

Data Wrangling and Visualization 101 in R

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Contents

1 This document	1
2 Overview	1
3 Data wrangling	2
3.1 An example data set	2
3.2 Dplyr's verbs	3
3.3 Magrittr's pipes	3
3.4 Putting it together: Wrangling through pipes	3
3.5 Exercises	4
4 Data visualization	6
4.1 Ggplot2's components (aesthetic mappings)	6
4.1.1 Adding geometric components (geoms)	7
4.1.2 Visualizing data summaries	9
4.1.3 Plotting data from multiple subjects	12
4.1.4 Facets	13
4.1.5 Scales and coordinate systems	16
4.2 Pipes (again)	18
4.3 Exercises	18
4.4 Other libraries	19
5 Session info	20

1 This document

This document is part of a series of lectures that introduce students to basic data wrangling, plotting, and general approaches to data analysis. Please see the [overview lecture](#). This and all other lectures are created in R markdown. R markdown combines text with R code, allowing us to see the code and its output, embedded within the text describing the code. If you have the original R markdown file (file extension .Rmd), you can ‘knit’ the document into an HMTL, PDF, or Word file.

2 Overview

This document provides an introduction to data wrangling and visualization in R. Following this class, you will be asked to apply the knowledge gain from this tutorial to *your own data*. **By this Wednesday, post at least one plot about your data on slack using the skills learned in this tutorial.** You are encouraged to ask questions (and help others) on slack.

The document also contains sections marked as exercises. **Please complete these exercises by Friday** and submit them on slack. As with everything else, you're encouraged to ask questions about these problem sets and provide help on slack.

3 Data wrangling

The *R* libraries *dplyr* provide us with efficient ways to transform ('wrangle') our data tables. The library *magrittr* let's us concatenate these operations in transparent and easy to read code. Like many of the packages we use in this tutorial, they are part of the *tidyverse*—an awesome and powerful collection of R packages for the data sciences (<https://www.tidyverse.org/>).

There are many video and interactive tutorials for R, RStudio, and the tidyverse online. I *highly* recommend that you invest a handful of ours to get your inner data scientist started. Your future self will thank you. R is increasingly used both in academia and in the data sciences, and that includes the libraries we use for this tutorial (which are also available in similar form for Python). I would recommend going through at least the first four Sections of [RStudio's R Primers](#): The basics, working with data, visualizing data, and tidying data.

3.1 An example data set

We will illustrate the use of *dplyr* with the following data from an experiment with a 2AFC task. On each trial, subjects had to fixate on a fixation cross. The fixation cross was then replaced by a small small number, and subjects had to quickly answer whether they saw the number "3" or "8". Half of the trials displayed "3", half displayed "8". Within subject, the experiment manipulated two variables, the size of the number (1, 2, or 4) and whether the number was surrounded by four other numbers above, below, left, and right of it (hard) or not (easy). The presence of other numbers presented close to the target number is known to make recognition of the target number harder—an effect known as "visual crowding". For each trial, the software recorded whether the subject's response was correct (1 = correct; 0 = incorrect) and the reaction time for the response (RT):

```
summary(d)
```

```
## #> #>   size    condition      trial      subject      correct
## #> 1:2400  easy:3600  Min.   : 1.00  1       : 720  Min.   :0.0000
## #> 2:2400  hard:3600  1st Qu.: 30.75  2       : 720  1st Qu.:0.0000
## #> 4:2400          Median : 60.50  3       : 720  Median :1.0000
## #>                  Mean   : 60.50  4       : 720  Mean   :0.6062
## #>                  3rd Qu.: 90.25  5       : 720  3rd Qu.:1.0000
## #>                  Max.   :120.00  6       : 720  Max.   :1.0000
## #>                  (Other):2880
## #> #>   RT
## #> 1: Min.   : 24.98
## #> 2: 1st Qu.: 103.18
## #> 3: Median : 212.79
## #> 4: Mean   : 256.55
## #> 5: 3rd Qu.: 350.44
## #> 6: Max.   :1207.55
## #>
```

```
glimpse(d)
```

```
## #> #> Rows: 7,200
## #> #> Columns: 6
## #> #> $ size      <fct> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
## #> #> $ condition <fct> easy, easy, easy, easy, easy, easy, easy, ~
```

```

## $ trial      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, ~
## $ subject    <fct> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10~
## $ correct    <int> 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 0, 0, 1, 0, 0, 1, 0, ~
## $ RT         <dbl> 612.445, 241.010, 283.580, 233.697, 330.521, 456.040, 589.33~

```

3.2 Dplyr's verbs

Dplyr has ‘verbs’ like filter, select, summarize, mutate, transmute, etc. to let us conduct operations on our data, and reshape the data frame into the format we need. We can use dplyr, for example, to calculate the proportion correct answers in our experiment by using *summarise*.

```
summarise(d, meanCorrect = mean(correct))
```

```

## # A tibble: 1 x 1
##   meanCorrect
##       <dbl>
## 1     0.606

```

Or just for number size 1:

```
d.1 = filter(d, size == "1")
summarise(d.1, meanCorrect = mean(correct))
```

```

## # A tibble: 1 x 1
##   meanCorrect
##       <dbl>
## 1     0.498

```

3.3 Magritte's pipes

Here we will use only of the ‘pipes’ magrittr provides:

- `x %>% f`: takes x and hands it to the function f on the right, as f’s first argument
- `x %>>% f1 %>% f2 %>% etc.`: takes x hands it to f1, takes the output of f1 and hands it to f2, etc. And since the first pipe was `%>>%` (rather than just `%>%`), the final result will be written back into x.



Figure 1: Magritte’s pipe

3.4 Putting it together: Wrangling through pipes

Remember how we got the mean proportion correct for just number size 1?

```
d.1 = filter(d, size == "1")
summarise(d.1, meanCorrect = mean(correct))
```

```

## # A tibble: 1 x 1
##   meanCorrect
##       <dbl>
## 1     0.498

```



Figure 2: Magrittr's pipe

This is inelegant and hard to read. Pipes let us make this more transparent:

```
d %>%
  filter(size == "1") %>%
  summarise(meanCorrect = mean(correct))

## # A tibble: 1 x 1
##   meanCorrect
##       <dbl>
## 1      0.498
```

And this advantage becomes even clearer, the more operations we concatenate. For example, `group_by` is an elegant operator that tells the pipes to conduct all subsequent operations for each of the groups (and then put all the separate outcomes back together into a single data frame). So if we want the proportion correct for all groups:

```
d %>%
  group_by(size) %>%
  summarise(meanCorrect = mean(correct))

## # A tibble: 3 x 2
##   size  meanCorrect
##   <fct>     <dbl>
## 1 1        0.498
## 2 2        0.592
## 3 4        0.729
```

3.5 Exercises

Remember [dplyr cheatsheet!](#) How can we:

- View the entire data set? (`View`)
- Calculate the by-subject averages for all three number sizes? (`group_by, summarise`)
- Calculate the by-subject standard deviations around those averages? (`group_by, summarise`)
- Attach this information (the averages and SDs) to each row of the present data.frame? (`group_by, mutate`)
- Determine whether RTs were on average faster for correct, as compared to incorrect, trials?
- Add a column for log-transformed RTs to the data set?
- Remove the old column for raw RTs? (`select`)

- Sort the data by log-transformed reaction times? (*arrange*)

Say we further have an additional data frame with information about our subjects:

```
## # A tibble: 10 x 3
## # Rowwise:
##   subject gender age
##   <fct>   <fct> <dbl>
## 1 1       male    21
## 2 2       male    20
## 3 3       female  20
## 4 4       male    18
## 5 5       male    19
## 6 6       male    20
## 7 7       female  20
## 8 8       male    21
## 9 9       male    18
## 10 10     male    20
```

- How can we join the information from the two data sources together? (*left_join*)

```
## # A tibble: 10 x 3
## # Rowwise:
##   subject gender age
##   <fct>   <fct> <dbl>
## 1 1       male    21
## 2 2       male    20
## 3 3       female  20
## 4 4       male    18
## 5 5       male    19
## 6 6       male    20
## 7 7       female  20
## 8 8       male    21
## 9 9       male    18
## 10 10     male    20

## Joining with `by = join_by(subject)`

## # A tibble: 7,200 x 8
##   size condition trial subject correct      RT gender age
##   <fct> <fct>   <int> <fct>   <int> <dbl> <fct> <dbl>
## 1 1     easy      1 1       1 612. male   21
## 2 1     easy      1 2       0 241. male   20
## 3 1     easy      1 3       1 284. female 20
## 4 1     easy      1 4       0 234. male   18
## 5 1     easy      1 5       1 331. male   19
## 6 1     easy      1 6       0 456. male   20
## 7 1     easy      1 7       1 589. female 20
## 8 1     easy      1 8       0 335. male   21
## 9 1     easy      1 9       1 698. male   18
## 10 1    easy      1 10      1 319. male   20
## # i 7,190 more rows
```

4 Data visualization

The two main libraries in R we will be using for visualization are *ggplot2* and *plotly*. Ggplot2 provides a grammar of graphics approach to plotting. Plotly let's us interact with our data. In particular, *ggplotly()* wrapped around a ggplot2 figure let's us interact with that figure. Before you start, make sure to get the superb [ggplot2 cheatsheet](#).

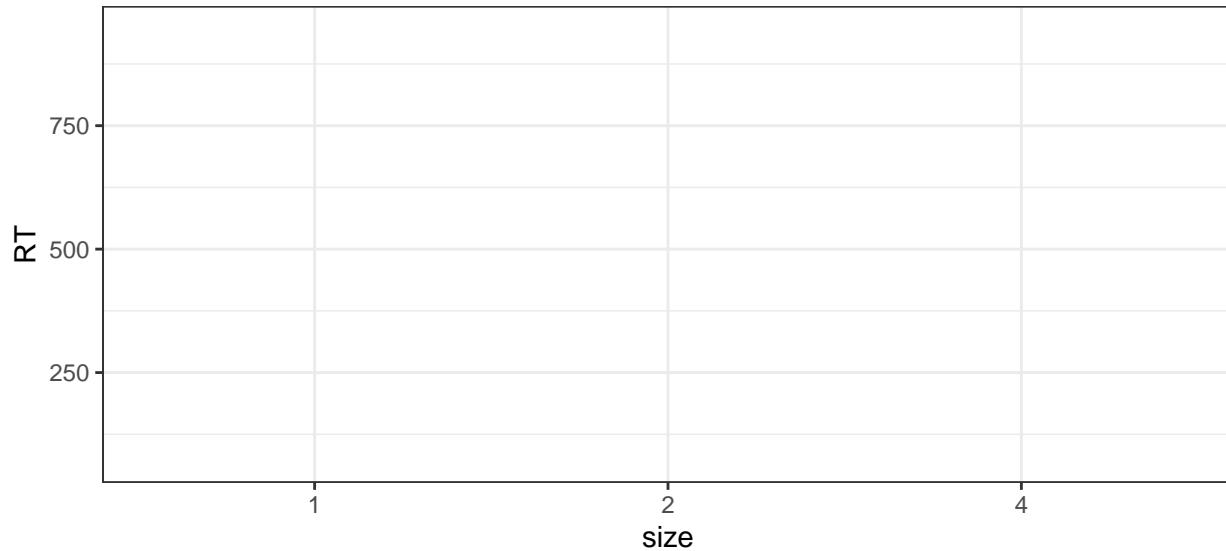
4.1 Ggplot2's components (aesthetic mappings)

In order to plot in ggplot2, we need to understand the way it thinks about visualization. There are excellent online course that explain all of this, so I focus on the basics. **For reasons that become apparent below, we start by just looking at one subject, subject 1.**

At the heart of a plot is a mapping between properties of your data (i.e., column in your data frame) and abstract properties of the plot (such as x- or y-coordinates, color, fill, transparency (alpha), linetype, shape, or label information). If we call the function `ggplot()` in order to create a figure, we specify two arguments: the name of the data frame we want to work with, and the mapping. The latter is done through a helpful function called `aes()`—for aesthetics:

```
d.s1 = d %>%
  filter(subject == 1)

ggplot(
  data = d.s1,
  mapping =
    aes(
      x = size,
      y = RT))
```



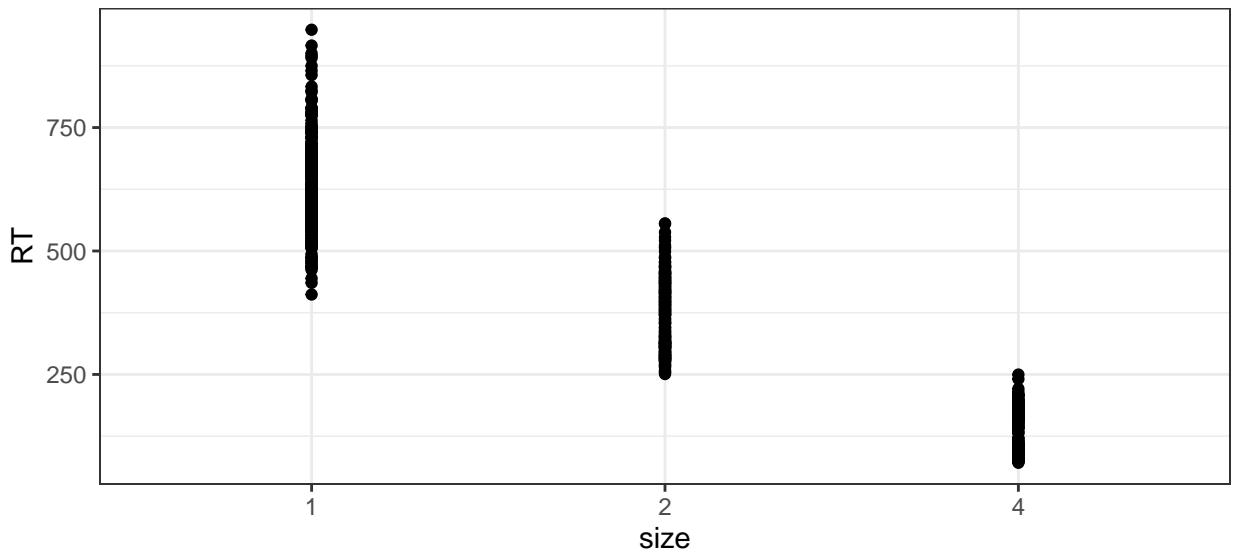
```
# or equivalently and shorter:
# ggplot(
#   d,
#   aes(
#     x = size,
#     y = RT))
```

4.1.1 Adding geometric components (geoms)

Notice that this by itself only returns an empty plot. That's the case because we have not yet specified how we want the abstract properties of the graph to be expressed visually. That's achieved by specifying *geoms* (for geometries), such as points (*geom_point*), lines (*geom_line*), histograms (*geom_histogram*), lineranges (*geom_linerange*), and many similar functions (I take it you're getting the hang for the naming scheme ...). You can find all of them on the [ggplot2 cheatsheet](#).

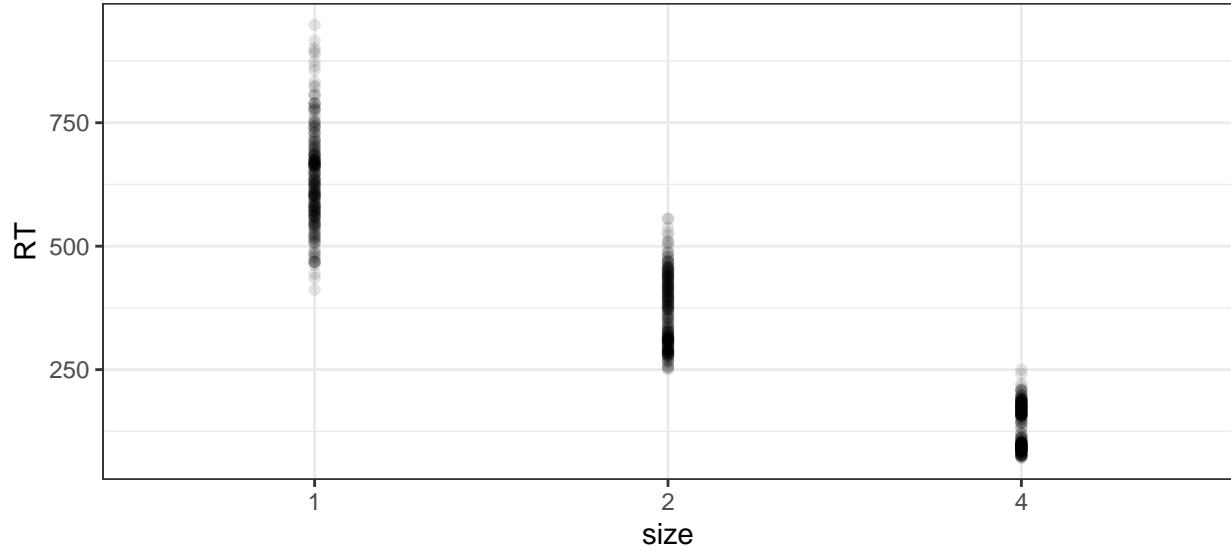
We add such components to a plot with “+”.

```
p = ggplot(  
  data = d.s1,  
  mapping =  
    aes(  
      x = size,  
      y = RT)) +  
  geom_point()  
  
plot(p)
```



Notice that this plot is not particularly helpful! There is a lot of points and they are all overlaid, making it hard to get a clear idea of the data. One way we can improve this plot is to add transparency to the points. Another way is to jitter the points along the x-axis. Both approaches help convey information about the distribution of RTs at each number size, and sometimes—especially, when we have a lot of data—we might want to combine both approaches. For example, here's the same plot with just transparency added. Since we have quite a bit of data, it still does not convey much information:

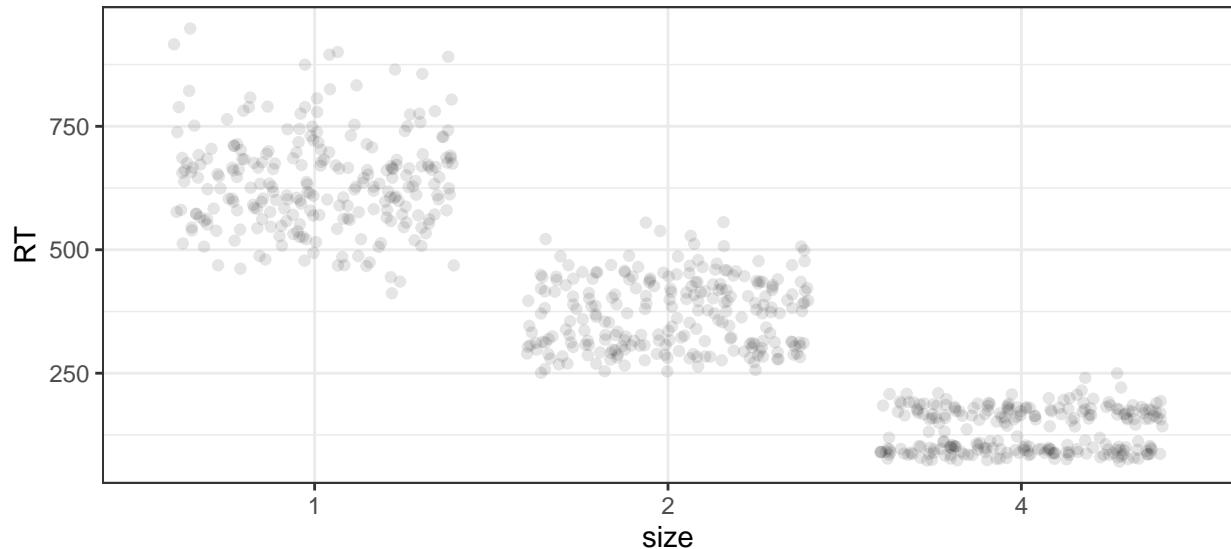
```
p = ggplot(  
  data = d.s1,  
  mapping =  
    aes(  
      x = size,  
      y = RT)) +  
  geom_point(alpha = .1)  
  
plot(p)
```



And here is the plot with some additional jitter added along the x-axis. Note that we intentionally avoid jitter along the y-axis:

```
p = ggplot(
  data = d.s1,
  mapping =
  aes(
    x = size,
    y = RT)) +
  geom_point(alpha = .1, position = position_jitter(height = 0))

plot(p)
```



That's much better already, giving us a much clearer idea of how the data is distributed! We are now in a position to think about how to include information about condition in this plot. There are a few ways to do this. For example, we could use different point shapes or colors for the easy and hard condition. Here, we do the latter:

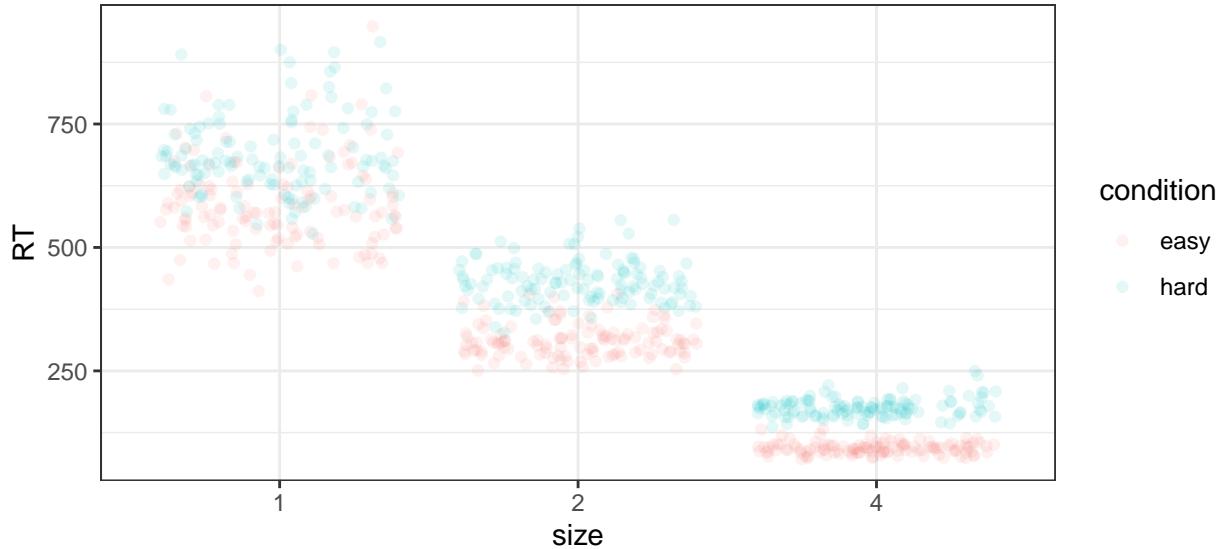
```
p = ggplot(
  data = d.s1,
```

```

mapping =
aes(
  x = size,
  y = RT,
  color = condition)) +
geom_point(alpha = .1, position = position_jitter(height = 0))

plot(p)

```

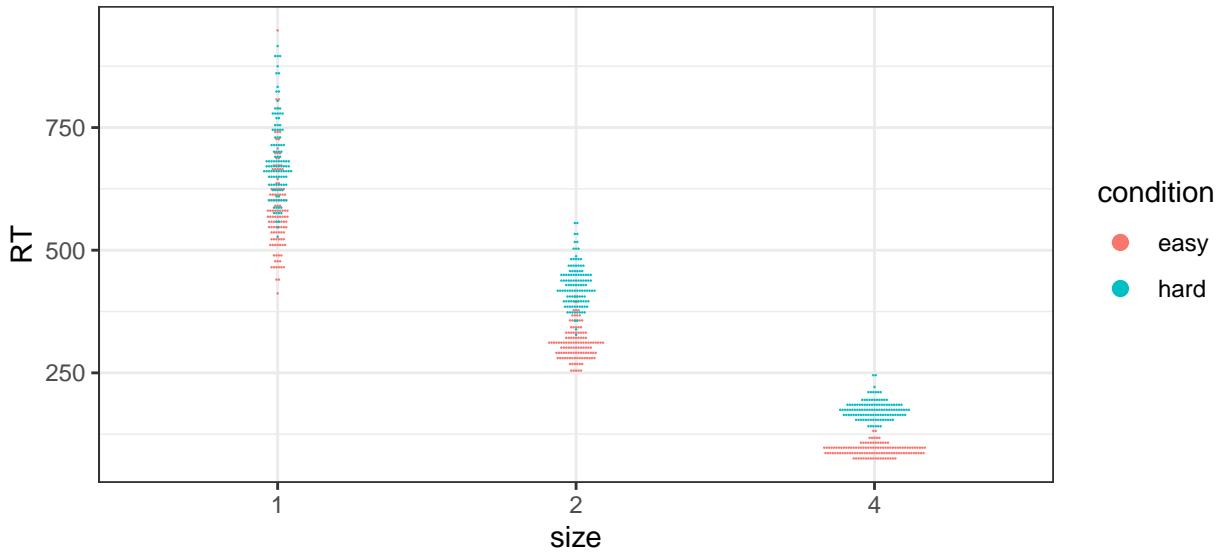


Notice the clear ‘stripes’ in the data

4.1.2 Visualizing data summaries

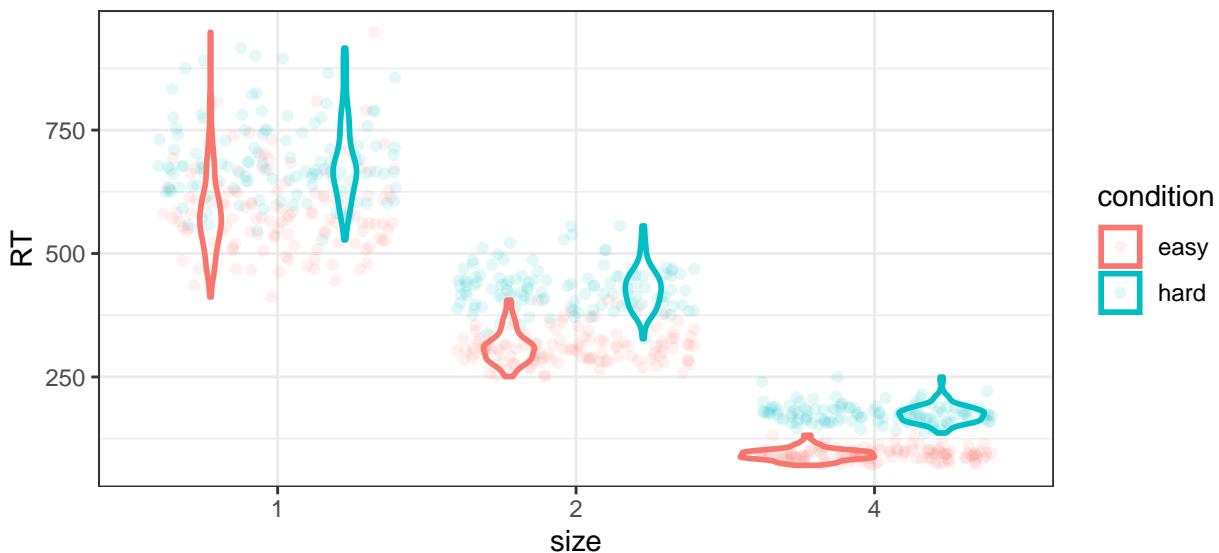
While it is often useful to see the raw data, this *alone* can be insufficient to communicate important aspects of the data. Specifically, we often are interested in whether the distributions of two conditions (e.g., the number size and easy vs. hard conditions) differ. The plots we have seen so far *suggest* that this might be the case, but we can’t be certain. In order to convey information about the distribution of our data, we often provide data *summaries* instead of—or in addition to—the raw data. Whenever possible, I would highly recommend to go with the “in addition to” option. There is a lot of value in seeing the raw data, as long as the overall tendencies we are interested in can also be recognized.

Data can be summarized down to various levels of abstraction. For example, we can *bin* the data, and report the binned ‘raw’ data:



Dotplots can be an effective means for a categorical outcome variable (or the proportions resulting from them). Try it out for plotting the correctness of responses, rather than RTs. For a continuous outcome variables, however, dotplots are difficult to read (as in the RT plot above), and you might be better off with plotting the histogram or density of the distribution. This can elegantly be done by adding so-called violins to the raw data:

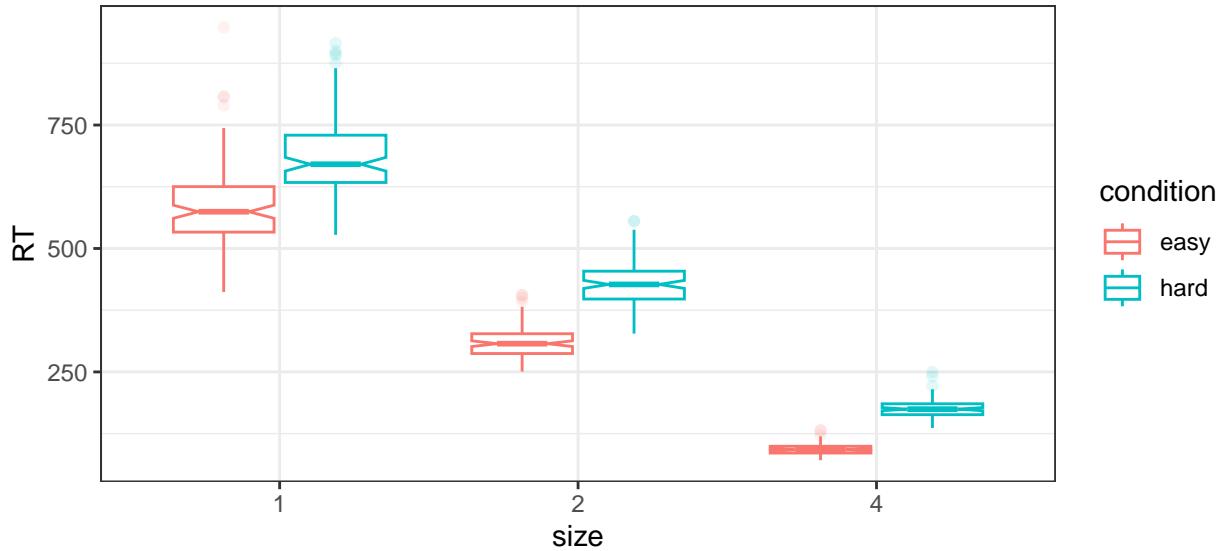
```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



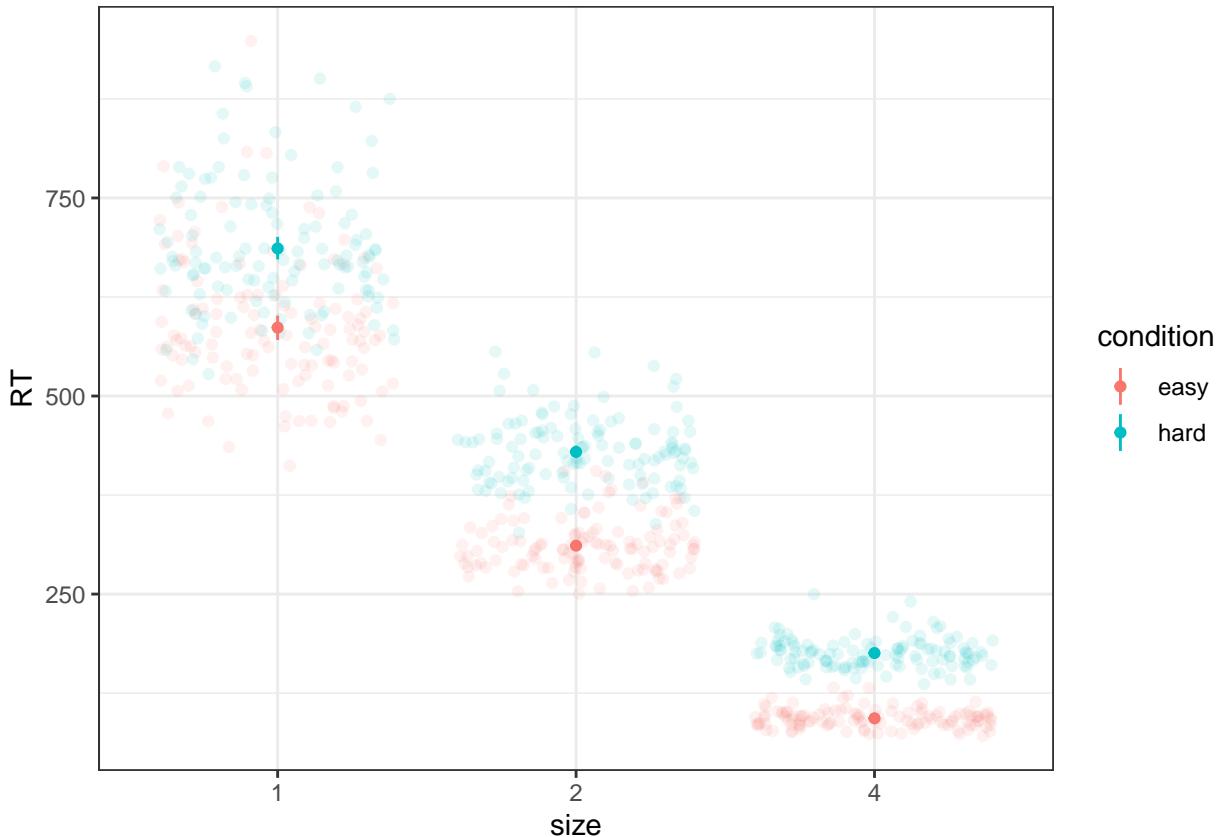
Some researchers also like dotplots, which try to provide a high-level summary of the data while also providing *some* information about the general distribution of the data and any potential outliers. Boxplots tend to be plotted *instead* of the raw data since boxplots already contain any raw data that is not captured well by the summary they provide (the outlier points). The line in the center of the box provides the median of the data in that condition. The upper and lower end of the box indicate the “inter-quartile range (IQR) from the 25th to the 75th quantile of the outcome (you can use the command `quantiles()` to get the quantiles yourself, if you want to compare them to what the plot provides). The whiskers (the lines below and above

the box) extend to the largest and smallest value at most 1.5-times larger/smaller than the end of the box. Just as the height of the box provides a summary of the middle 50% of the data (the IQR), the whiskers give an idea of the distribution beyond that middle part. Any points outside of that range are plotted and are referred to as "outliers". Notably all outliers in the present case are high RT outliers, not low RT outliers. This is quite common for variables that have highly skewed distributions: RTs have a lower, but no upper bound.

Finally, the notches (indentation on the sides of the box) provide the 95% confidence intervals around the means (CIs). We'll learn later *how CIs are obtained*, and what exactly they mean. For now, it suffices to say that (appropriately obtained) CIs are a critical visual component in plots when we want to know whether the means differ between conditions.



In publications, you will find that the data is often summarized even further into just the central tendency (mean) and its 95% CIs. Here we plot the mean and 95% CIs on top of the raw data. In this case, we have so much data that the CIs are very narrow and not even recognizable in the plot:



Here have used a pointrange to summarize the data. Alternatives include linerange (geom_linerange; no mean shown) or bar graphs with error intervals (geom_bar and geom_errorbar).

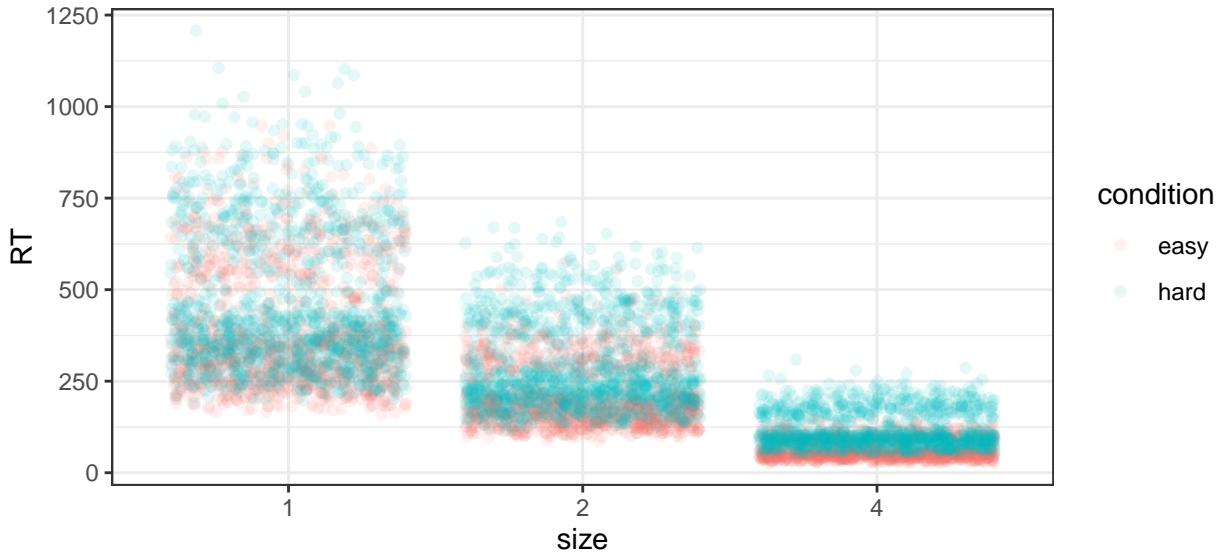
It is important that we summarize the data at an appropriate level when obtained CIs. We will cover this in more detail in a later class, but for now remember that what we do here is ok if we're looking at the data from one subject, but that we need to do things a bit differently when we look at the combined data from multiple subjects.

4.1.3 Plotting data from multiple subjects

So far we have plotted just one subject. Notice what happens when we update the scatter plot with the data from *all* subjects. There are now multiple ‘stripes’ visible in the data. Think about why that is the case. Any ideas?

```
# We can update a plot with new data using %+%
p = p %+%
  d

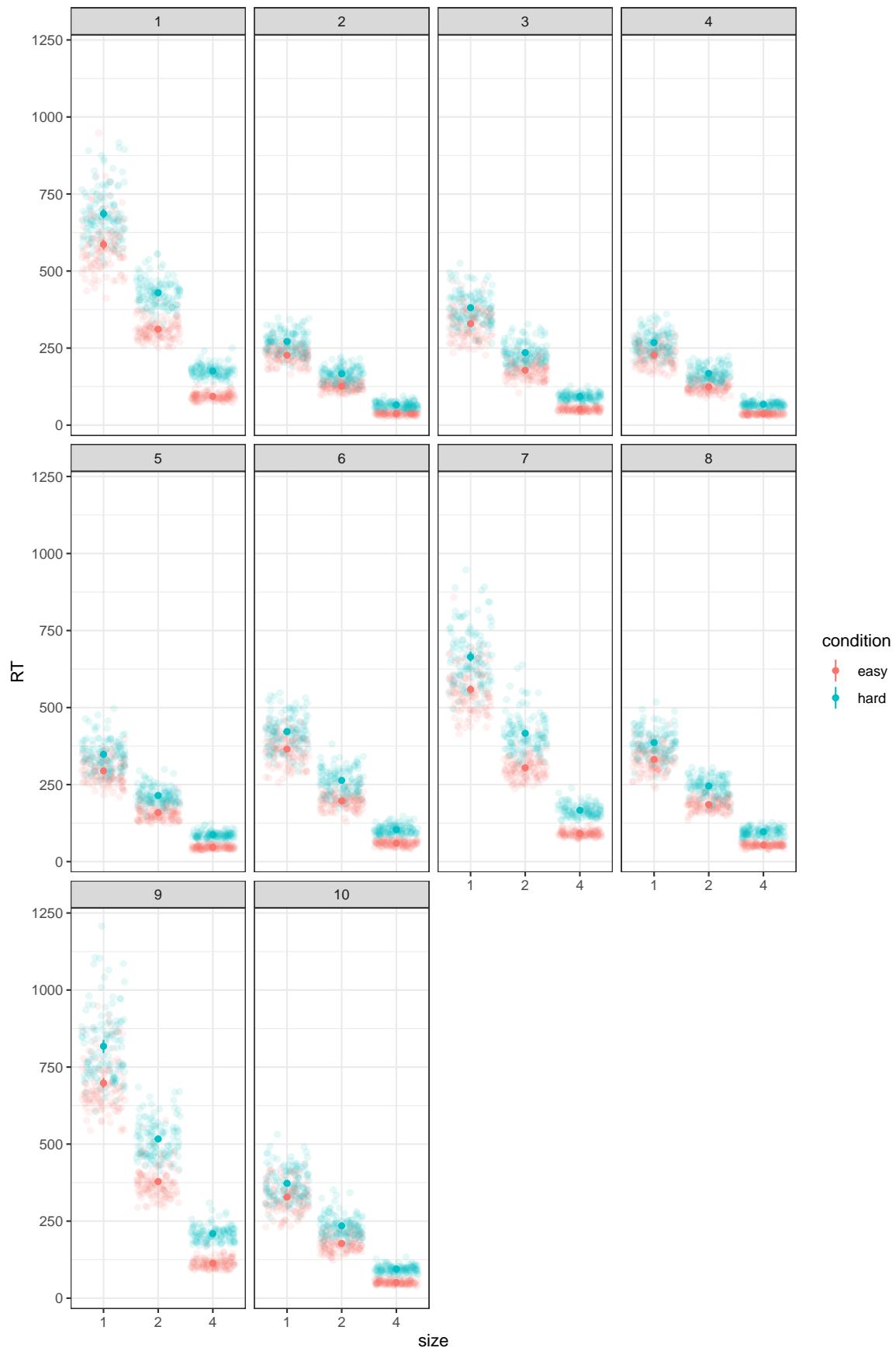
plot(p)
```



Correct: subjects differ from each other. This includes how fast they are overall, and might also include differences in how they are affected by the experimental conditions. This also means that the individual observations we are *not* independent of each other because the data points from the same subject resemble each other. We talk about “repeated measures” from the subject and call such data “repeated measures data”. Another term that is used to refer to such data is *hierarchical* data or `*hierarchically organized()` data. Whenever we deal with such data, we need to be careful, for example, when we calculate CIs. We will return to that issue in our class on confidence intervals. For now, the next section focuses on how we can effectively visualize the data for all subjects without having to make many individual plots.

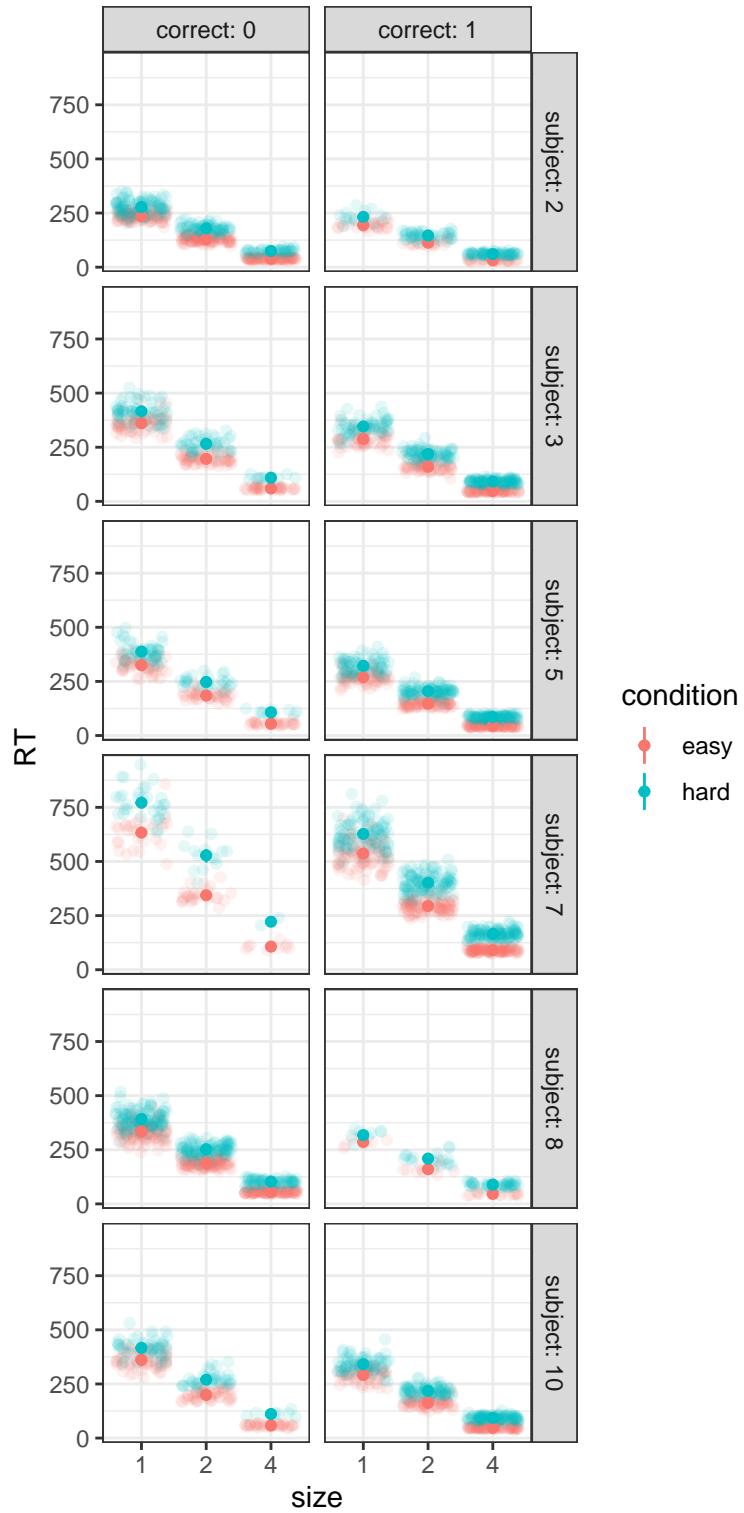
4.1.4 Facets

If we want to have separate panels conditional on another variable, we can do so through *facets*. There are two major facet functions, `facet_wrap` (to have panels conditional on one variable) and `facet_grid` (conditional on two variables). For example, we can have separate panels for each subject:



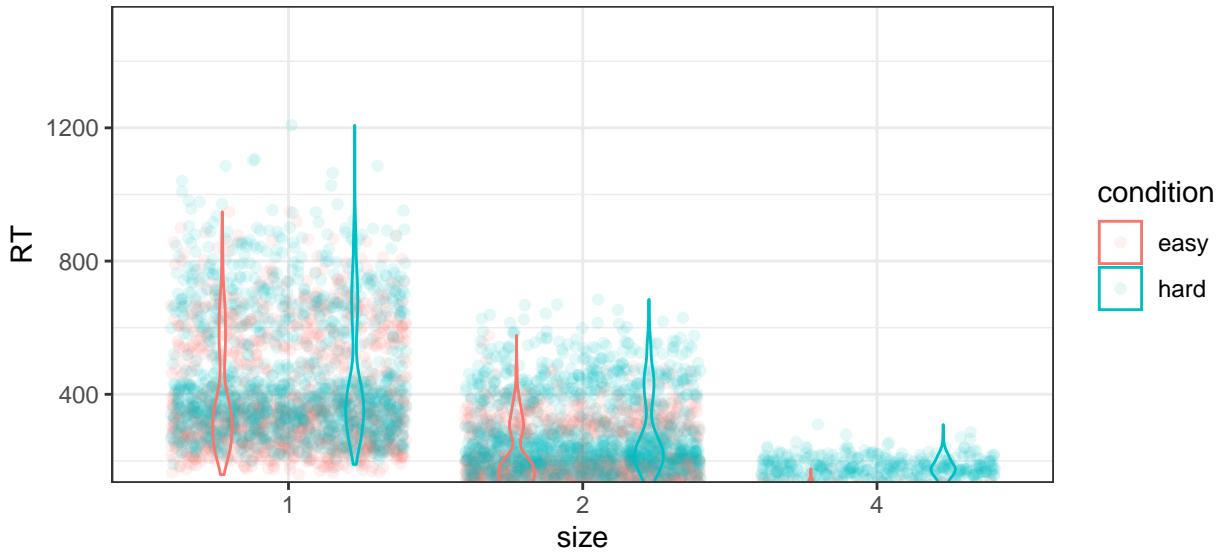
Or we could show by-subject RTs in two columns, separately for false and correct answers. Here, we do so after first sampling 6 random subjects (since the plot would otherwise be rather large).

```
## Warning: The `facets` argument of `facet_grid()` is deprecated as of ggplot2 2.2.0.  
## i Please use the `rows` argument instead.  
## This warning is displayed once every 8 hours.  
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was  
## generated.
```



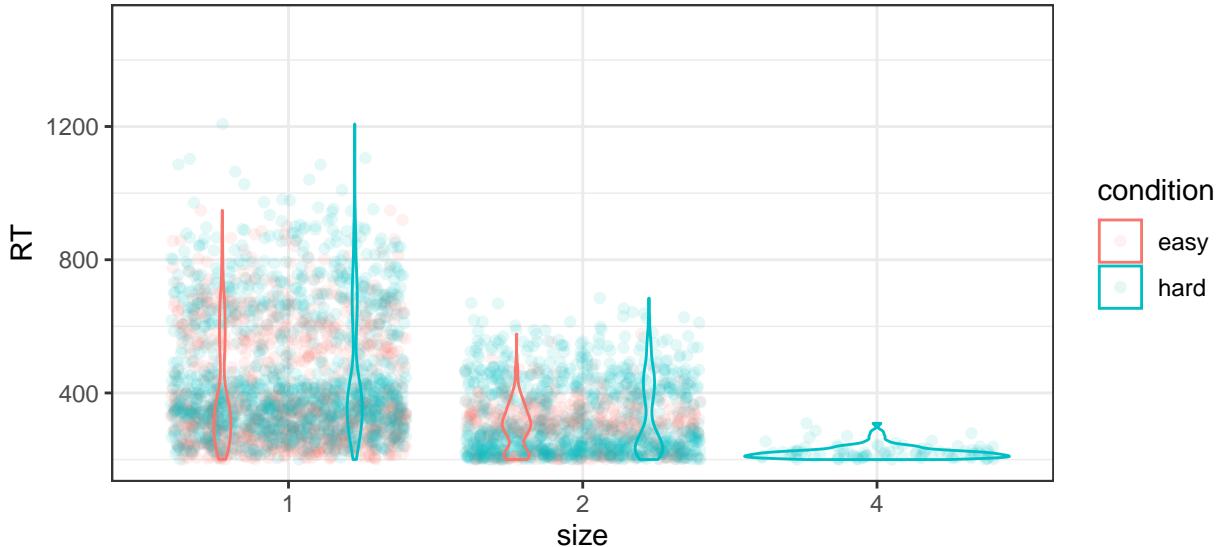
4.1.5 Scales and coordinate systems

Sometimes we don't want to see all of the data, or we want to zoom into some ranges of our data. We can do so by explicitly specifying the x- and y-limits of our coordinate system:

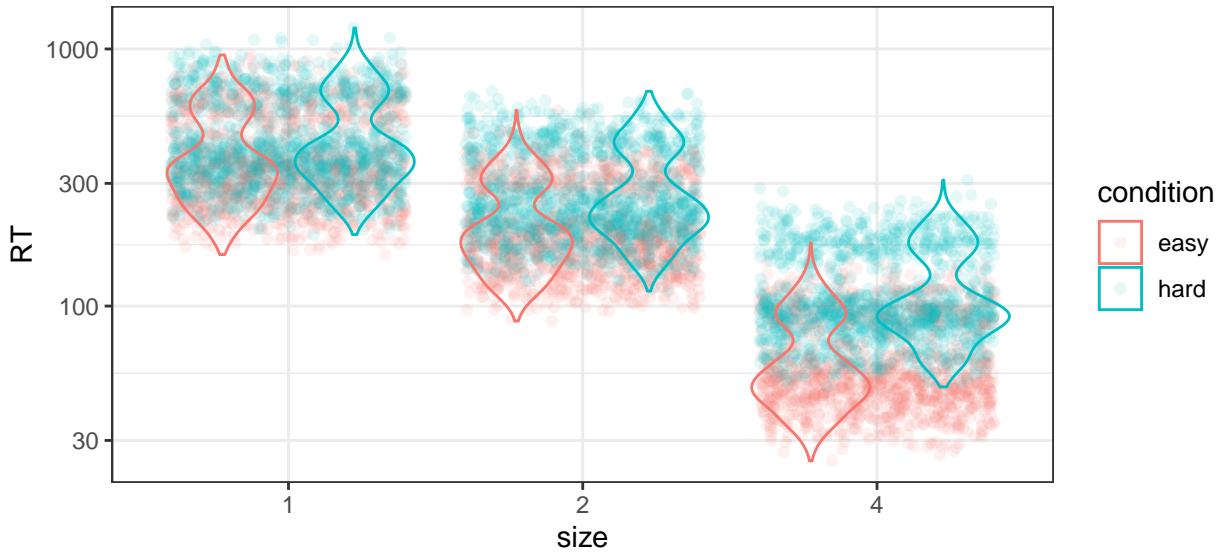


Note that this zooms into parts of our data without excluding any data (e.g., from the calculation of the violins, which have the same shape as above). If we want to exclude data, transform data or in other ways change the way the aesthetical mappings are interpreted, this is achieved through *scales*. For example, the following excludes all RTs below 300 and above 2000. Note how that changes the violin plots (as it should: they estimate the ditribution of RTs):

```
## Warning: Removed 3353 rows containing non-finite values (`stat_ydensity()`).
## Warning: Removed 3353 rows containing missing values (`geom_point()`).
```



More generally, **scales are applied before *ggplot2* applies any statistics, whereas coordinate systems do only affect how we see the data**. This is important to remember. For example, since reaction times often have distributions that are more lognormal, rather than normal, let's update our original plot to use a log-transformed y-axis. This does not only affect how we *see* the data, it also affects how the densities that are plotted by the violin geom are estimated:

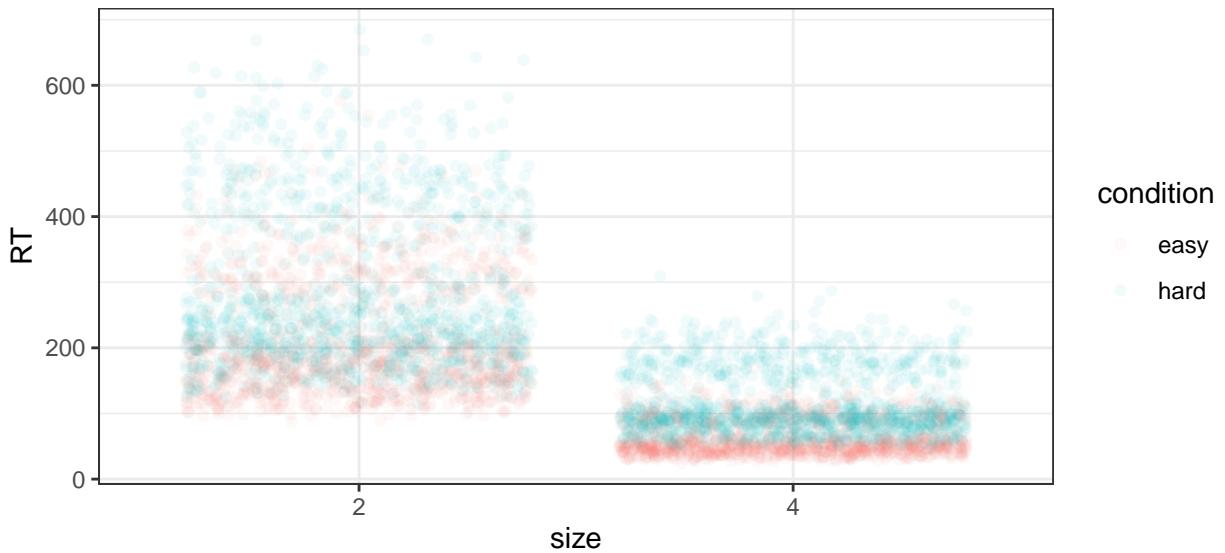


4.2 Pipes (again)

Of course, we can use pipes to pipe the data frame into the plotting function, optionally after first piping the data through some additional *dplyr* operations (since the output of that entire pipe is again a data frame):

```
p = d %>%
  filter(size != "1") %>%
  ggplot(
    aes(
      x = size,
      y = RT,
      color = condition)) +
  geom_point(alpha = .05, position = position_jitter())

plot(p)
```



4.3 Exercises

Remember [ggplot2 cheatsheet!](#)

- Plot a histogram of the RTs by number size. Make one version where you plots the histograms in different facets, and another version where you have only one facet and use fill color to distinguish between number sizes. (*geom_histogram*)
- Plot the average proportion of correct answers by number size as a pointrange.
- Do the same, but first average by subject and number size, and then plot the average (and confidence interval) of those by-subject averages of correct responses.
- Try to make a pie chart that shows the proportion correct for the three number sizes. (*coord_polar*)

4.4 Other libraries

There's a huge number of additional libraries that build on *ggplot2*, and they keep changing. Many of the libraries introduce additional geoms, incl. single-line commands for complex plots (e.g., k -by- k correlation plots; trees diagrams; field-specific plot types like map types, dendograms, ridge plots, 3D plots). Other packages extend what *ggplot2* can do or make it easier to use.

Here I just note a few:

- Extend functionality:
 - ganimate for animations, movies, gifs, etc.
 - plotly to turn any ggplot into an interactive graph
 - cowplot to combine multiple ggplots into a single figure
 - Make it easier to do things that ggplot can already do:
 - ggforce to add powerful functionality
 - ggthemes to add themes
 - ggraph to visualize graphs
 - ggeffects to help with plotting model summaries
 - ggsignif to add significance brackets (seen in many publications)
 - ggpubr to make ggplots publication ready
 - ggsci to add scientifically themed palettes
 - viridis to add highly contrastive color schemes (beautiful)
 - Shiny to make web-based apps in which users can interact with your plots.

For further inspiration, check out these galleries:

- [Gallery of R plots](#)
- [List of ggplot2 extensions](#)

For example, instead of faceting our data by subject, we might animate it by subject. Gganimate can create movies, but here I am embedding the animation directly into the PDF. This will only work if you work the document in Acrobat Reader. Try it out:

5 Session info

```
## - Session info -
## setting value
## version R version 4.3.0 (2023-04-21)
## os      macOS Ventura 13.4.1
## system aarch64, darwin20
## ui      X11
## language (EN)
## collate en_US.UTF-8
## ctype   en_US.UTF-8
## tz      Europe/Stockholm
## date    2023-08-19
## pandoc  3.1.1 @ /Applications/RStudio.app/Contents/Resources/app/quarto/bin/tools/ (via rmarkdown)
##
## - Packages -
## package     * version  date (UTC) lib source
## backports     1.4.1    2021-12-13 [1] CRAN (R 4.3.0)
## base64enc     0.1-3    2015-07-28 [1] CRAN (R 4.3.0)
## bit          4.0.5    2022-11-15 [1] CRAN (R 4.3.0)
## bit64         4.0.5    2020-08-30 [1] CRAN (R 4.3.0)
## cachem        1.0.8    2023-05-01 [1] CRAN (R 4.3.0)
## callr         3.7.3    2022-11-02 [1] CRAN (R 4.3.0)
## cellranger    1.1.0    2016-07-27 [1] CRAN (R 4.3.0)
## checkmate     2.2.0    2023-04-27 [1] CRAN (R 4.3.0)
## cli           3.6.1    2023-03-23 [1] CRAN (R 4.3.0)
## cluster       2.1.4    2022-08-22 [1] CRAN (R 4.3.0)
## colorspace    2.1-0    2023-01-23 [1] CRAN (R 4.3.0)
## cowplot       * 1.1.1    2020-12-30 [1] CRAN (R 4.3.0)
## crayon        1.5.2    2022-09-29 [1] CRAN (R 4.3.0)
## data.table    1.14.8   2023-02-17 [1] CRAN (R 4.3.0)
## devtools      2.4.5    2022-10-11 [1] CRAN (R 4.3.0)
## digest         0.6.33   2023-07-07 [1] CRAN (R 4.3.0)
## dplyr         * 1.1.2    2023-04-20 [1] CRAN (R 4.3.0)
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## ellipsis      0.3.2   2021-04-29 [1] CRAN (R 4.3.0)
## evaluate     0.21    2023-05-05 [1] CRAN (R 4.3.0)
## fansi        1.0.4   2023-01-22 [1] CRAN (R 4.3.0)
## farver       2.1.1   2022-07-06 [1] CRAN (R 4.3.0)
## fastmap      1.1.1   2023-02-24 [1] CRAN (R 4.3.0)
##forcats      * 1.0.0   2023-01-29 [1] CRAN (R 4.3.0)
## foreign      0.8-84   2022-12-06 [1] CRAN (R 4.3.0)
## Formula      1.2-5   2023-02-24 [1] CRAN (R 4.3.0)
## fs           1.6.2   2023-04-25 [1] CRAN (R 4.3.0)
## generics     0.1.3   2022-07-05 [1] CRAN (R 4.3.0)
## gganimate    * 1.0.8   2022-09-08 [1] CRAN (R 4.3.0)
## ggplot2      * 3.4.2   2023-04-03 [1] CRAN (R 4.3.0)
## gifski       1.12.0-1 2023-06-08 [1] CRAN (R 4.3.0)
## glue          1.6.2   2022-02-24 [1] CRAN (R 4.3.0)
## gridExtra     2.3     2017-09-09 [1] CRAN (R 4.3.0)
## gtable        0.3.3   2023-03-21 [1] CRAN (R 4.3.0)
## Hmisc         5.1-0   2023-05-08 [1] CRAN (R 4.3.0)
## hms          1.1.3   2023-03-21 [1] CRAN (R 4.3.0)
## htmlTable     2.4.1   2022-07-07 [1] CRAN (R 4.3.0)
## htmltools     0.5.5   2023-03-23 [1] CRAN (R 4.3.0)
## htmlwidgets   1.6.2   2023-03-17 [1] CRAN (R 4.3.0)
## httpuv        1.6.11   2023-05-11 [1] CRAN (R 4.3.0)
## httr          1.4.6   2023-05-08 [1] CRAN (R 4.3.0)
## jsonlite      1.8.7   2023-06-29 [1] CRAN (R 4.3.0)
## knitr         1.43    2023-05-25 [1] CRAN (R 4.3.0)
## labeling      0.4.2   2020-10-20 [1] CRAN (R 4.3.0)
## later         1.3.1   2023-05-02 [1] CRAN (R 4.3.0)
## lazyeval      0.2.2   2019-03-15 [1] CRAN (R 4.3.0)
## lifecycle     1.0.3   2022-10-07 [1] CRAN (R 4.3.0)
## lubridate     * 1.9.2   2023-02-10 [1] CRAN (R 4.3.0)
## magrittr      * 2.0.3   2022-03-30 [1] CRAN (R 4.3.0)
## memoise       2.0.1   2021-11-26 [1] CRAN (R 4.3.0)
## mime          0.12    2021-09-28 [1] CRAN (R 4.3.0)
## miniUI        0.1.1.1  2018-05-18 [1] CRAN (R 4.3.0)
## munsell       0.5.0   2018-06-12 [1] CRAN (R 4.3.0)
## nnet          7.3-19   2023-05-03 [1] CRAN (R 4.3.0)
## pillar         1.9.0   2023-03-22 [1] CRAN (R 4.3.0)
## pkgbuild      1.4.2   2023-06-26 [1] CRAN (R 4.3.0)
## pkgconfig     2.0.3   2019-09-22 [1] CRAN (R 4.3.0)
## pkgload       1.3.2.1  2023-07-08 [1] CRAN (R 4.3.0)
## plotly        * 4.10.2  2023-06-03 [1] CRAN (R 4.3.0)
## prettyunits   1.1.1   2020-01-24 [1] CRAN (R 4.3.0)
## processx      3.8.2   2023-06-30 [1] CRAN (R 4.3.0)
## profvis       0.3.8   2023-05-02 [1] CRAN (R 4.3.0)
## progress      1.2.2   2019-05-16 [1] CRAN (R 4.3.0)
## promises      1.2.0.1  2021-02-11 [1] CRAN (R 4.3.0)
## ps             1.7.5   2023-04-18 [1] CRAN (R 4.3.0)
## purrr        * 1.0.1   2023-01-10 [1] CRAN (R 4.3.0)
## R.matlab      * 3.7.0   2022-08-25 [1] CRAN (R 4.3.0)
## R.methodsS3   1.8.2   2022-06-13 [1] CRAN (R 4.3.0)
## R.oo          1.25.0   2022-06-12 [1] CRAN (R 4.3.0)
## R.utils       2.12.2   2022-11-11 [1] CRAN (R 4.3.0)
## R6             2.5.1   2021-08-19 [1] CRAN (R 4.3.0)
## Rcpp          1.0.11   2023-07-06 [1] CRAN (R 4.3.0)

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##  readr      * 2.1.4   2023-02-10 [1] CRAN (R 4.3.0)
##  readxl     * 1.4.3   2023-07-06 [1] CRAN (R 4.3.0)
##  remotes    2.4.2   2021-11-30 [1] CRAN (R 4.3.0)
##  rlang       1.1.1   2023-04-28 [1] CRAN (R 4.3.0)
##  rmarkdown   2.23    2023-07-01 [1] CRAN (R 4.3.0)
##  rpart      4.1.19   2022-10-21 [1] CRAN (R 4.3.0)
##  rstudioapi 0.15.0   2023-07-07 [1] CRAN (R 4.3.0)
##  scales      1.2.1   2022-08-20 [1] CRAN (R 4.3.0)
##  sessioninfo 1.2.2   2021-12-06 [1] CRAN (R 4.3.0)
##  shiny       1.7.4.1  2023-07-06 [1] CRAN (R 4.3.0)
##  stringi     1.7.12   2023-01-11 [1] CRAN (R 4.3.0)
##  stringr     * 1.5.0   2022-12-02 [1] CRAN (R 4.3.0)
##  tibble      * 3.2.1   2023-03-20 [1] CRAN (R 4.3.0)
##  tidyverse    * 2.0.0   2023-01-24 [1] CRAN (R 4.3.0)
##  tidyselect   1.2.0   2022-10-10 [1] CRAN (R 4.3.0)
##  tidyverse    * 2.0.0   2023-02-22 [1] CRAN (R 4.3.0)
##  timechange   0.2.0   2023-01-11 [1] CRAN (R 4.3.0)
##  tweenr      2.0.2   2022-09-06 [1] CRAN (R 4.3.0)
##  tzdb        0.4.0   2023-05-12 [1] CRAN (R 4.3.0)
##  urlchecker  1.0.1   2021-11-30 [1] CRAN (R 4.3.0)
##  usethis     2.2.2   2023-07-06 [1] CRAN (R 4.3.0)
##  utf8         1.2.3   2023-01-31 [1] CRAN (R 4.3.0)
##  vctrs        0.6.3   2023-06-14 [1] CRAN (R 4.3.0)
##  viridisLite 0.4.2   2023-05-02 [1] CRAN (R 4.3.0)
##  vroom        1.6.3   2023-04-28 [1] CRAN (R 4.3.0)
##  withr       2.5.0   2022-03-03 [1] CRAN (R 4.3.0)
##  xfun         0.39    2023-04-20 [1] CRAN (R 4.3.0)
##  xtable      1.8-4   2019-04-21 [1] CRAN (R 4.3.0)
##  yaml        2.3.7   2023-01-23 [1] CRAN (R 4.3.0)
##
## [1] /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library
##
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