

But this gets complicated and error prone very quickly

# The pipe |>

The pipe operator makes it very easy to combine multiple operations:

```
vertebrates_new <- vertebrates |>
  filter(!is.na(unittype)) |>
  count(year, species, section)

vertebrates_new
```

You can read from top to bottom and interpret the |> as an “and then do”.

# The pipe |>

But what is happening?

The pipe is “pushing” the result of one line into the first argument of the function from the next line.

```
vertebrates |>
  count(year)

# instead of
count(vertebrates, year)
```

Piping works perfectly with the **tidyverse** functions because they are designed to return a tibble **and** take a tibble as first argument.



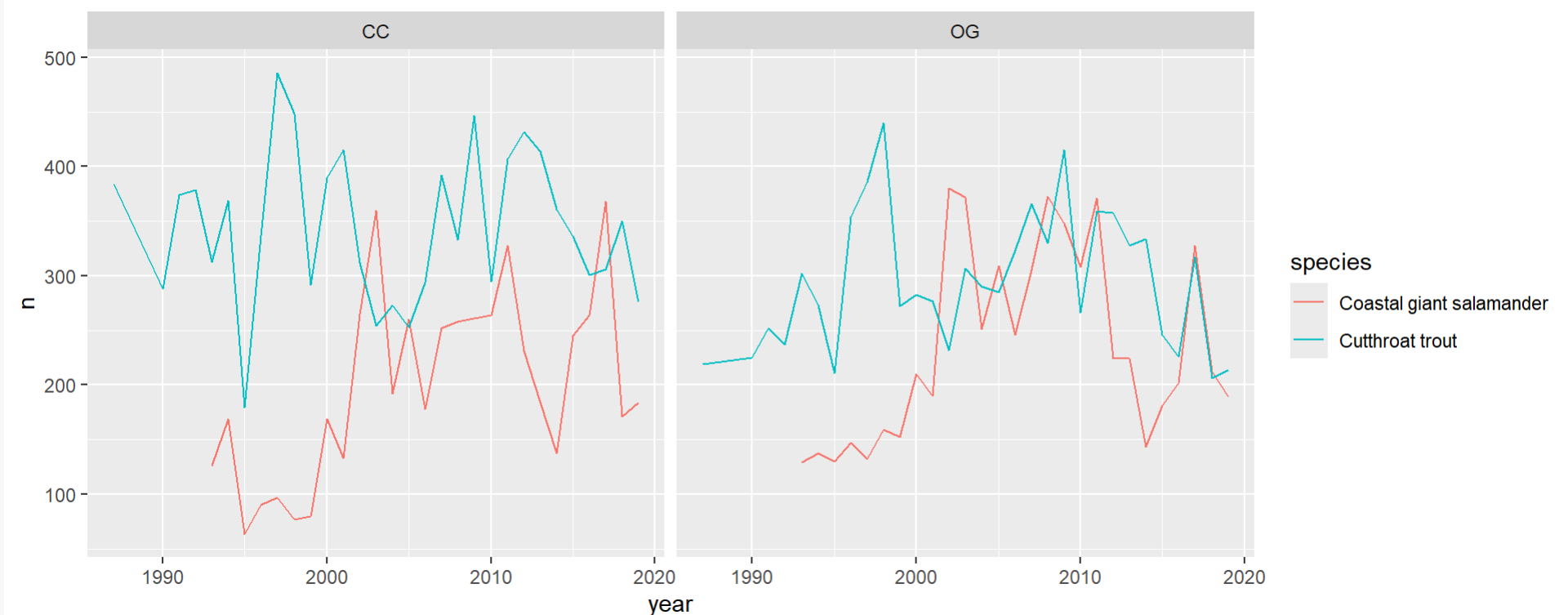
Tip

Use the keyboard shortcut **Ctrl/Cmd + Shift + M** to insert |>

# The pipe |>

Piping also works well together with `ggplot`

```
vertebrates |>
  filter(!is.na(unittype)) |>
  count(year, species, section) |>
  ggplot(aes(x = year, y = n, color = species)) +
  geom_line() +
  facet_wrap(~section)
```



# Combining multiple tables

# Combine two tibbles by row `bind_rows`

Situation: Two (or more) `tibbles` with the same variables (column names)

```
tbl_a <- vertebrates[1:2, ] # first two rows
tbl_b <- vertebrates[2:nrow(vertebrates), ] # the rest
```

tbl\_a

```
#> # A tibble: 2 × 6
#>   year section unitttype species      length_1_mm weight_g
#>   <dbl> <chr>   <chr>   <chr>          <dbl>     <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75
#> 2  1987 CC      R      Cutthroat trout      61      1.95
```

tbl\_b

```
#> # A tibble: 32,190 × 6
#>   year section unitttype species      length_1_mm weight_g
#>   <dbl> <chr>   <chr>   <chr>          <dbl>     <dbl>
#> 1  1987 CC      R      Cutthroat trout      61      1.95
#> 2  1987 CC      R      Cutthroat trout      89      5.6
#> # i 32,188 more rows
```



# Combine two tibbles by row `bind_rows`

Bind the rows together with `bind_rows()`:

```
bind_rows(tbl_a, tbl_b)
```

```
#> # A tibble: 32,192 × 6
#>   year section unittype species      length_1_mm weight_g
#>   <dbl> <chr>   <chr>   <chr>         <dbl>     <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75
#> 2  1987 CC      R      Cutthroat trout      61      1.95
#> # i 32,190 more rows
```

You can also add an ID-column to indicate which line belonged to which table:

```
bind_rows(a = tbl_a, b = tbl_b, .id = "id")
```

```
#> # A tibble: 32,192 × 7
#>   id      year section unittype species      length_1_mm weight_g
#>   <chr> <dbl> <chr>   <chr>   <chr>         <dbl>     <dbl>
#> 1 a      1987 CC      R      Cutthroat trout      58      1.75
#> 2 a      1987 CC      R      Cutthroat trout      61      1.95
#> 3 b      1987 CC      R      Cutthroat trout      61      1.95
#> # i 32,189 more rows
```

You can use `bind_rows()` to bind as many tables as you want:

```
bind_rows(a = tbl_a, b = tbl_b, c = tbl_c, ..., .id = "id")
```

# Join tibbles with `left_join()`

Situation: Two tables that share some but not all columns.

```
vertebrates
```

```
#> # A tibble: 32,191 × 6
#>   year section unittype species      length_1_mm weight_g
#>   <dbl> <chr>    <chr>    <chr>          <dbl>      <dbl>
#> 1  1987 CC      R      Cutthroat trout      58      1.75
#> 2  1987 CC      R      Cutthroat trout      61      1.95
#> # i 32,189 more rows
```

```
# table with more information on the species
```

```
species
```

```
#> # A tibble: 2 × 2
#>   species      type
#>   <chr>      <chr>
#> 1 Cutthroat trout      Fish
#> 2 Coastal giant salamander Amphibian
```

# Join tibbles with `left_join()`

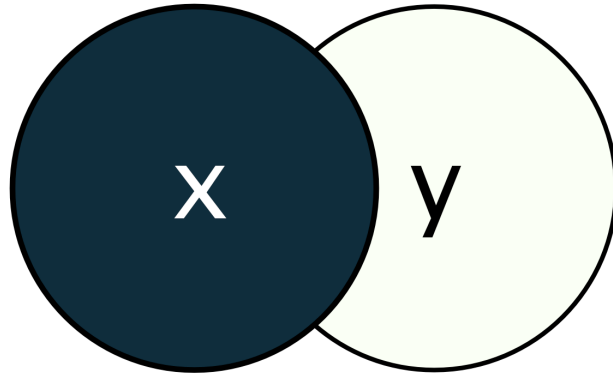
Join the two tables by the common column `species`

```
left_join(vertebrates, species, by = "species")
#> # A tibble: 32,191 × 7
#>   year section unittype species length_1_mm weight_g type
#>   <dbl> <chr>   <chr>   <chr>         <dbl>    <dbl> <chr>
#> 1  1987 CC      R      Cutthroat trout      58      1.75 Fish
#> 2  1987 CC      R      Cutthroat trout      61      1.95 Fish
#> 3  1987 CC      R      Cutthroat trout      89      5.6  Fish
#> 4  1987 CC      R      Cutthroat trout      58      2.15 Fish
#> 5  1987 CC      R      Cutthroat trout      93      6.9  Fish
#> 6  1987 CC      R      Cutthroat trout      86      5.9  Fish
#> 7  1987 CC      R      Cutthroat trout     107     10.5 Fish
#> 8  1987 CC      R      Cutthroat trout     131     20.6 Fish
#> 9  1987 CC      R      Cutthroat trout     103      9.55 Fish
#> 10 1987 CC      R      Cutthroat trout     117      13   Fish
#> # i 32,181 more rows
```

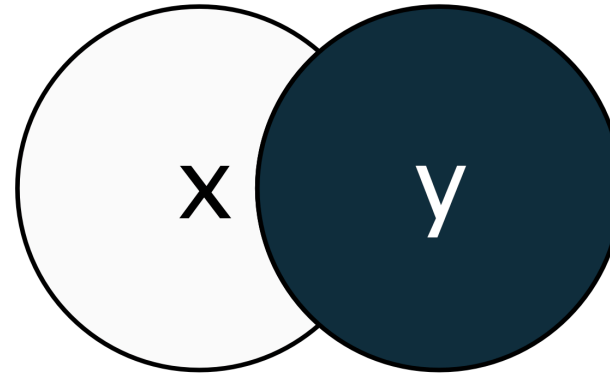
`left_join()` means that the resulting tibble will contain all rows of `vertebrates`, but not necessarily all rows of `species` (in this case it does though).

# Different `*_join()` functions

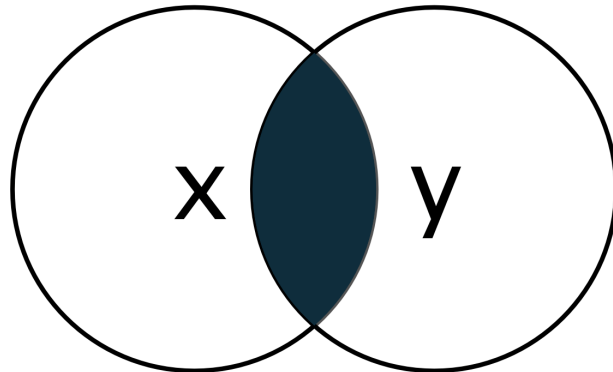
`left_join(x, y)`



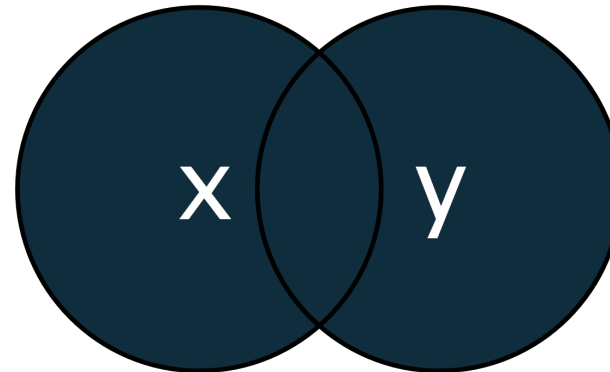
`right_join(x, y)`



`inner_join(x, y)`



`full_join(x, y)`



# Summary

Data transformation with dplyr

# Summary I

All `dplyr` functions take a tibble as first argument and return a tibble.

## `filter()`

- **pick rows** with helpers
  - relational and logical operators
  - `%in%`
  - `is.na()`
  - `between()`
  - `near()`

# Summary II

All `dplyr` functions take a tibble as first argument and return a tibble.

## `select()`

- pick columns with helpers
  - `starts_with()`, `ends_with()`
  - `contains()`
  - `matches()`
  - `any_of()`, `all_of()`

# Summary III

## `arrange()`

- **change order** of rows (ascending)
  - or descending with `desc()`

## `mutate()`

- **add columns** but keep all columns
  - `case_when()` for conditional values



# Summary IV

## `summarize()`

- **collapse rows** into one row by some summary
  - use `.by` argument to summarize by group

## `count`

- **count rows** based on a group

# Summary V

## `bind_rows()`

- **combine rows** of multiple tibbles into one
  - the tibbles need to have the same columns
  - add an id column with the argument `.id = "id"`
  - function `bind_cols()` works similarly just for columns

## `left_join()`

- **combine tables** based on common columns

# Now you

Task (45 min)

Transform the penguin data set

Find the task description [here](#)