

Tidy R programming with data in databases and Apache Arrow: applications with the OMOP common data model

Edward Burn, Adam Black, Marti Catala, Berta Raventós

2022-09-23T00:00:00+01:00

Table of contents

Preface	3
1 Getting started with R	4
1.1 Installing R and R Studio	4
1.2 A first data analysis	4
3 summarise()	10
4 right_join(), left_join(), inner_join(), and anti_join()	11
5 filter(), select(), mutate()	12
5.0.1 working with dates	12
5.0.2 working with strings	12
6 Getting to tidy data	13
6.1.2 compute()	13
6.1.3 collect()	13
7 Analysis in R	14
8 Structure of an analysis	15
8.1 Using projects to organise data analyses	15
8.2 A note on file paths	15
8.4 Adding renv	15
8.5 Structure of an R project	15
References	16

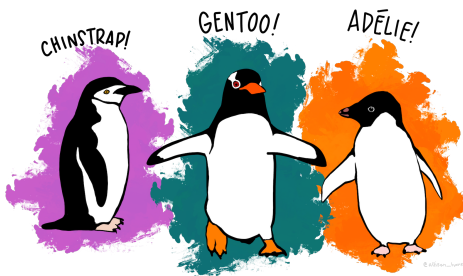
Preface

This book is written for analysts writing analytic code with R to run against the OMOP CDM. This source code for the book can be found at this [Github repository](#). Please open an issue there if you have a question or suggestion. Pull requests with suggested changes and additions are also most welcome.

1 Getting started with R

1.1 Installing R and R Studio

1.2 A first data analysis



Artwork by @allison_horst

For a quick example of a data analysis with R, let's use the data from palmerpenguins package (<https://allisonhorst.github.io/palmerpenguins/>), which contains data on penguins collected from the [Palmer Station](#) in Antarctica.

Because we'll be using a few packages not included in base R, first we need to install these if we don't already have them.

```
install.packages("dplyr")
install.packages("ggplot2")
install.packages("palmerpenguins")
```

Once installed, we can load them like so.

```
library(dplyr)
library(ggplot2)
library(palmerpenguins)
```

We can get an overview of the data using the `glimpse()` command.

```
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~
```

Let's get a count by species

```
penguins %>%
  group_by(species) %>%
  count()
```

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

Now suppose we are particularly interested in the body mass variable. We can first notice that there are a couple of missing records for this.

```
penguins %>%
  group_by(species) %>%
  summarise(not_missing_body_mass_g=sum(!is.na(body_mass_g)==TRUE),
            missing_body_mass_g=sum(is.na(body_mass_g)==TRUE))
```

```
# A tibble: 3 x 3
  species    not_missing_body_mass_g missing_body_mass_g
<fct>                <int>             <int>
1 Adelie              151                1
2 Chinstrap           68                0
3 Gentoo             123                1
```

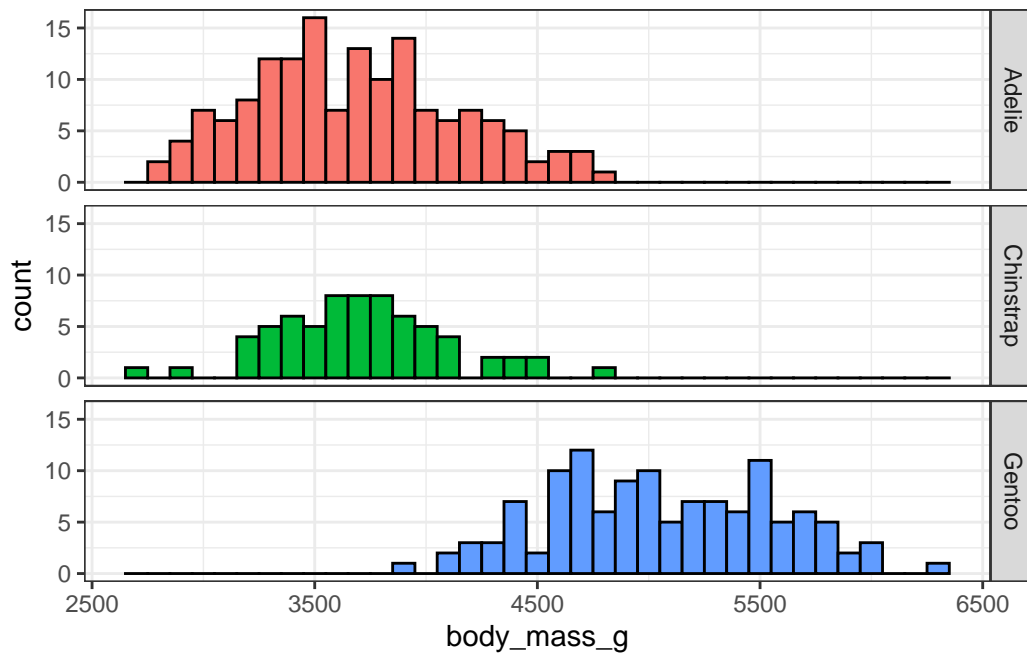
We can get the mean for each of the species (dropping those two missing records).

```
penguins %>%  
  group_by(species) %>%  
  summarise(mean_body_mass_g=round(mean(body_mass_g, na.rm=TRUE)))
```

```
# A tibble: 3 x 2  
  species    mean_body_mass_g  
  <fct>          <dbl>  
1 Adelie        3701  
2 Chinstrap    3733  
3 Gentoo       5076
```

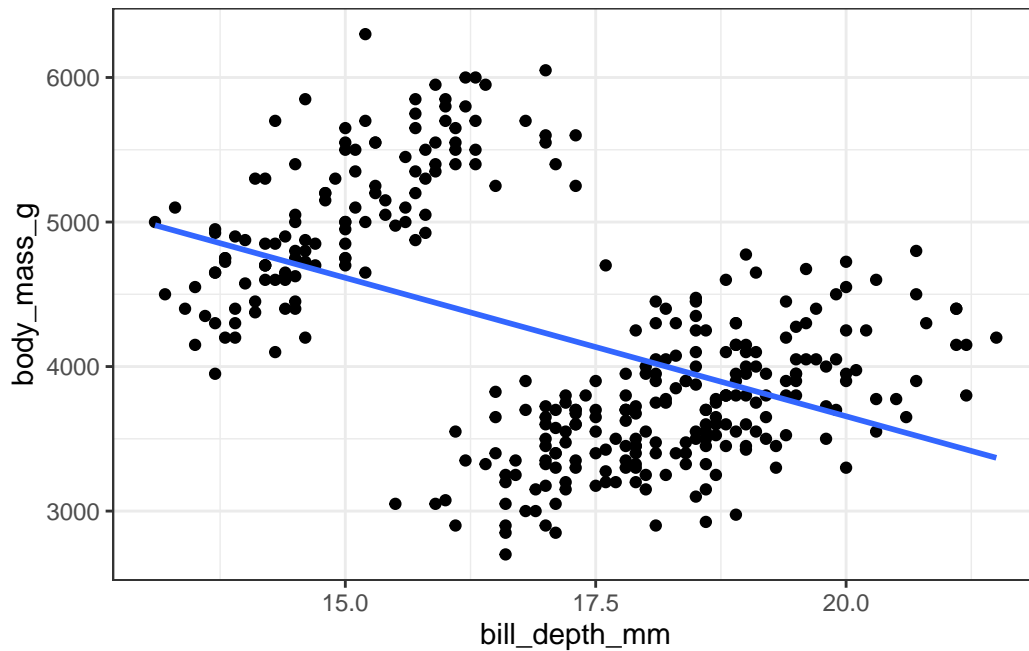
We can then also do a histogram for each of the species.

```
penguins %>%  
  ggplot(aes(group=species, fill=species))+  
  facet_grid(species~ .) +  
  geom_histogram(aes(body_mass_g), colour="black", binwidth = 100)+  
  theme_bw()+  
  theme(legend.position = "none")
```



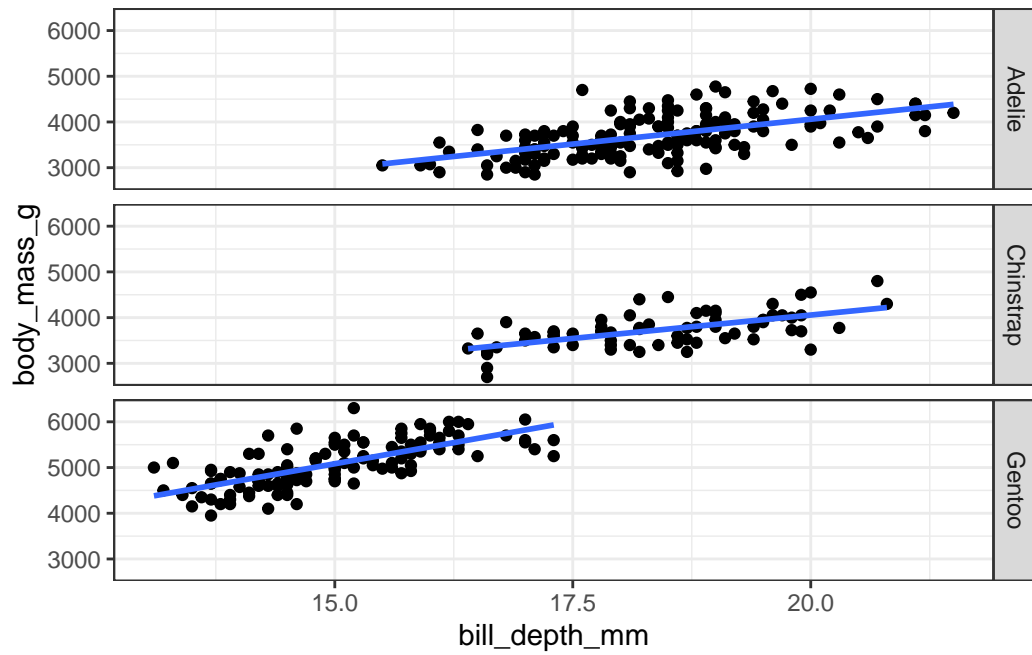
How about the relationship between body mass and bill depth?

```
penguins %>%  
  ggplot(aes(x=bill_depth_mm,y=body_mass_g))+  
  geom_point()+  
  geom_smooth(method="lm",se=FALSE )+  
  theme_bw()+  
  theme(legend.position = "none")
```



But what about by species?

```
penguins %>%  
  ggplot(aes(x=bill_depth_mm,y=body_mass_g))+  
  facet_grid(species~ .) +  
  geom_point()+  
  geom_smooth(method="lm",se=FALSE )+  
  theme_bw()+  
  theme(legend.position = "none")
```



Oh, your first data analysis and you have already found an example of [Simpson's paradox](#)!

2

3 summarise()

4 `right_join()`, `left_join()`, `inner_join()`, and `anti_join()`

5 filter(), select(), mutate()

5.0.1 working with dates

5.0.2 working with strings

5.1

6 Getting to tidy data

6.1

6.1.1

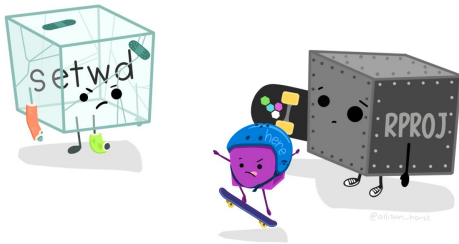
6.1.2 `compute()`

6.1.3 `collect()`

7 Analysis in R

8 Structure of an analysis

8.1 Using projects to organise data analyses



Artwork by @allison_horst

8.2 A note on file paths

8.3

8.4 Adding renv

8.5 Structure of an R project

References