# **Aggregating**

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#LOAD PACKAGES library(tidyverse)



## palmerpenguins dataset

Size measurements, clutch observations, and blood isotope ratios for adult foraging Adélie, Chinstrap, and Gentoo penguins observed on islands in the Palmer Archipelago near Palmer Station, Antarctica. Data were collected and made available by Dr. Kristen Gorman and the Palmer Station Long Term Ecological Research (LTER) Program.

```
#LOAD DATA
library(palmerpenguins) #<1>
data(penguins) #<2>
```

- 1 Load the palmerpenguins package
- (2) Display the penguins dataset in the environment

### Remove rows with missing data with drop\_na()

```
penguins <- penguins %>% #<2>
  drop_na() #<1>
```

- (1) Drops all the rows in the penguins dataset which has missing data (NA values)
- 2 overwrite the penguins dataset with the penguins dataset without the missing rows

#### ⚠ Warning

Is it appropriate to remove rows with missing data? How many rows have missing data? Do the missing rows have something in common?

Removing rows can affect the validity and generalizability of your analysis!

#### count()

count() lets you quickly count the unique values of one or more variables. Suppose you want the number of penguins on each island.

## summarize() or summarise() (either works)

Suppose we are interested in the average bill length of all Adelie penguins:

```
penguins %>%
  filter(species == "Adelie") %>% #<1>
  summarize(average_bill_length = mean(bill_length_mm)) #<2>
```

- (1) only include the rows where the species is Adelie
- (2) calculate the average bill length; save this as average\_bill\_length

Suppose we are interested in the average bill length AND average bill depth of all Adelie penguins:

- (1) calculate the average bill length; save this as average\_bill\_length
- (2) calculate the average bill depth; save this as average\_bill\_depth

Typically, we separate each calculation with a new line to keep things pretty. These new values will print out on the same table.

There are lots of other functions available:

- min: minimum value
- max: maximum value
- mean: average or mean value
- median: median value
- var: variance
- sd: standard deviation
- n: count or number of values
- n\_distinct: counts number of distinct values

Suppose we are interested in the average bill length AND the median bill length of all Adelie penguins:

#### group\_by()

Let's say we were interested in the average bill length and bill depth of all penguin species in this dataset. We could repeat this for the other species (Gentoo and Chinstrap). This would be a fair amount of work AND the results would not end up in the same table.

OR we could use the group\_by command!

1 Repeats the calculate below for each different species.

#### Multiple Groups

Suppose we wish to have the average bill length and average bill depth broken down by sex AND species:

```
penguins %>%
    group_by(species, sex) %>%
    summarise(average bill length = mean(bill length mm),
               average_bill_depth = mean(bill_depth_mm))
# A tibble: 6 x 4
# Groups:
            species [3]
  species
                   average_bill_length average_bill_depth
  <fct>
            <fct>
                                  <dbl>
                                                      <dbl>
1 Adelie
            female
                                   37.3
                                                       17.6
                                                       19.1
2 Adelie
            male
                                   40.4
3 Chinstrap female
                                   46.6
                                                       17.6
4 Chinstrap male
                                   51.1
                                                       19.3
5 Gentoo
                                   45.6
                                                       14.2
            female
6 Gentoo
            male
                                   49.5
                                                       15.7
```

## across() (Optional)

If you wish to apply the same calculation to many columns, you may wish to check out the across function.

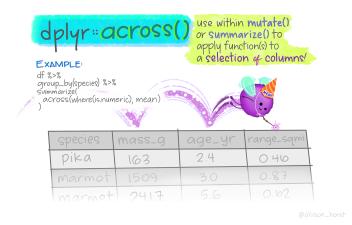


Figure 1: Artwork by @allisonhorst

```
penguins %>%
    group_by(species, sex) %>%
    summarise(across(where(is.numeric), mean))
# A tibble: 6 x 7
# Groups:
            species [3]
  species sex
                bill_length_mm bill_depth_mm flipper_length_mm body_mass_g year
  <fct>
          <fct>
                          <dbl>
                                         <dbl>
                                                            <dbl>
                                                                         <dbl> <dbl>
1 Adelie fema~
                           37.3
                                          17.6
                                                             188.
                                                                         3369. 2008.
2 Adelie male
                           40.4
                                          19.1
                                                             192.
                                                                         4043. 2008.
3 Chinst~ fema~
                                          17.6
                                                                         3527. 2008.
                           46.6
                                                             192.
4 Chinst~ male
                                          19.3
                                                             200.
                                                                         3939. 2008.
                           51.1
5 Gentoo fema~
                                                             213.
                                                                         4680. 2008.
                           45.6
                                          14.2
6 Gentoo male
                           49.5
                                          15.7
                                                             222.
                                                                         5485. 2008.
```

#### Recall: mutate()

The mutate function allows you create a new column which is a function of other columns. This can be useful to converting units.

For example, let's calculate create a new column which displays the body length weight in pounds (lbs) instead of grams. Recall: to convert from grams to pounds we need to multiply by 0.00220462

```
penguins <- penguins %>%
  mutate(body_mass_lbs = body_mass_g*0.00220462) #<1>
```

① Creates a new column in the penguins dataset called body\_mass\_lbs calculated by taking the value of the body mass (in g) and multiplying by 0.00220562.

### case\_when()

Case when can be used in combination with mutate to create a new column with a categorical variable conditional on the values in another column.

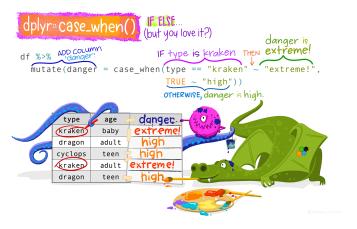


Figure 2: Artwork by @allisonhorst

#### For example:

```
penguins <- penguins %>%
  mutate(penguin_length_cat = case_when(bill_length_mm > 50 ~ 'whoa! huge bill!', TRUE ~ '
```



For those of you who have taken a computer science class before, you may notice that case\_when is similar to using an ifelse statement. You can also use ifelse in R if you'd prefer!

```
penguins <- penguins %>%
   mutate(penguin_length_cat = ifelse(bill_length_mm > 50, 'whoa! huge bill!', '--' ))
```

## Brain Break: Jingjing!

https://youtu.be/oks2R4LqWtE