11 Data transformation

(AST230) R for Data Science

Md Rasel Biswas

Tibble review

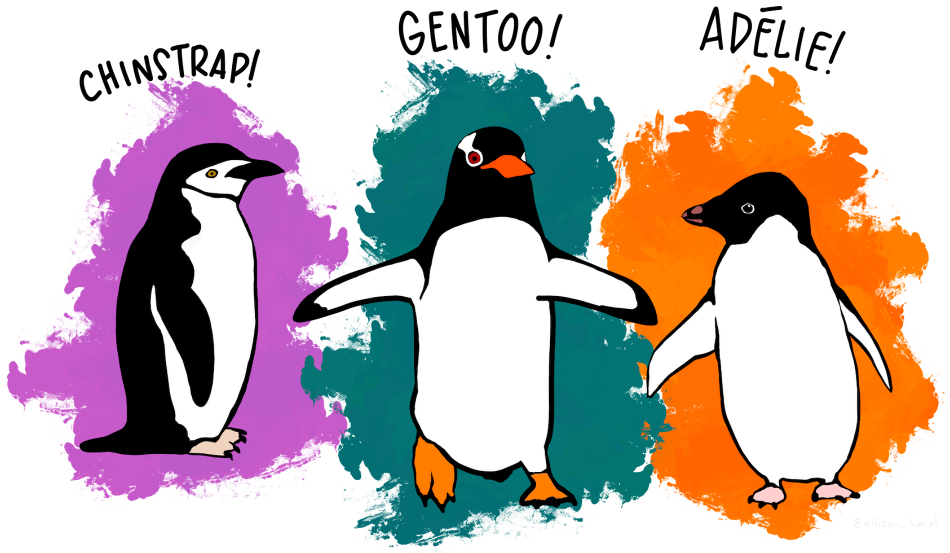
- `tibble()` is similar to `data.frame()`, but has some advantages
- A data frame can be transformed into a `tibble()` by `as_tibble()`
- E.g. create a `tibble` object `mtcars_t` from a data frame `mtcars`

```r
mtcars_t <- as_tibble(mtcars)
mtcars_t
```

```
# A tibble: 32 × 11
     mpg   cyl  disp    hp  drat    wt  qsec    vs    am  gear  carb
   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
 1  21       6  160    110  3.9   2.62  16.5     0     1     4     4
 2  21       6  160    110  3.9   2.88  17.0     0     1     4     4
 3  22.8     4  108     93  3.85  2.32  18.6     1     1     4     1
 4  21.4     6  258    110  3.08  3.22  19.4     1     0     3     1
 5  18.7     8  360    175  3.15  3.44  17.0     0     0     3     2
 6  18.1     6  225    105  2.76  3.46  20.2     1     0     3     1
 7  14.3     8  360    245  3.21  3.57  15.8     0     0     3     4
 8  24.4     4  147.    62  3.69  3.19  20       1     0     4     2
 9  22.8     4  141.    95  3.92  3.15  22.9     1     0     4     2
10  19.2     6  168.   123  3.92  3.44  18.3     1     0     4     4
# ℹ 22 more rows
```

Penguins data

- The `palmerpenguins::penguins` data contains size measurements for three penguin species observed on three islands in the Palmer Archipelago, Antarctica.



- These data were collected from 2007 - 2009 by Dr. Kristen Gorman

- The `penguins` data contains information (8 variables) on 344 penguins
- Load the package `palmerpenguins` to access the `penguins` data

```r
library(palmerpenguins)
data(penguins)
glimpse(penguins)
```

```
Rows: 344
Columns: 8
$ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adel…
$ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgerse…
$ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, …
$ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, …
$ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186…
$ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, …
$ sex               <fct> male, female, female, NA, female, male, female, male…
$ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007…
```

Overview of `dplyr`

- **`dplyr`**: A powerful package for data manipulation with a consistent and flexible grammar.
- dplyr package is helpful for different types of data transformations (e.g. creating new variables, computing summaries, renaming variables, reorders the observations, etc).
- dplyr has versatile verbs to handle most data manipulation tasks.
- It has a unified syntax:
  - first argument is a data frame
  - output is always a data frame

- dplyr’s verbs are organized into four groups based on what they operate on:
  - **rows**,
  - **columns**,
  - **groups**,
  - **tables**

Verbs for Rows

Two most important verbs that operate on rows without changing the columns:

1. `filter()` keeps rows based on the values of the columns (variables)
2. `arrange()` reorders the rows (observations)
3. `distinct()` which finds rows with unique values.
   - but it can also optionally modify the columns

1 `filter()`

Filter rows with `filter()`

- The function `filter()` allows to obtain a subset of observations based on given conditions
  - For example, we could find all the penguins of Chinstrap species

```
filter(penguins, species == "Chinstrap")
```

Equivalently,

```
penguins |>
  filter(species == "Chinstrap")
```

```
# A tibble: 68 × 8
   species   island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>     <fct>           <dbl>         <dbl>             <int>       <int>
 1 Chinstrap Dream            46.5          17.9               192        3500
 2 Chinstrap Dream            50            19.5               196        3900
 3 Chinstrap Dream            51.3          19.2               193        3650
 4 Chinstrap Dream            45.4          18.7               188        3525
 5 Chinstrap Dream            52.7          19.8               197        3725
 6 Chinstrap Dream            45.2          17.8               198        3950
 7 Chinstrap Dream            46.1          18.2               178        3250
 8 Chinstrap Dream            51.3          18.2               197        3750
 9 Chinstrap Dream            46            18.9               195        4150
10 Chinstrap Dream            51.3          19.9               198        3700
```

Filter rows with filter()

- We can use `>`, `>=`, `<`, `<=`, `==`, and `!=` to write conditions
- We can combine multiple conditions with
  - `&` or `,` $\rightarrow$ “and”
  - `|` $\rightarrow$ “or”

Filter rows with filter()

Question: Find Chinstrap penguins whose bill length is greater than 52 mm

```r
penguins |>
  filter(species == "Chinstrap", bill_length_mm > 52)
```

```
# A tibble: 7 × 8
  species   island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>     <fct>           <dbl>         <dbl>             <int>       <int>
1 Chinstrap Dream            52.7          19.8               197        3725
2 Chinstrap Dream            58            17.8               181        3700
3 Chinstrap Dream            52.8          20                 205        4550
4 Chinstrap Dream            54.2          20.8               201        4300
5 Chinstrap Dream            53.5          19.9               205        4500
6 Chinstrap Dream            52.2          18.8               197        3450
7 Chinstrap Dream            55.8          19.8               207        4000
# ℹ 2 more variables: sex <fct>, year <int>
```

Filter rows with filter()

Question: Find the penguins of the types Chinstrap or Gentoo

```
penguins |>
  filter(species == "Chinstrap" | species == "Gentoo")
```

```
# A tibble: 192 × 8
   species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>           <dbl>         <dbl>             <int>       <int>
 1 Gentoo  Biscoe           46.1          13.2               211        4500
 2 Gentoo  Biscoe           50            16.3               230        5700
 3 Gentoo  Biscoe           48.7          14.1               210        4450
 4 Gentoo  Biscoe           50            15.2               218        5700
 5 Gentoo  Biscoe           47.6          14.5               215        5400
 6 Gentoo  Biscoe           46.5          13.5               210        4550
 7 Gentoo  Biscoe           45.4          14.6               211        4800
 8 Gentoo  Biscoe           46.7          15.3               219        5200
 9 Gentoo  Biscoe           43.3          13.4               209        4400
10 Gentoo  Biscoe           46.8          15.4               215        5150
# ℹ 182 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

Filter rows with filter()

- There's a useful shortcut when you're combining `|` and `==`. That is: `%in%`

```
penguins |>
  filter(species %in% c("Chinstrap", "Gentoo"))
```

```
# A tibble: 192 × 8
   species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>           <dbl>         <dbl>             <int>       <int>
 1 Gentoo  Biscoe           46.1          13.2               211        4500
 2 Gentoo  Biscoe           50            16.3               230        5700
 3 Gentoo  Biscoe           48.7          14.1               210        4450
 4 Gentoo  Biscoe           50            15.2               218        5700
 5 Gentoo  Biscoe           47.6          14.5               215        5400
 6 Gentoo  Biscoe           46.5          13.5               210        4550
 7 Gentoo  Biscoe           45.4          14.6               211        4800
 8 Gentoo  Biscoe           46.7          15.3               219        5200
 9 Gentoo  Biscoe           43.3          13.4               209        4400
10 Gentoo  Biscoe           46.8          15.4               215        5150
# ℹ 182 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

Exercise 1

1. Create a subset from penguins that only contains Gentoo penguins with a bill depth greater than or equal to 15.5 millimeters.
2. Create a subset from penguins that contains observations for male penguins recorded at *Dream* or *Biscoe* Islands.
3. Create a subset from penguins that contains penguins that are either Gentoo or have a body mass greater than 4500 g.

2 `arrange()`

Arrange rows with `arrange()`

- `arrange()` reorders the observations by one or more variables (column names)
- As inputs, `arrange()` takes a data frame and a set of column names (variables) to order by
- If more than one columns are used in the arguments then each additional column will be used to break ties in the values of preceding column
- Default is ascending order (lowest to highest)

Arrange rows with arrange()

```r
penguins |>
  arrange(bill_length_mm)
```

```
# A tibble: 344 × 8
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Dream               32.1          15.5               188        3050
 2 Adelie  Dream               33.1          16.1               178        2900
 3 Adelie  Torgersen           33.5          19                 190        3600
 4 Adelie  Dream               34            17.1               185        3400
 5 Adelie  Torgersen           34.1          18.1               193        3475
 6 Adelie  Torgersen           34.4          18.4               184        3325
 7 Adelie  Biscoe              34.5          18.1               187        2900
 8 Adelie  Torgersen           34.6          21.1               198        4400
 9 Adelie  Torgersen           34.6          17.2               189        3200
10 Adelie  Biscoe              35            17.9               190        3450
# ℹ 334 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

Arrange rows with arrange()

```r
# arrange in descending order
penguins |>
  arrange(desc(bill_depth_mm))
```

```
# A tibble: 344 × 8
   species   island    bill_length_mm bill_depth_mm
flipper_length_mm body_mass_g
   <fct>     <fct>              <dbl>         <dbl>
<int>        <int>
 1 Adelie    Torgers…            46            21.5
194         4200
 2 Adelie    Torgers…            38.6          21.2
191         3800
 3 Adelie    Dream               42.3          21.2
191         4150
 4 Adelie    Torgers…            34.6          21.1
198         4400
 5 Adelie    Dream               39.2          21.1
196         4150
 6 Adelie    Biscoe              41.3          21.1
195         4400
 7 Chinstrap Dream               54.2          20.8
201         4300
```

Arrange rows with arrange()

```
# arrange with more than one variables
penguins |>
  arrange(desc(bill_depth_mm),
          desc(flipper_length_mm))
```

```
# A tibble: 344 × 8
   species   island    bill_length_mm bill_depth_mm
flipper_length_mm body_mass_g
   <fct>     <fct>              <dbl>         <dbl>
<int>       <int>
 1 Adelie    Torgers…            46            21.5
194         4200
 2 Adelie    Torgers…            38.6          21.2
191         3800
 3 Adelie    Dream               42.3          21.2
191         4150
 4 Adelie    Torgers…            34.6          21.1
198         4400
 5 Adelie    Dream               39.2          21.1
196         4150
 6 Adelie    Biscoe              41.3          21.1
195         4400
 7 Chinstrap Dream               54.2          20.8
201         4300
```

3 `distinct()`

Find unique rows with `distinct()`

- `distinct()` finds all the unique rows in a dataset

```r
# Remove duplicate rows, if any
penguins |>
  distinct()
```

```
# A tibble: 344 × 8
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Torgersen           39.1          18.7               181        3750
 2 Adelie  Torgersen           39.5          17.4               186        3800
 3 Adelie  Torgersen           40.3          18                 195        3250
 4 Adelie  Torgersen           NA            NA                  NA          NA
 5 Adelie  Torgersen           36.7          19.3               193        3450
 6 Adelie  Torgersen           39.3          20.6               190        3650
 7 Adelie  Torgersen           38.9          17.8               181        3625
 8 Adelie  Torgersen           39.2          19.6               195        4675
 9 Adelie  Torgersen           34.1          18.1               193        3475
10 Adelie  Torgersen           42            20.2               190        4250
# ℹ 334 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

Find unique rows with distinct()

- Most of the time, however, you'll want the distinct combination of some variables, so you can also optionally supply column names

```
#Find all unique species and year pairs
penguins |>
  distinct(species, year)
```

```
# A tibble: 9 × 2
  species    year
  <fct>     <int>
1 Adelie     2007
2 Adelie     2008
3 Adelie     2009
4 Gentoo     2007
5 Gentoo     2008
6 Gentoo     2009
7 Chinstrap  2007
8 Chinstrap  2008
9 Chinstrap  2009
```

Find unique rows with distinct()

- If you want to find the number of occurrences instead, you're better off swapping `distinct()` for `count()`.
  - With the `sort = TRUE` argument, you can arrange them in descending order of the number of occurrences

```r
#Find count for species and year pairs
penguins |>
  count(species, year, sort = TRUE)
```

```
# A tibble: 9 × 3
  species    year     n
  <fct>     <int> <int>
1 Adelie     2009    52
2 Adelie     2007    50
3 Adelie     2008    50
4 Gentoo     2008    46
5 Gentoo     2009    44
6 Gentoo     2007    34
7 Chinstrap  2007    26
8 Chinstrap  2009    24
9 Chinstrap  2008    18
```

Verbs for Columns

There are four important verbs that affect the columns without changing the rows:

4. `mutate()` creates new columns that are derived from the existing columns,
5. `select()` changes which columns are present, and
6. `rename()` changes the names of the columns

4 `mutate()`

Add new variables with `mutate()`

- `mutate()` is used to create new variables to the existing data frame
- E.g. create a new variable `body_mass_kg` (body mass in kg) by `body_mass_g/1000`

```
penguins |>
  mutate(body_mass_kg = body_mass_g / 1000)
```

```
# A tibble: 344 × 9
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Torgersen           39.1          18.7               181        3750
 2 Adelie  Torgersen           39.5          17.4               186        3800
 3 Adelie  Torgersen           40.3          18                 195        3250
 4 Adelie  Torgersen          NA            NA                   NA          NA
 5 Adelie  Torgersen           36.7          19.3               193        3450
 6 Adelie  Torgersen           39.3          20.6               190        3650
 7 Adelie  Torgersen           38.9          17.8               181        3625
 8 Adelie  Torgersen           39.2          19.6               195        4675
 9 Adelie  Torgersen           34.1          18.1               193        3475
10 Adelie  Torgersen           42            20.2               190        4250
# ℹ 334 more rows
# ℹ 3 more variables: sex <fct>, year <int>, body_mass_kg <dbl>
```

- By default, `mutate()` adds new columns on the right side of your data

Add new variables with mutate()

- We can use the `.before` argument to add the variables to the left-hand side (.before=1 means before the 1st variable).

```
penguins |>
 mutate(body_mass_kg = body_mass_g / 1000,
         .before = 1)
```

```
# A tibble: 344 × 9
   body_mass_kg species island    bill_length_mm bill_depth_mm flipper_length_mm
          <dbl> <fct>   <fct>              <dbl>         <dbl>             <int>
 1         3.75 Adelie  Torgersen           39.1          18.7               181
 2         3.8  Adelie  Torgersen           39.5          17.4               186
 3         3.25 Adelie  Torgersen           40.3          18                 195
 4        NA    Adelie  Torgersen           NA            NA                  NA
 5         3.45 Adelie  Torgersen           36.7          19.3               193
 6         3.65 Adelie  Torgersen           39.3          20.6               190
 7         3.62 Adelie  Torgersen           38.9          17.8               181
 8         4.68 Adelie  Torgersen           39.2          19.6               195
 9         3.48 Adelie  Torgersen           34.1          18.1               193
10         4.25 Adelie  Torgersen           42            20.2               190
# ℹ 334 more rows
# ℹ 3 more variables: body_mass_g <int>, sex <fct>, year <int>
```

Re-coding with `mutate()`

- Suppose we want to classify penguins by their flipper size, so create a new variable `flip_size`, which will be either "large" or "short"
  - "large" if flipper size is greater than 210 mm
  - "short" if flipper size is less than or equal to 210 mm
- `if_else(condition, true, false)` is used to obtain a variable with two levels depending on whether `condition` is satisfied or not

Re-coding with mutate()

```
penguins |>
  mutate(
    flip_size = if_else(
      flipper_length_mm > 210, "large", "short")
    )
```

```
# A tibble: 344 × 9
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Torgersen           39.1          18.7               181        3750
 2 Adelie  Torgersen           39.5          17.4               186        3800
 3 Adelie  Torgersen           40.3          18                 195        3250
 4 Adelie  Torgersen          NA            NA                   NA          NA
 5 Adelie  Torgersen           36.7          19.3               193        3450
 6 Adelie  Torgersen           39.3          20.6               190        3650
 7 Adelie  Torgersen           38.9          17.8               181        3625
 8 Adelie  Torgersen           39.2          19.6               195        4675
 9 Adelie  Torgersen           34.1          18.1               193        3475
10 Adelie  Torgersen           42            20.2               190        4250
# ℹ 334 more rows
# ℹ 3 more variables: sex <fct>, year <int>, flip_size <chr>
```

Re-coding with mutate()

- To re-code a variable in more than two categories, `case_when()` function is used
- For example, we are interested in classifying penguins into three categories (large, medium, and small) by their body mass where
  - "small" (<=3000], "medium" (3000-4500), "large" (>=4500),

```
penguins |>
  mutate(
    mass_c = case_when(
      body_mass_g > 4500 ~ "large",
      body_mass_g > 3000 &
        body_mass_g <= 4500 ~ "medium",
      body_mass_g <= 3000 ~ "small"
    ), .before = 1
  )
```

Re-coding with mutate()

```
# A tibble: 344 × 9
   mass_c species island    bill_length_mm bill_depth_mm flipper_length_mm
   <chr>  <fct>   <fct>              <dbl>         <dbl>             <int>
 1 medium Adelie  Torgersen           39.1          18.7               181
 2 medium Adelie  Torgersen           39.5          17.4               186
 3 medium Adelie  Torgersen           40.3          18                 195
 4 <NA>   Adelie  Torgersen           NA            NA                  NA
 5 medium Adelie  Torgersen           36.7          19.3               193
 6 medium Adelie  Torgersen           39.3          20.6               190
 7 medium Adelie  Torgersen           38.9          17.8               181
 8 large  Adelie  Torgersen           39.2          19.6               195
 9 medium Adelie  Torgersen           34.1          18.1               193
10 medium Adelie  Torgersen           42            20.2               190
# ℹ 334 more rows
# ℹ 3 more variables: body_mass_g <int>, sex <fct>, year <int>
```

5 `select()`

Select columns with `select()`

- In practice, only a subset of variables from the original data frame are used, the original data frame may contain thousands of variables
- `select()` is used to create a new data frame with the variables mentioned in the arguments (selected variables)
- As inputs, a data frame, and column names to be selected are used in `select()`

Select columns with select()

- Create a data frame with three variables:
  - `year`, `island`, and `species`

```
penguins |>
  select(year, island, species)
```

```
# A tibble: 344 × 3
    year island    species
   <int> <fct>     <fct>
 1  2007 Torgersen Adelie
 2  2007 Torgersen Adelie
 3  2007 Torgersen Adelie
 4  2007 Torgersen Adelie
 5  2007 Torgersen Adelie
 6  2007 Torgersen Adelie
 7  2007 Torgersen Adelie
 8  2007 Torgersen Adelie
 9  2007 Torgersen Adelie
10  2007 Torgersen Adelie
# ℹ 334 more rows
```

Select columns with select()

```
names(penguins)
```

```
[1] "species"           "island"            "bill_length_mm"
[4] "bill_depth_mm"     "flipper_length_mm" "body_mass_g"
[7] "sex"               "year"
```

- A colon (`:`) can be used to select a number of consecutive variables

```
penguins |>
  select(species:body_mass_g)
```

```
# A tibble: 344 × 6
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Torgersen           39.1          18.7               181        3750
 2 Adelie  Torgersen           39.5          17.4               186        3800
 3 Adelie  Torgersen           40.3          18                 195        3250
 4 Adelie  Torgersen           NA            NA                  NA          NA
 5 Adelie  Torgersen           36.7          19.3               193        3450
 6 Adelie  Torgersen           39.3          20.6               190        3650
 7 Adelie  Torgersen           38.9          17.8               181        3625
 8 Adelie  Torgersen           39.2          19.6               195        4675
 9 Adelie  Torgersen           34.1          18.1               193        3475
10 Adelie  Torgersen           42            20.2               190        4250
# ℹ 334 more rows
```

Select columns with select()

- We can also **omit** variables using the negative sign.

```
penguins |>
  select(species:bill_depth_mm, -island)
```

```
# A tibble: 344 × 3
   species bill_length_mm bill_depth_mm
   <fct>            <dbl>         <dbl>
 1 Adelie            39.1          18.7
 2 Adelie            39.5          17.4
 3 Adelie            40.3          18  
 4 Adelie            NA            NA  
 5 Adelie            36.7          19.3
 6 Adelie            39.3          20.6
 7 Adelie            38.9          17.8
 8 Adelie            39.2          19.6
 9 Adelie            34.1          18.1
10 Adelie            42            20.2
# ℹ 334 more rows
```

Select columns with select()

- `select()` can also be used to **rename** a variable and **reordering** the sequence of variables

```
penguins |>
  select(species, year, bill_len = bill_length_mm)
```

```
# A tibble: 344 × 3
   species  year bill_len
   <fct>   <int>    <dbl>
 1 Adelie   2007     39.1
 2 Adelie   2007     39.5
 3 Adelie   2007     40.3
 4 Adelie   2007     NA
 5 Adelie   2007     36.7
 6 Adelie   2007     39.3
 7 Adelie   2007     38.9
 8 Adelie   2007     39.2
 9 Adelie   2007     34.1
10 Adelie   2007     42
# ℹ 334 more rows
```

Select columns with select()

- `select()` has some helper functions that can be used to select a subset of variables
  - `starts_with("abc")`, `ends_with("th")`, `contains("co")`, etc.

```r
names(penguins)
```

```
[1] "species"           "island"
"bill_length_mm"
[4] "bill_depth_mm"     "flipper_length_mm"
"body_mass_g"
[7] "sex"               "year"
```

```r
penguins |>
  select(starts_with("bill"))
```

```
# A tibble: 344 × 2
   bill_length_mm bill_depth_mm
            <dbl>         <dbl>
 1           39.1          18.7
 2           39.5          17.4
 3           40.3          18
 4           NA            NA
 5           36.7          19.3
 6           39.3          20.6
 7           38.9          17.8
 8           39.2          19.6
 9           34.1          18.1
10           42            20.2
# ℹ 334 more rows
```

6 `rename()`

- If you want to keep all the existing variables and just want to rename a few, you can use `rename()` instead of `select()`

```
penguins |>
  rename(location = island)
```

```
# A tibble: 344 × 8
   species location  bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Torgersen           39.1          18.7               181        3750
 2 Adelie  Torgersen           39.5          17.4               186        3800
 3 Adelie  Torgersen           40.3          18                 195        3250
 4 Adelie  Torgersen           NA            NA                  NA          NA
 5 Adelie  Torgersen           36.7          19.3               193        3450
 6 Adelie  Torgersen           39.3          20.6               190        3650
 7 Adelie  Torgersen           38.9          17.8               181        3625
 8 Adelie  Torgersen           39.2          19.6               195        4675
 9 Adelie  Torgersen           34.1          18.1               193        3475
10 Adelie  Torgersen           42            20.2               190        4250
# ℹ 334 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

Practice 2

1. Starting with the penguins data, only keep the `body_mass_g` variable.
2. Starting with the penguins data, keep columns from `bill_length_mm` to `body_mass_g`, and `year`
3. Starting with the penguins data, keep all columns except `island`
4. From penguins, keep the species column and any columns that end with "mm".

The pipe

The pipe

- We've shown you simple examples of the pipe above, but its real power arises when you start to combine multiple verbs.
- E.g. We want to find the female Adelie penguins with the largest bill sizes.

```r
penguins |>
  filter(species == "Adelie" & sex == "female") |>
  arrange(desc(bill_length_mm))
```

```
# A tibble: 73 × 8
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Dream               42.2          18.5               180        3550
 2 Adelie  Torgersen           41.1          17.6               182        3200
 3 Adelie  Torgersen           40.9          16.8               191        3700
 4 Adelie  Biscoe              40.5          17.9               187        3200
 5 Adelie  Torgersen           40.3          18                 195        3250
 6 Adelie  Torgersen           40.2          17                 176        3450
 7 Adelie  Dream               40.2          17.1               193        3400
 8 Adelie  Biscoe              39.7          17.7               193        3200
 9 Adelie  Biscoe              39.6          17.7               186        3500
10 Adelie  Torgersen           39.6          17.2               196        3550
# ℹ 63 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

The pipe

What would happen if we didn’t have the pipe?

- We could nest each function call inside the previous call?

```r
arrange(
  filter(
    penguins,
    species == "Adelie" & sex == "female"
    ),
  desc(bill_length_mm))
```

- Or we could use a bunch of intermediate objects:

```r
penguins1 <- filter(species == "Adelie" & sex == "female")
arrange(penguins1, desc(bill_length_mm))
```

- While both forms do the work, the pipe generally produces data analysis code that is easier to write and read

The pipe

- Behind the scenes
- `x |> f(y)` $\rightarrow$ `f(x, y)`
- `x |> f(y) |> g(z)` $\rightarrow$ `f(x, y) |> g(z)` $\rightarrow$ `g(f(x, y), z)`

Another pipe

- There is another pipe operator (`%>%`) provided by the `magrittr` package
- The `magrittr` package is included in the core tidyverse, so you can use `%>%` whenever you load the `tidyverse`
- For simple cases, `|>` and `%>%` behave identically

```r
penguins %>%
  filter(species == "Adelie" & sex == "female") %>%
  arrange(desc(bill_length_mm))
```

```
# A tibble: 73 × 8
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Dream               42.2          18.5               180        3550
 2 Adelie  Torgersen           41.1          17.6               182        3200
 3 Adelie  Torgersen           40.9          16.8               191        3700
 4 Adelie  Biscoe              40.5          17.9               187        3200
 5 Adelie  Torgersen           40.3          18                 195        3250
 6 Adelie  Torgersen           40.2          17                 176        3450
 7 Adelie  Dream               40.2          17.1               193        3400
 8 Adelie  Biscoe              39.7          17.7               193        3200
 9 Adelie  Biscoe              39.6          17.7               186        3500
10 Adelie  Torgersen           39.6          17.2               196        3550
# ℹ 63 more rows
```

Exercise

1. In a piped sequence, starting from penguins:

- Only keep observations for female penguins observed on Dream Island, then
- Keep variables `species` and any variable starting with "bill"

2. Add a column to penguins that contains a new column `flipper_m`, which is the `flipper_length_mm` (flipper length in millimeters) converted to units of meters.

Exercise

3. The year column in penguins is currently an integer. Add a new column named `year_fct` that is the year converted to a factor (hint: `as.factor()`)
4. Starting with penguins, do the following within a single `mutate()` function:

a. Convert the `species` variable to a character

b. Add a new column (called `flipper_cm` with flipper length in centimeters)

c. Convert the `island` column to lowercase

Verbs for Groups

- So far you've learned about functions that work with rows and columns.
- dplyr gets even more powerful when you add in the ability to work with groups.
- In this section, we'll focus on the most important functions: `group_by()`, and `summarize()`

7 `group_by()`

- Use `group_by()` to divide dataset into groups meaningful for your analysis

```
penguins |>
  group_by(species)
```

```
# A tibble: 344 × 8
# Groups:   species [3]
   species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
   <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
 1 Adelie  Torgersen           39.1          18.7               181        3750
 2 Adelie  Torgersen           39.5          17.4               186        3800
 3 Adelie  Torgersen           40.3          18                 195        3250
 4 Adelie  Torgersen           NA            NA                  NA          NA
 5 Adelie  Torgersen           36.7          19.3               193        3450
 6 Adelie  Torgersen           39.3          20.6               190        3650
 7 Adelie  Torgersen           38.9          17.8               181        3625
 8 Adelie  Torgersen           39.2          19.6               195        4675
 9 Adelie  Torgersen           34.1          18.1               193        3475
10 Adelie  Torgersen           42            20.2               190        4250
# ℹ 334 more rows
# ℹ 2 more variables: sex <fct>, year <int>
```

- `group_by()` doesn't change the data but, the output indicates that it is "grouped by" species (`Groups: species [3]`). This means subsequent operations will now work "by species".

8 `summarize()`

`summarize()`

- `summarize()` collapses a data frame into a single row
  - E.g. to create a data frame with mean and standard deviation of penguins' body mass

```r
penguins |>
  summarize(
    mean_mass = mean(body_mass_g, na.rm = T),
    sd_mass = sd(body_mass_g, na.rm = T)
  )
```

```
# A tibble: 1 × 2
  mean_mass sd_mass
      <dbl>   <dbl>
1     4202.    802.
```

- `summarise()` requires that each argument returns a single value

`summarize()` with `group_by()`

- `group_by()` is used to (single-value) summarize a variable at different levels of a categorical variable
- E.g. we want to obtain mean and standard deviation of penguins’ body mass for different species

```r
penguins |>
  group_by(species) |>
  summarise(
    mean_mass = mean(body_mass_g, na.rm = T),
    sd_mass = sd(body_mass_g, na.rm = T)
  )
```

```
# A tibble: 3 × 3
  species   mean_mass sd_mass
  <fct>         <dbl>   <dbl>
1 Adelie        3701.    459.
2 Chinstrap     3733.    384.
3 Gentoo        5076.    504.
```

`.by`

- There is an alternative to `group_by()` known as `.by` argument.
- We use the `.by` argument with the `summarize()`, and `mutate()` functions to create temporary groups.

```
penguins |>
  summarise(
    mean_mass = mean(body_mass_g, na.rm = T),
    sd_mass = sd(body_mass_g, na.rm = T),
    .by = species
  )
```

```
# A tibble: 3 × 3
  species   mean_mass sd_mass
  <fct>         <dbl>   <dbl>
1 Adelie        3701.    459.
2 Gentoo        5076.    504.
3 Chinstrap     3733.    384.
```

- with `.by`, the result is always ungrouped, regardless of the number of grouping columns

Practice

- Starting with penguins, create a summary table containing the maximum and minimum length of flippers (call the columns `flip_max` and `flip_min`) for chinstrap penguins, grouped by island.

Practice

- Starting with penguins, in a piped sequence:
    - Add a new column called `bill_ratio` that is the ratio of bill length to bill depth (hint: mutate())
    - Only keep columns species and `bill_ratio`
    - Group the data by species
    - Create a summary table containing the mean of the `bill_ratio` variable, by species (name the column in the summary table `bill_ratio_mean`)

9 `slice`

`slice`

`slice`: - A function in the `dplyr` package for selecting rows from a data frame or tibble based on their position.

- **Key Features**:
  - Operates on row indices rather than row values.
  - Useful for sampling, filtering specific rows, or working with sorted data.
- **`slice()`**: Select specific rows by position.

```r
slice(mtcars, 1:5)  # Select rows 1 to 5
```

Find frequency distributions

10 `count()`

- The function `count()` provides frequency distribution of a variable

```r
penguins |>
  count(species)
```

```
# A tibble: 3 × 2
  species       n
  <fct>     <int>
1 Adelie      152
2 Chinstrap    68
3 Gentoo      124
```

slice

- By default `count()` creates a variable `n` in the resulting data frame, which can be renamed using `name` argument of `count()`

```
penguins |>
  count(species, name = "freq")
```

```
# A tibble: 3 × 2
  species    freq
  <fct>     <int>
1 Adelie      152
2 Chinstrap    68
3 Gentoo      124
```

Proporions with `count()`

- **Frequency distribution of `species`**

```
penguins |>
  count(species)
```

```
# A tibble: 3 × 2
  species       n
  <fct>     <int>
1 Adelie      152
2 Chinstrap    68
3 Gentoo      124
```

- **Relative frequency distribution of `species`**

```
penguins |>
  count(species) |>
  mutate(prop = n / sum(n))
```

```
# A tibble: 3 × 3
  species       n  prop
  <fct>     <int> <dbl>
1 Adelie      152 0.442
2 Chinstrap    68 0.198
3 Gentoo      124 0.360
```

Distribution of penguins flipper size

```
penguins |>
  mutate(flip_s = if_else(
    flipper_length_mm > 210, "large", "short")) |>
  count(flip_s)
```

```
# A tibble: 3 × 2
  flip_s      n
  <chr>   <int>
1 large     100
2 short     242
3 <NA>        2
```

Distribution of penguins body mass

```r
penguins |>
  mutate(mass_c = case_when(
    body_mass_g > 4500 ~ "large",
    body_mass_g > 3000 & body_mass_g <= 4500 ~ "medium",
    body_mass_g <= 3000 ~ "small")
    ) |>
  count(mass_c)
```

```
# A tibble: 4 × 2
  mass_c      n
  <chr>   <int>
1 large     115
2 medium    216
3 small      11
4 <NA>        2
```

Joint distribution of two categorical variables

- Distribution of species and year of measurements of penguins, can be described in a contingency table

(a)

year	Adelie	Chinstrap	Gentoo
2007	50	26	34
2008	50	18	46
2009	52	24	44

Joint distribution of two categorical variables

Similarly, the following frequency (with proportions) tables can also be constructed.

- Frequency and overall proportions

(b)

year	Adelie	Chinstrap	Gentoo
2007	50 (0.145)	26 (0.076)	34 (0.099)
2008	50 (0.145)	18 (0.052)	46 (0.134)
2009	52 (0.151)	24 (0.070)	44 (0.128)

- Freq. with (species) marginal proportions

(c)

year	Adelie	Chinstrap	Gentoo
2007	50 (0.329)	26 (0.382)	34 (0.274)
2008	50 (0.329)	18 (0.265)	46 (0.371)
2009	52 (0.342)	24 (0.353)	44 (0.355)

- Freq. with (year) marginal proportions

(d)

year	Adelie	Chinstrap	Gentoo
2007	50 (0.455)	26 (0.236)	34 (0.309)
2008	50 (0.439)	18 (0.158)	46 (0.404)
2009	52 (0.433)	24 (0.200)	44 (0.367)

Joint distribution of species and year

Let’s see how these tables can be constructed using `count()`:

- Frequency

```r
penguins |>
  count(year, species)
```

```
# A tibble: 9 × 3
   year species       n
  <int> <fct>     <int>
1  2007 Adelie       50
2  2007 Chinstrap    26
3  2007 Gentoo       34
4  2008 Adelie       50
5  2008 Chinstrap    18
6  2008 Gentoo       46
7  2009 Adelie       52
8  2009 Chinstrap    24
9  2009 Gentoo       44
```

Joint distribution of species and year

- Frequency and overall proportions

```r
penguins |>
  count(species, year) |>
  mutate(prop = n / sum(n))
```

```
# A tibble: 9 × 4
  species    year     n   prop
  <fct>     <int> <int>  <dbl>
1 Adelie     2007    50 0.145
2 Adelie     2008    50 0.145
3 Adelie     2009    52 0.151
4 Chinstrap  2007    26 0.0756
5 Chinstrap  2008    18 0.0523
6 Chinstrap  2009    24 0.0698
7 Gentoo     2007    34 0.0988
8 Gentoo     2008    46 0.134
9 Gentoo     2009    44 0.128
```

Joint distribution of species and year

- Frequency and (species) marginal proportions

```r
penguins |>
  count(species, year)  |>
  mutate(prop = n / sum(n),
         .by= species)
```

```
# A tibble: 9 × 4
  species    year     n  prop
  <fct>     <int> <int> <dbl>
1 Adelie     2007    50 0.329
2 Adelie     2008    50 0.329
3 Adelie     2009    52 0.342
4 Chinstrap  2007    26 0.382
5 Chinstrap  2008    18 0.265
6 Chinstrap  2009    24 0.353
7 Gentoo     2007    34 0.274
8 Gentoo     2008    46 0.371
9 Gentoo     2009    44 0.355
```

Joint distribution of species and year

- Frequency and (year) marginal proportions

```
penguins |>
  count(species, year)  |>
  mutate(prop = n / sum(n),
         .by = year)
```

```
# A tibble: 9 × 4
  species    year     n  prop
  <fct>     <int> <int> <dbl>
1 Adelie     2007    50 0.455
2 Adelie     2008    50 0.439
3 Adelie     2009    52 0.433
4 Chinstrap  2007    26 0.236
5 Chinstrap  2008    18 0.158
6 Chinstrap  2009    24 0.2
7 Gentoo     2007    34 0.309
8 Gentoo     2008    46 0.404
9 Gentoo     2009    44 0.367
```