

Data transformation with dplyr

Day 2 - Introduction to Data Analysis with R

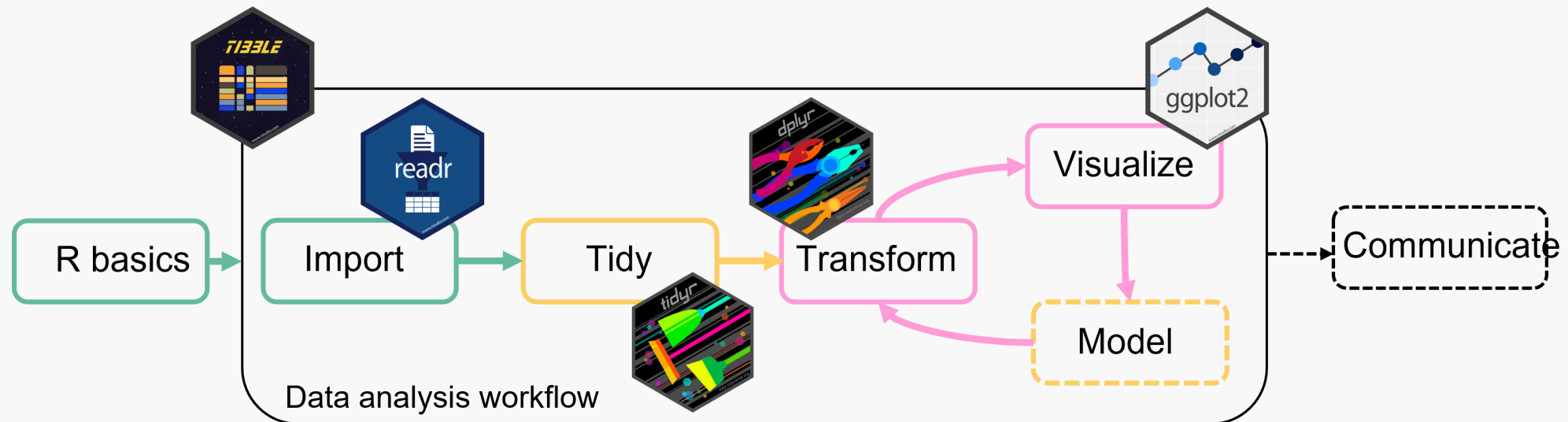
Selina Baldauf

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 **dplyr** 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 **dplyr** 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(lterdatasampler)
and_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
#> 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(and_vertebrates, species == "Cutthroat trout")
#> # A tibble: 20,433 × 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 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(and_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

```
unittype_select <- c("R", "C", "S")
filter(and_vertebrates, unittype %in% unittype_select)
#> # A tibble: 19,619 × 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 19,609 more rows
```

filter() + is.na()

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

```
filter(and_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(and_vertebrates, !is.na(weight_g))
```

filter() + between()

Combine different filters:

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

```
filter(and_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(and_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(and_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(and_vertebrates, -species, -length_1_mm, -year)
```

select() + ends_with()

Select all columns that start with "s"

```
select(and_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 `starts_with()` and `contains()`.

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


select() + from:to

Multiple consecutive columns can be selected using the **from:to** structure with either column id or name:

```
select(and_vertebrates, 1:3)
select(and_vertebrates, year:unitttype)
```

```
#> # A tibble: 32,191 × 3
#>   year section unitttype
#>   <dbl> <chr>    <chr>
#> 1  1987 CC      R
#> 2  1987 CC      R
#> 3  1987 CC      R
#> # i 32,188 more rows
```

Be a bit careful with these commands: They are not robust if you e.g. change the order of your columns at some point.

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(and_vertebrates, weight_kg = weight_g/1000)
```

```
#> # A tibble: 32,191 × 7  
#>   year section unitttype 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(and_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(and_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
```

summarize()

summarizes data

summarize()

`summarize` will collapse the data to a single row

```
summarize(and_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(and_vertebrates,
  mean_length = mean(length_l_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
```


count()

Counts observations by group

```
# count rows grouped by year
count(and_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 | >

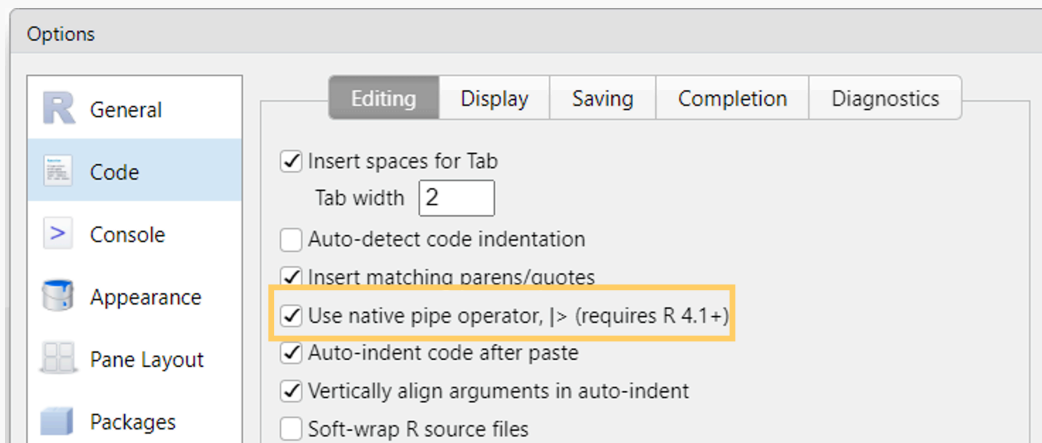
Combine multiple data operations into one command

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
and_vertebrates_new <- filter(and_vertebrates, !is.na(unittype))

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

How could we make this more efficient?

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

```
and_vertebrates_new <- count(
  filter(and_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:

```
and_vertebrates_new <- and_vertebrates |>
  filter(!is.na(unitttype)) |>
  count(year, species, section)

and_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.

```
and_vertebrates |>
  count(year)

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

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



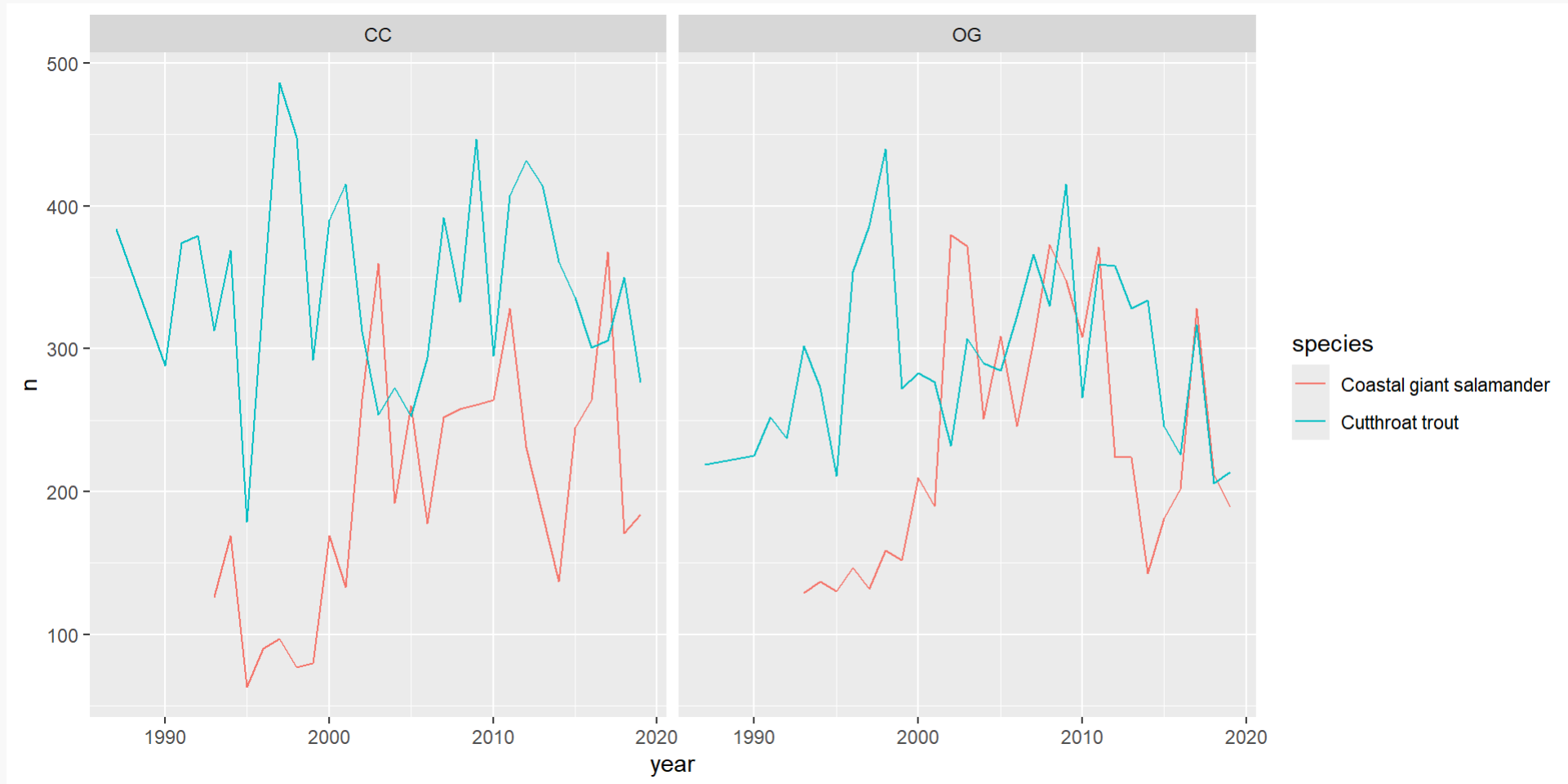
Tip

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

The pipe | >

Piping also works well together with **ggplot**

```
and_vertebrates |>
  filter(!is.na(unitttype)) |>
  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 <- and_vertebrates[1:2, ] # first two rows
tbl_b <- and_vertebrates[2:nrow(and_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.

```
and_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()`

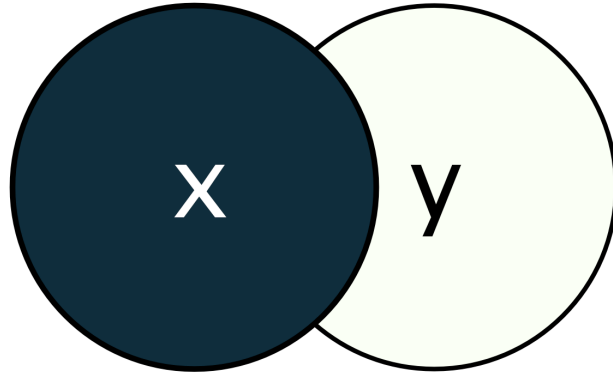
Join the two tables by the common column `species`

```
left_join(and_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
```

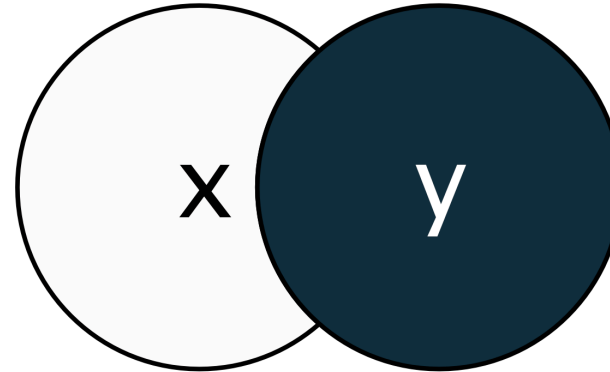
`left_join()` means that the resulting tibble will contain all rows of `and_vertebrates`, but not necessarily all rows of `species` (in this case it does though).

Different `*_join()` functions

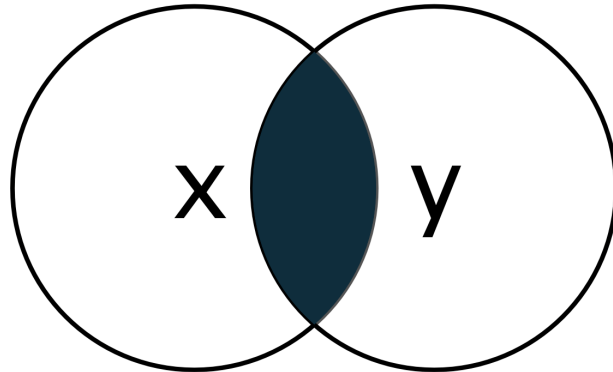
`left_join(x, y)`



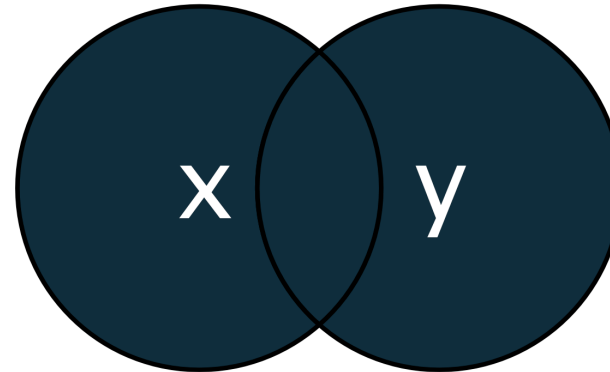
`right_join(x, y)`



`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 (60 min)

Transform the penguin data set

Find the task description [here](#)

