

How to enter the tidyverse of madness

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What's wrong with R?

R is old (circa 1993).

It was originally designed for doing **statistics** with relatively small, simple datasets.

Since then, it has become one of the most popular tools for the new discipline called **data science**.

"Data science is an interdisciplinary field that uses scientific methods, processes, algorithms and systems to extract knowledge and insights from noisy, structured and unstructured data, and apply knowledge and actionable insights from data across a broad range of application domains." https://en.wikipedia.org/wiki/Data_science

Shortcomings of R for data science

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2. Often surprising

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2. Often **surprising**
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5. Functional language can be **awkward** to use

1. Lacks consistency

function naming

```
names, colnames  
row.names, rownames  
rowSums, rowsum  
rowMeans, (no parallel rowmean exists)  
browseURL, contrib.url, fixup.package.URLs  
package.contents, packageStatus  
getMethod, getS3method  
read.csv and write.csv, load and save, readRDS and  
Sys.time, system.time
```

[\[https://r4stats.com/articles/why-r-is-hard-to-learn/\]](https://r4stats.com/articles/why-r-is-hard-to-learn/)

multiple ways to do things

e.g. two different object-oriented systems: S3 and
S4 systems

missing values

```
> x <- c(1, 2, 3, 4, NA)  
> y <- c(1.1, 2.2, 3.3, 4.4, 5.5)  
## missing values not okay  
> quantile(x)  
Error in quantile.default(x) :  
  missing values not allowed if 'na.rm' is FALSE  
## missing values okay  
> fit <- lm(y ~ x)  
> length(x)  
[1] 5  
> length(residuals(fit))  
[1] 4
```

2. Often surprising

R often converts between data types behind the scenes, e.g. characters to factors, matrices to vectors, numeric to characters

```
> x <- matrix(1:12, ncol=3)
> x
[,1] [,2] [,3]
[1,]    1    5    9
[2,]    2    6   10
[3,]    3    7   11
[4,]    4    8   12
```

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[3,] [3,] [3,]
[4,] [4,] [4,]
```

```
> class(x[,1:2])
[1] "matrix" "array"
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[3,] [3,] [3,]
[4,] [4,] [4,]
```

```
> class(x[,1:2])
[1] "matrix" "array"
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```
> class(x[,3]) ## what is this?
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[4,] [4,] [4,]
```

```
> class(x[,1:2])
[1] "matrix" "array"
```

```
> class(x[,3]) ## what is this?
```

```
[1] "integer"
```

```
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> x
[1,] [1,] [,2] [,3]
[1,] 1   5   9
[2,] 2   6   10
[3,] 3   7   11
[4,] 4   8   12
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[3,] [3] [3] [3]
[4,] [4] [4] [4]
```

```
> x[1,1]
1
```

```
> x <- matrix(1:12, ncol=3)
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[1,] [1,] [,2] [,3]
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> x[1,3] <- "a"
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> x[1,1] + 1 ## what is this equal to?
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Error in x[1, 1] + 1 : non-numeric argument to binary operator
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```
> class(x[1, 1])
[1] "character"
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```
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3. Tends to be slow and memory-intensive

R was designed for small datasets, so it tends to do things

- the *simple* way
rather than
 - the *efficient* way.

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• the *efficient* way.

e.g. it is designed to **slurp** data

Slurping means loading entire datasets into memory before analysing them.

This is not efficient when the analysis really only needs to see a table row-by-row.

But, this is simpler to just load (slurp) the entire dataset in one simple step.

4. Built around **vectors** and **matrices**

... whereas data science analyses **data frames** like this:

participant	age	sex	arm
1	23.58224	F	arm3
2	24.69102	M	arm4
3	25.42567	F	arm2
4	24.96019	F	arm2
5	23.35406	M	arm4

Each column has its own data type.

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Each column has its own data type.

Although R implements data frames, most functions are designed for vectors and matrices.

5. Functional language that can be **awkward** to use

e.g. even if you know what all the functions do, this expression is difficult to understand!

```
summarize(group_by(left_join(filter(visits, wave=="wave2"),  
participants, by="participant"), arr, sex), n=n(),  
age=mean(age), bmi=mean(bmi), blink=mean(blink))
```

tidyverse

Tidyverse is a collection of R packages that aim to make the analysis of large datasets more convenient.

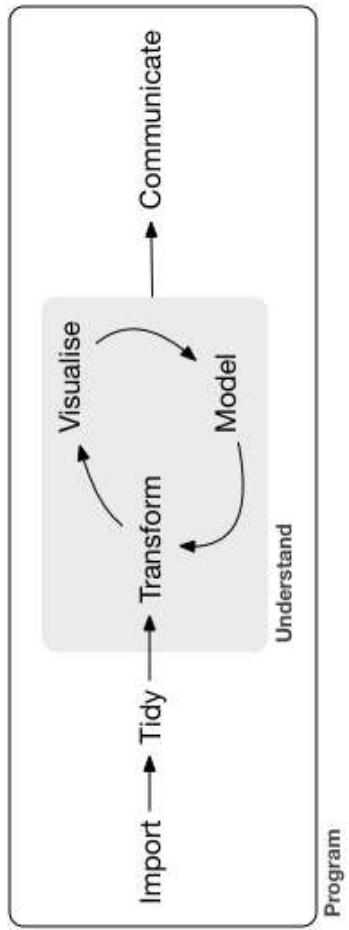


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Here is intended workflow in the tidyverse:



- Data is **imported** and made **tidy** so it can be analysed
- Analysis involves **transforming** the data
- Relationships in the data are **visualised**
- **Models** are applied to test relationships
- Finally, conclusions are **communicated**

tidyverse book

<https://r4ds.had.co.nz/>

R for Data Science

Search

Welcome

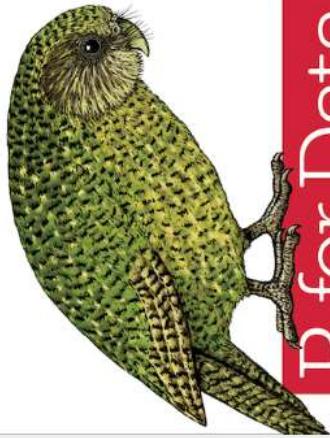
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This is the website for “**R for Data Science**”. This book will teach you how to do data science with R: You’ll learn how to get your data into R, get it into the most useful structure, transform it, visualise it and model it. In this book, you will find a practicum of skills for data science. Just as a chemist learns how to clean test tubes and stock a lab, you’ll learn how to clean data and draw plots—and many other things besides. These are the skills that allow data science to happen, and here you will find the best practices for doing each of these things with R. You’ll learn how to use the grammar of graphics, literate programming, and reproducible research to save time. You’ll also learn how to manage

O'REILLY.



R for Data Science

VISUALIZE, MODEL, TRANSFORM, TIDY, AND IMPORT DATA

Hadley Wickham &
Garrett Grolemund

Using tidyverse packages

Installing all tidyverse packages.

```
install.packages("tidyverse")
```

Loading all tidyverse packages.

```
library(tidyverse)
```

Our dataset

In this session, we will explore the tidyverse by performing a basic data analysis of a simulated dataset from a randomized control trial.



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Background (Pretend) studies have shown that blink rate is positively associated with disengaged attention. A drug has been developed that is known to reduce blink rate.

Aim Determine if the drug will reduce attention deficits by reducing blink rate.

Methods

The were 4 arms:

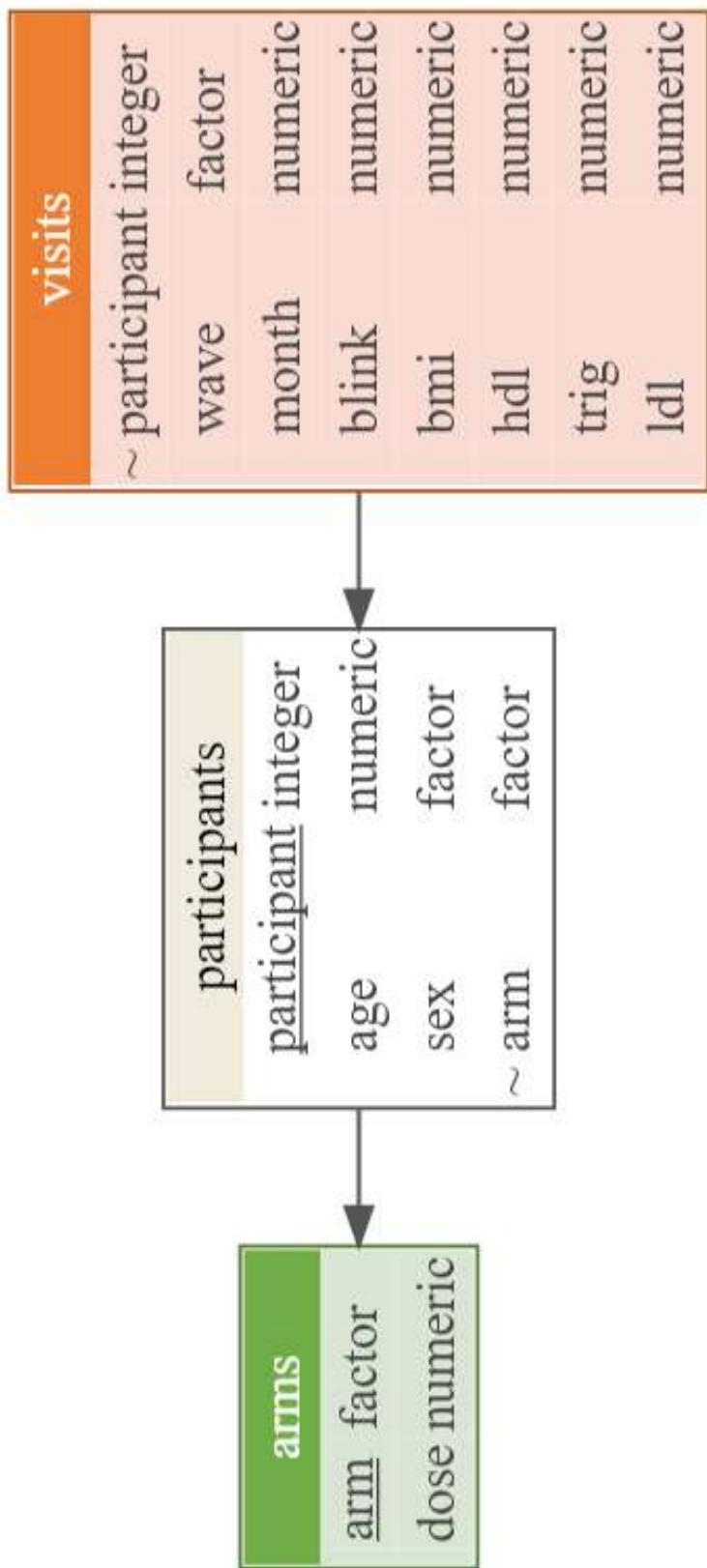
controls (arm 1), low dose (arm 2), medium (arm 3), high (arm 4)

Each arm had 100 randomly selected individuals.

Data was collected in 3 waves:

baseline (wave 0), 6 months (wave 1), 12 months (wave 2)

Dataset schema



Import the dataset

The dataset is available as CSV files.

These can be imported into R using tidyverse function `readr::read_csv()`.

```
data.dir <- "https://raw.githubusercontent.com/perishky/perishky.github.io/master/r/enter-the-tidyverse"  
  
arms <- read_csv(file.path(data.dir, "arms.csv"))  
participants <- read_csv(file.path(data.dir, "participants.csv"))  
visits <- read_csv(file.path(data.dir, "visits.csv"))
```

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visits <- read_csv(file.path(data.dir, "visits.csv"))

> arms <- read_csv("arms.csv")
Rows: 4 Columns: 2
── Column specification ───────────────────────────────────────────────
Delimiter: ","
chr(1): arm
dbl(1): dose

> arms
# A tibble: 4 × 2
   arm    dose
   <chr> <dbl>
 1 arm3     2
 2 arm4     4
 3 arm2     1
 4 arm1     0
```

Why use `read_csv` rather than `read.csv`?

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Tidy format `read_csv` creates tibbles rather than data frames. (we'll discuss tibbles vs data frames on the next slide)

```
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# A tibble: 4 × 2
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Tidy

Tidy data is stored in tables called 'tibbles'.

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Convenience Whereas tibble can create data frames column-by-column, there is a tribble function to create data frames row-by-row.

Pretty printing Tibbles are nicer to look at!

Typing the name of a data frame in R and pressing enter will print the entire data frame to the screen, regardless of its length or width! Tibbles will only show the first few rows and columns along with the dimensions of the data frame and data type of each column.

Creating tibbles

Tibbles can be created by column (just like a data frame)

```
tibble(  
  x=c("a", "b"),  
  y=c(3,1),  
  z=c(pi,2*pi)  
)
```

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)
```

or by row like they'd be written in a data file

```
tribble(  
  ~x, ~y, ~z,  
  #--|---|----  
  "a", 3, pi,  
  "b", 1, 2*pi  
)
```

Answering questions

How many participants are in each study arm?

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We'll use the **participants tibble**.

```
> participants
# A tibble: 400 × 4
  participant age sex   arm
  <dbl>    <dbl> <chr> <chr>
1 1         23.6 F    arm3
2 2         24.7 M    arm4
3 3         25.4 F    arm2
4 4         25.0 F    arm2
5 5         23.4 M    arm4
6 6         25.9 M    arm2
7 7         26.5 M    arm4
8 8         26.6 F    arm1
9 9         25.3 F    arm2
10 10        25.3 F   arm3
# ... with 390 more rows
```

Answering questions

How many participants are in each study arm?

We'll use the **participants tibble**.

We'll use the **count()** function to count participants in each arm.

```
> participants
# A tibble: 400 × 4
  participant    age   sex   arm
  <dbl>     <dbl> <chr> <chr>
1 1         23.6 F      arm3
2 2         24.7 M      arm4
3 3         25.4 F      arm2
4 4         25.0 F      arm2
5 5         23.4 M      arm4
6 6         25.9 M      arm2
7 7         26.5 M      arm4
8 8         26.6 F      arm1
9 9         25.3 F      arm2
10 10        25.3 F      arm3
# ... with 390 more rows
```

```
> count(participants, arm)
# A tibble: 4 × 2
  arm   n
  <chr> <int>
1 arm1 100
2 arm2 100
3 arm3 100
4 arm4 100
```

count() is very similar to the **table()** function in base R.

Challenge!

See if you can count the number of female participants in each arm.

Challenge!

See if you can count the number of female participants in each arm.

```
> count(participants, arm, sex)
# A tibble: 8 × 3
  arm   sex     n
  <chr> <chr> <int>
1 arm1  F      48
2 arm1  M      52
3 arm2  F      43
4 arm2  M      57
5 arm3  F      50
6 arm3  M      50
7 arm4  F      46
8 arm4  M      54
```

Filtering

That last output gives more information than we wanted. To focus on just females, we'll need to filter out information about males.

To do this, we use the `filter()` function.

```
> counts <- count(participants, arm, sex)
> filter(counts, sex == "F")
# A tibble: 4 × 3
  arm   sex     n
<chr> <chr> <int>
 1 arm1  F      48
 2 arm2  F      43
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 4 arm4  F      46
```

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See if you can obtain the same result by

1. first applying the filter function to participants to remove males
2. and then applying the count function to the result.

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1. first applying the filter function to participants to remove males
2. and then applying the count function to the result.

```
> females <- filter(participants, sex=="F")
> count(females, arm, sex)
# A tibble: 4 × 3
  arm   sex     n
<chr> <chr> <int>
1 arm1  F      48
2 arm2  F      43
3 arm3  F      50
4 arm4  F      46
```

Intermediate variables

For longer queries, it can get a little tedious creating variable names for each step.

In the queries above, we had to create counts and females even though we aren't directly interested in those variables, e.g.

```
counts <- count(participants, arm, sex)
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One solution is called **function composition**.

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filter(count(participants, arm, sex), sex=="F")
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```
count(filter(participants, sex=="F"), arm, sex)
```

Function composition gets extreme

Although function composition avoids having to name intermediate variables, they can make the code difficult to read.

For example, the following command summarizes information about each study arm (we'll discuss the functions used here later).

```
summarize(group_by(left_join(filter(visits, wave=="wave2"),  
participants, by="participant"), arm, sex), n=n(), age=mean(age),  
bmi=mean(bmi), blink=mean(blink))
```

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```

To be fair, we can split it across lines to make it a little easier to read.

```
summarize(
  group_by(
    left_join(
      filter(visits, wave=="wave2"),
      participants,
      by="participant"),
    arm,
    sex),
  n=n(),
  age=mean(age),
  bmi=mean(bmi),
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```

Pipes

The "pipe" operator (%>%) was invented to solve this problem.

This command ...

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filter(count(participants, arm, sex), sex=="F")
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... can be written like this

```
participants %>% filter(sex=="F") %>% count(arm, sex)
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The "pipe" operator (%>%) was invented to solve this problem.

This command ...

```
filter(count(participants, arm, sex), sex=="F")
```

... can be written like this

```
participants %>% filter(sex=="F") %>% count(arm, sex)
```

... or even better, split across multiple lines

```
participants %>%
  filter(sex=="F") %>%
  count(arm, sex)
```

i.e.

- we 'pipe' participants to filter,
- and then the output of filter to count

Challenge!

See if you can rewrite the following using pipes:

```
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```
participants %>%
  count(arm, sex) %>%
  filter(sex=="F")
```

Challenge!

Now see if you can rewrite this command using pipes:

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summarize(  
  group_by(  
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    left_join(  
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      by="participant"),  
    arm,  
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  bmi=mean(bmi),  
  blink=mean(blink))
```

```
visits %>%  
  filter(wave=="wave2") %>%  
  left_join(participants, by="participant") %>%  
  group_by(arm, sex) %>%  
  summarize(n=n(), age=mean(age), bmi=mean(bmi), blink=mean(blink))
```

Calculating data summaries

The `summarise(<tibble>, <summary1>, <summary2>, ...)` summarizes the columns of a tibble.

For example, we can use it to calculate

1. the average participant age, and
2. how many of them are females.

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1. the average participant age, and
2. how many of them are females.

```
> summarise(participants, age=median(age), nfemales=sum(sex=="F"))
# A tibble: 1 × 2
  age nfemales
  <dbl>    <int>
1  25.0      187
```

Calculating data summaries

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> summarise(participants, age=median(age), nemales=sum(sex=="F"))
# A tibble: 1 × 2
  age nemales
  <dbl>    <int>
1 25.0      187
```

Here is what it looks like using pipes.

```
participants %>%
  summarise(age=median(age), nemales=sum(sex=="F"))
```

Calculating summaries of subsets

The previous example above provided summaries across *all*/rows.

It is also possible to summarize subsets of rows using `group_by(<tibble>, <groupby1>, <groupby2>, ...)`.

For example, we can calculate, *for each arm of the study*

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For example, we can calculate, *for each arm of the study*

1. the average participant age, and
2. the number of males and females.

```
> participants %>%
  group_by(arm, sex) %>%
  summarise(n=n(), age=mean(age))

# A tibble: 8 × 4
# Groups:   arm [4]
  arm   sex     n    age
<chr> <chr> <int> <dbl>
  1 arm1  F      48  25.1
  2 arm1  M      52  25.1
  3 arm2  F      43  25.1
  4 arm2  M      57  24.8
  5 arm3  F      50  25.1
  6 arm3  M      50  24.8
  7 arm4  F      46  24.9
  8 arm4  M      54  25.1
```

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  summarise(n=n(), age=mean(age))

# A tibble: 8 × 4
# Groups:   arm [4]
  arm   sex     n    age
  <chr> <chr> <int> <dbl>
1 arm1  F      48  25.1
2 arm1  M      52  25.1
3 arm2  F      43  25.1
4 arm2  M      57  24.8
5 arm3  F      50  25.1
6 arm3  M      50  24.8
7 arm4  F      46  24.9
8 arm4  M      54  25.1
```

Did you notice some **magic**?

1. `summarise()` magically knows when a tibble has come from `group_by()` and that it should summarize by the resulting groups.
2. `n()` function magically knows about the tibble subsets being processed by `summarise`.

Challenge!

Can you think of an alternative to the mysterious n() function? (*this is a tricky question*)

```
participants %>%
  group_by(arm, sex) %>%
  summarise(n=n(), age=mean(age))
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```
participants %>%
  group_by(arm, sex) %>%
  summarise(n=n(), age=mean(age))
```

Hint: Use the length function ...

```
participants %>%
  group_by(arm, sex) %>%
  summarise(n=length(age), age=mean(age))
```

Merging datasets

We'd like to augment the summary with measurements from the first visit.

This information is in the visits dataset.

To do this, we'll first need to:

1. filter visits to get just the first visit (there were 3 visits)
2. merge the result with participants
3. group the result by arm and by sex
4. calculate the mean of age, BMI and blink rate

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We've seen how to do each of these steps except step 2, merging.

```
visits %>%
  filter(wave=="wave0") %>%
  ??????? merge with participants ?????????? %>%
  group_by(arm,sex) %>%
  summarise(n=n(), age=mean(age), bmi=mean(bmi), blink=mean(blink))
```

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  ??????? merge with participants ?????????? %>%
  group_by(arm,sex) %>%
  summarise(n=n(), age=mean(age), bmi=mean(bmi), blink=mean(blink))
```

In base R, we'd use the function `merge()`.

For tibbles, we have four different functions: `left_join()`, `right_join()`, `inner_join()` and `full_join()`.

left_join()

To illustrate, we'll use a small version of visits.

```
> visits.s <- visits %>% filter(participant %in% 1  
> visits.s  
# A tibble: 9 × 8  
  participant wave month blink bmi   hdl   trig   ldl  
  <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
1 1         wave0 0     17.6 15.4 1.38 1.52 2.11  
2 1         wave1 6.18 16.0 16.5 1.35 1.33 1.88  
3 1         wave2 10.4 15.6 14.9 1.39 1.39 2.01  
4 2         wave0 0     16.3 19.4 1.64 1.70 4.06  
5 2         wave1 5.50 14.5 20.6 1.61 1.31 3.90  
6 2         wave2 13.0 11.2 21.8 1.57 1.62 4.04  
7 3         wave0 0     18.6 22.0 1.61 1.12 2.11  
8 3         wave1 6.58 17.8 20.8 1.75 1.14 1.82  
9 3         wave2 13.5 17.3 23.1 1.53 1.11 2.21
```

left_join()

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Recall participants.

```
> visits.s <- visits %>% filter(participant %in% 1  
> visits.s  
# A tibble: 9 × 8  
  participant wave month blink bmi hdl trig ldl  
  <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
1 1 wave0 0 17.6 15.4 1.38 1.52 2.11  
2 1 wave1 6.18 16.0 16.5 1.35 1.33 1.88  
3 1 wave2 10.4 15.6 14.9 1.39 1.39 2.01  
4 2 wave0 0 16.3 19.4 1.64 1.70 4.06  
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6 2 wave2 13.0 11.2 21.8 1.57 1.62 4.04  
7 3 wave0 0 18.6 22.0 1.61 1.12 2.11  
8 3 wave1 6.58 17.8 20.8 1.75 1.14 1.82  
9 3 wave2 13.5 17.3 23.1 1.53 1.11 2.21
```



```
> participants  
# A tibble: 400 × 4  
  participant age sex arm  
  <dbl> <dbl> <chr> <chr>  
1 1 23.6 F arm3  
2 2 24.7 M arm4  
3 3 25.4 F arm2  
4 4 25.0 F arm2  
5 5 23.4 M arm4  
# ... with 390 more rows
```

... with 390 more rows



left_join()

`left_join()` adds data from participants that match the three participants in `visits.s.`

```
> left_join(visits.s, participants, by="participant")
Joining, by = "participant"
# A tibble: 9 × 11
  participant wave month blink bmi <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> age sex arm
    <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
  1 wave0 0 17.6 15.4 1.38 1.52 2.11 23.6 F
  2 wave1 6.18 16.0 16.5 1.35 1.33 1.88 23.6 F
  3 wave2 10.4 15.6 14.9 1.39 1.39 2.01 23.6 F
  4 wave0 0 16.3 19.4 1.64 1.70 4.06 24.7 M
  5 wave1 5.50 14.5 20.6 1.61 1.31 3.90 24.7 M
  6 wave2 13.0 11.2 21.8 1.57 1.62 4.04 24.7 M
  7 wave0 0 18.6 22.0 1.61 1.12 2.11 25.4 F
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  9 wave2 13.5 17.3 23.1 1.53 1.11 2.21 25.4 F
```

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```
> left_join(visits.s, participants, by="participant")
Joining, by = "participant"
# A tibble: 9 × 11
  participant wave month blink bmi hdl trig ldl age sex arm
  <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
1 1          wave0 0     17.6 15.4 1.38 1.52 2.11 23.6 F
2 1          wave1 6.18 16.0 16.5 1.35 1.33 1.88 23.6 F
3 1          wave2 10.4 15.6 14.9 1.39 1.39 2.01 23.6 F
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6 2          wave2 13.0 11.2 21.8 1.57 1.62 4.04 24.7 M
7 3          wave0 0     18.6 22.0 1.61 1.12 2.11 25.4 F
8 3          wave1 6.58 17.8 20.8 1.75 1.14 1.82 25.4 F
9 3          wave2 13.5 17.3 23.1 1.53 1.11 2.21 25.4 F
```

Notice how the result is just `visits.s` but with some additional columns from participants.

Rows in participants that do not match are omitted.

Challenge!

What do you think happens if some participants in visits do not match a participant in participants?

```
> parts.s <- participants %>% filter(participant %in% 1:2)
> parts.s
# A tibble: 2 × 4
  participant age sex   arm
  <dbl>     <dbl> <chr> <chr>
1 1         23.6 F    arm3
2 2         24.7 M    arm4
```

Challenge!

What do you think happens if some participants in visits do not match a participant in participants?

```
> parts.s <- participants %>% filter(participant %in% 1:2)  
> parts.s  
# A tibble: 2 × 4  
  participant age sex arm  
  <dbl> <dbl> <chr> <chr>  
1 1 23.6 F arm3  
2 2 24.7 M arm4
```

```
> left_join(visits.s, parts.s, by="participant")  
# A tibble: 9 × 11  
  participant wave month blink bmi <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> age sex arm  
<dbl> <chr> <dbl>  
1 wave0 0 17.6 15.4 1.38 1.52 2.11 23.6 F arm3  
2 wave1 6.18 16.0 16.5 1.35 1.33 1.88 23.6 F arm3  
3 wave2 10.4 15.6 14.9 1.39 1.39 2.01 23.6 F arm3  
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7 wave0 0 18.6 22.0 1.61 1.12 2.11 NA NA  
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9 wave2 13.5 17.3 23.1 1.53 1.11 2.21 NA NA
```

Putting it altogether

Recall that we want to summarize information from all participants, grouped by age and sex.

```
visits %>%
  filter(wave=="wave0") %>%
  left_join(participants,by="participant") %>% ## merging step
  group_by(arm,sex) %>%
  summarise(n=n(), age=mean(age), bmi=mean(bmi), blink=mean(blink))
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Putting it altogether

Recall that we want to summarize information from all participants, grouped by age and sex.

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visits %>%
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```

```
# A tibble: 8 × 6
# Groups:   arm [4]
  arm   sex     n    age    bmi  blink
  <chr> <chr> <int> <dbl> <dbl> <dbl>
  1 arm1  F      48   25.1  21.4  17.7
  2 arm1  M      52   25.1  23.9  17.5
  3 arm2  F      43   25.1  21.3  17.6
  4 arm2  M      57   24.8  23.4  17.5
  5 arm3  F      50   25.1  21.0  17.7
  6 arm3  M      50   24.8  23.8  17.6
  7 arm4  F      46   24.9  21.4  17.2
  8 arm4  M      54   25.1  22.9  17.6
```

Challenge!

The previous output wasn't interesting because we're looking at the data before any treatment.

Modify the command to see the same data from the final visit.

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```
visits %>%
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  group_by(arm, sex) %>%
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```

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```

```
# A tibble: 8 × 6
# Groups:   arm [4]
  arm  sex    n    age    bmi  blink
<chr> <chr> <int> <dbl> <dbl> <dbl>
  1 arm1 F     48   25.1  21.6  17.7
  2 arm1 M     52   25.1  24.0  17.5
  3 arm2 F     43   25.1  21.6  16.5
  4 arm2 M     57   24.8  24.0  16.3
  5 arm3 F     50   25.1  22.1  15.3
  6 arm3 M     50   24.8  25.1  15.2
  7 arm4 F     46   24.9  23.7  12.6
  8 arm4 M     54   25.1  25.2  13.0
```

Can you see differences between the study arms now?

Merging multiple tables

To remember the treatment within each study arm, we'll add 'dose' to the output found in the arms tibble.

Merging multiple tables

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```
query <- visits %>%
  filter(wave=="wave2") %>%
  left_join(participants,by="participant") %>%
  left_join(arms,by="arm") %>%
  group_by(arm,sex) %>%
  summarise(dose=dose[1],n=n(), age=mean(age), bmi=mean(bmi), blink=mean(blink))
```

Merging multiple tables

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query <- visits %>%
  filter(wave=="wave2") %>%
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  left_join(arms,by="arm") %>%
  group_by(arm,sex) %>%
  summarise(dose=dose[1],n=n(), age=mean(age), bmi=mean(bmi), blink=mean(blink))
```

```
> query
```

```
# A tibble: 8 × 7
# Groups:   arm [4]
  arm   sex   dose    n   age   bmi   blink
  <chr> <chr> <dbl> <int> <dbl> <dbl> <dbl>
1 arm1  F     0     48   25.1  21.6  17.7
2 arm1  M     0     52   25.1  24.0  17.5
3 arm2  F     1     43   25.1  21.6  16.5
4 arm2  M     1     57   24.8  24.0  16.3
5 arm3  F     2     50   25.1  22.1  15.3
6 arm3  M     2     50   24.8  25.1  15.2
7 arm4  F     4     46   24.9  23.7  12.6
8 arm4  M     4     54   25.1  25.2  13.0
```

Selecting columns

Having both 'arm' and 'dose' columns is a bit redundant, we just want to show 'dose'.

For this, we can use the `select()` function.

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For this, we can use the `select()` function.

```
> query %>%
  ungroup() %>%
  select(dose, sex, n, age, bmi, blink)
```

#	A tibble: 8 × 6	dose	sex	n	age	bmi	blink
1	0	F	48	25.1	21.6	17.7	
2	0	M	52	25.1	24.0	17.5	
3	1	F	43	25.1	21.6	16.5	
4	1	M	57	24.8	24.0	16.3	
5	2	F	50	25.1	22.1	15.3	
6	2	M	50	24.8	25.1	15.2	
7	4	F	46	24.9	23.7	12.6	
8	4	M	54	25.1	25.2	13.0	

The `ungroup` command is necessary to turn 'off' grouping.

Omitting columns

It's a bit tedious to type all the column names when we just want to remove one. There is a way to do this.

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select(-arm)
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```
query <- query %>%
  ungroup() %>%
  select(-arm)
```

```
> query
# A tibble: 8 × 6
  sex   dose    n    age   bmi  blink
  <chr> <dbl> <int> <dbl> <dbl> <dbl>
1 F     0     48  25.1  21.6  17.7
2 M     0     52  25.1  24.0  17.5
3 F     1     43  25.1  21.6  16.5
4 M     1     57  24.8  24.0  16.3
5 F     2     50  25.1  22.1  15.3
6 M     2     50  24.8  25.1  15.2
7 F     4     46  24.9  23.7  12.6
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```

Reordering rows

With male rows next to female rows, it is difficult to see if there were any treatment effects on BMI.

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We'll reorder/arrange the rows by sex and then by dose.

Before reordering ...

```
> query

# A tibble: 8 × 6
  sex   dose    n    age   bmi  blink
  <chr> <dbl> <int> <dbl> <dbl> <dbl>
1 F     0     48   21.6  17.7 
2 M     0     52   25.1  24.0  17.5 
3 F     1     43   25.1  21.6  16.5 
4 M     1     57   24.8  24.0  16.3 
5 F     2     50   25.1  22.1  15.3 
6 M     2     50   24.8  25.1  15.2 
7 F     4     46   24.9  23.7  12.6 
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```
> query

# A tibble: 8 × 6
  sex   dose    n   age   bmi  blink
  <chr> <dbl> <int> <dbl> <dbl>
1 F     0     48  25.1 21.6 17.7
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3 F     1     43  25.1 21.6 16.5
4 M     1     57  24.8 24.0 16.3
5 F     2     50  25.1 22.1 15.3
6 M     2     50  24.8 25.1 15.2
7 F     4     46  24.9 23.7 12.6
8 M     4     54  25.1 25.2 13.0
```

After reordering ...

```
> query %>%
  arrange(sex,dose)

# A tibble: 8 × 6
  sex   dose    n   age   bmi  blink
  <chr> <dbl> <int> <dbl> <dbl> <dbl>
1 F     0     48  25.1 21.6 17.7
2 F     1     43  25.1 21.6 16.5
3 F     2     50  25.1 22.1 15.3
4 F     3     46  24.9 23.7 12.6
5 M     4     46  24.9 23.7 12.6
6 M     5     52  25.1 24.0 17.5
7 M     6     57  24.8 24.0 16.3
8 M     7     50  24.8 25.1 15.2
```

Now we can more easily see that BMI appears to be increasing with dose.

Running statistical tests

We'd like to determine statistically if treatment actually increases BMI.

We can do this by fitting the following linear model:

$$\text{BMI}_{\text{wave } 2} \sim \text{BMI}_{\text{wave } 0} + \text{age} + \text{sex} + \text{dose}$$

Running statistical tests

We'd like to determine statistically if treatment actually increases BMI.

We can do this by fitting the following linear model:

```
BMIwave 2 ~ BMIwave 0 + age + sex + dose
```

For this, we'll need to prepare a tibble like this:

bmi.wave0 bmi.wave2 age sex dose

5.4	14.9	23.5	F	2
19.3	21.8	24.7	M	4
22.0	23.1	25.4	F	1
20.6	19.7	24.9	F	1
26.1	28.6	23.4	M	4

...

Running statistical tests

Here are the steps:

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1. Create a wave 0 subset of 'visits'

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1. Create a wave 0 subset of 'visits'
2. Create a wave 2 subset of 'visits'
3. Merge these two so we have a data frame with bmi at wave 0 and wave 2
4. Merge this with 'participants' and 'arms' to add participant age, sex and dose
5. Fit the linear model and extract the coefficients and p-values

```
## 1. Create a wave 0 subset of 'visits'
```

```
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dat.wave0 <- visits %>% filter(wave=="wave0") %>% select(participant, bmi)
```

```
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dat.wave0 <- visits %>% filter(wave=="wave0") %>% select(participant, bmi)

## 2. Create a wave 2 subset of 'visits'
```

```
## 1. Create a wave 0 subset of 'visits'

dat.wave0 <- visits %>% filter(wave=="wave0") %>% select(participant, bmi)

## 2. Create a wave 2 subset of 'visits'

dat.wave2 <- visits %>% filter(wave=="wave2") %>% select(participant, bmi)
```

```
## 1. Create a wave 0 subset of 'visits'

dat.wave0 <- visits %>% filter(wave=="wave0") %>% select(participant, bmi)

## 2. Create a wave 2 subset of 'visits'

dat.wave2 <- visits %>% filter(wave=="wave2") %>% select(participant, bmi)

## 3. Merge these two so we have a data frame with bmi at wave 0 and wave 2
```

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  left_join(dat.wave2, by="participant", suffix=c(" .wave0" , " .wave2")) %>%
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lm(bmi.wave2 ~ bmi.wave0 + age + sex + dose, data=.) %>%
  summary() %>% coef()

```

Wait, what does that mysterious '.' mean?

```
... %>%  
lm(bmi.wave2 ~ bmi.wave0 + age + sex + dose, data=.) %>%  
...  
...
```

Wait, what does that mysterious '.' mean?

```
... %>%  
lm(bmi.wave2 ~ bmi.wave0 + age + sex + dose, data=. ) %>%  
...
```

The `:` refers to the input coming from the pipe ("%>%") to the `lm` function. We want the incoming data frame/tibble to be passed to `lm` via the data argument.

By default, pipe input is passed as the first argument to the function. Most tidyverse functions are written with this default in mind.

Running statistical tests

```
dat.wave0 <- visits %>% filter(wave=="wave0") %>% select(participant, bmi)
dat.wave2 <- visits %>% filter(wave=="wave2") %>% select(participant, bmi)
dat.wave0 %>%
  left_join(dat.wave2, by="participant", suffix=c(" .wave0" , " .wave2")) %>%
  left_join(participants, by="participant") %>%
  left_join(arms, by="arm") %>%
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```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-2.47273674	1.77929008	-1.3897322	1.653930e-01
bmi.wave0	1.01448861	0.01752561	57.8860586	4.790746e-195
age	0.08544156	0.06725427	1.2704259	2.046808e-01
sexM	0.08955528	0.14346982	0.6242099	5.328501e-01
dose	0.57515357	0.04672540	12.3092276	1.072305e-29

Running statistical tests

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dat.wave0 <- visits %>% filter(wave=="wave0") %>% select(participant, bmi)
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dat.wave0 %>%
  left_join(dat.wave2, by="participant", suffix=c(" .wave0" , " .wave2")) %>%
  left_join(participants, by="participant") %>%
  left_join(arms, by="arm") %>%
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dose	0.57515357	0.04672540	12.3092276	1.072305e-29

Treatment dose is strongly associated with increasing BMI ($p=1.1e-29$).

As expected, BMI is strongly associated across waves ($p = 4.8e-195$).

Beyond that, age and sex have almost no effect ($p > 0.2$).

Data pivots

The data transformation we just applied is called a 'pivot from long to wide'.

Data pivots

The data transformation we just applied is called a 'pivot from long to wide'.

1. Initially, the data is **'long'** with one row per BMI measurement per participant.

```
> visits %>% subset(c("participant", "wave", "bmi"))  
#> #> #> #> #>  
#> #>   participant wave      bmi  
#> #>   1          1  wave0    15.4  
#> #>   2          1  wave1    16.5  
#> #>   3          1  wave2    14.9  
#> #> ...  
#> #>
```

Data pivots

The data transformation we just applied is called a 'pivot from long to wide'.

1. Initially, the data is '**long**' with one row per BMI measurement per participant.

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> visits %>% subset(c("participant", "wave", "bmi"))  
  
  participant wave      bmi  
1           1  wave0    15.4  
2           1  wave1    16.5  
3           1  wave2    14.9  
...  
...
```

2. After the pivot, the data is '**shorter**' with one row per participant, but '**wider**' due to having two columns providing BMI measurements.

```
> dat.wave0 %>%  
  left_join(dat.wave2, by="participant", suffix=c(".wave0", ".wave2"))  
  
  participant bmi.wave0 bmi.wave2  
1           1    15.4    14.9  
2           2    19.4    21.8  
3           3    22.0    23.1
```

Because pivots are so common, `tidyR` has created `pivot_wider()` and its inverse `pivot_longer()`.

Because pivots are so common, tidyverse has created `pivot_wider()` and its inverse `pivot_longer()`.

As before ...

With `pivot_wider` ...

```
## 1. Create a wave 0 subset of 'visits'  
> dat.wave0 <- visits %>%  
  filter(wave=="wave0") %>%  
  select(participant, bmi)  
  
## 2. Create a wave 2 subset of 'visits'  
> dat.wave2 <- visits %>%  
  filter(wave=="wave2") %>%  
  select(participant, bmi)  
  
## 3. Merge these two  
> dat.wave0 %>%  
  left_join(dat.wave2,  
            by="participant",  
            suffix=c(" .wave0", " .wave2")) %>%  
  
## 4. Merge this with 'participants' and 'arms'  
left_join(participants, by="participant") %>%  
left_join(arms, by="arm") %>%  
  
## 5. Fit the linear model  
lm(bmi.wave2~bmi.wave0+age+sex+dose, data=.) %>%  
summary() %>%  
coef()
```

```
## 1-2. Create a wave 0 and 2 subset of 'visits'  
> visits %>%  
  filter(wave %in% c("wave0", "wave2")) %>%  
  
## 3. pivot dataset (and rename columns)  
pivot_wider(  
  id_cols=participant, ## individuals  
  names_from=wave, ## new column names  
  values_from=bmi) %>%  
  ## new column values  
  rename(bmi.wave0=wave0, bmi.wave2=wave2) %>%  
  
## 4. Merge this with 'participants' and 'arms'  
left_join(participants, by="participant") %>%  
left_join(arms, by="arm") %>%  
  
## 5. Fit the linear model  
lm(bmi.wave2~bmi.wave0+age+sex+dose, data=.) %>%  
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Visualizing data with `ggplot2`

We've looked at a lot of tables of statistics.

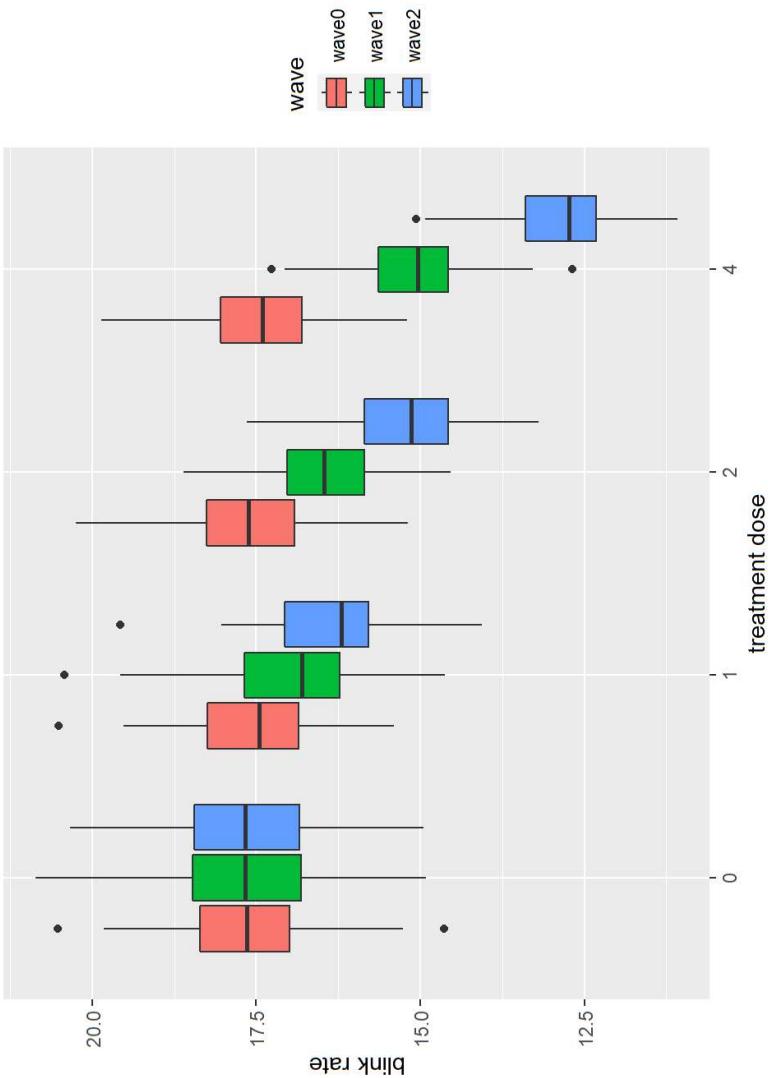
We can visualise these using `ggplot()`.

Visualizing data with ggplot2

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We can visualise blink rate, treatment dose and time as follows:



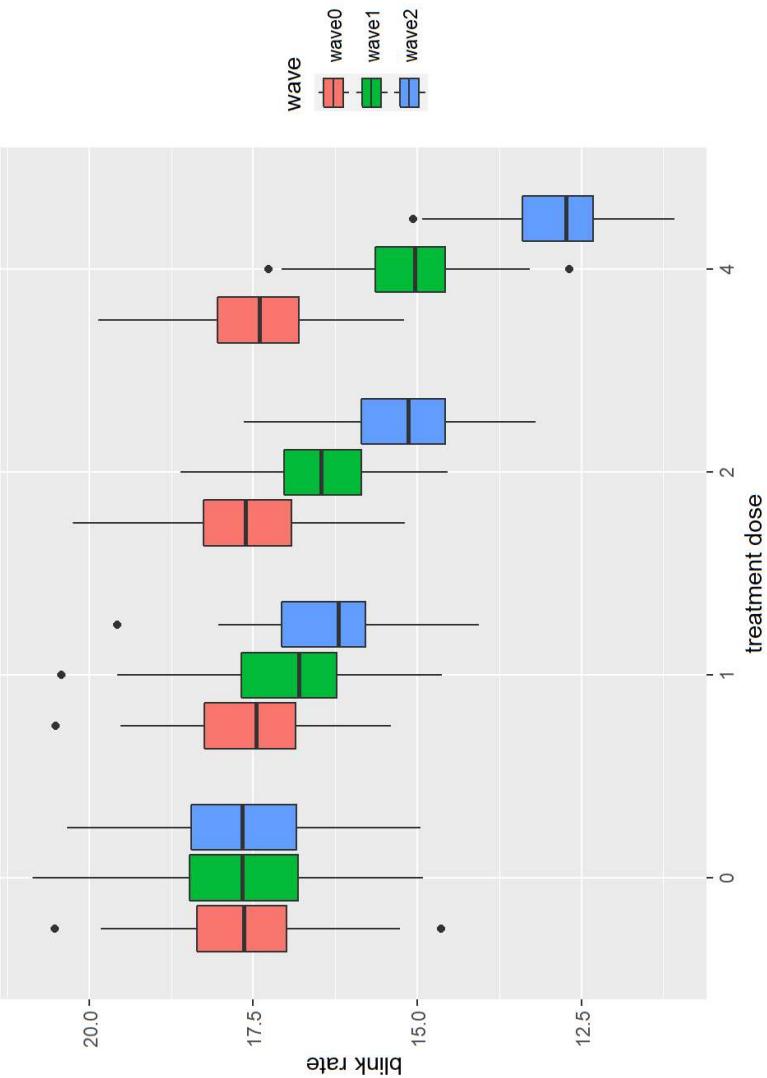
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1. pipe the data to `ggplot()`



Visualizing data with ggplot2

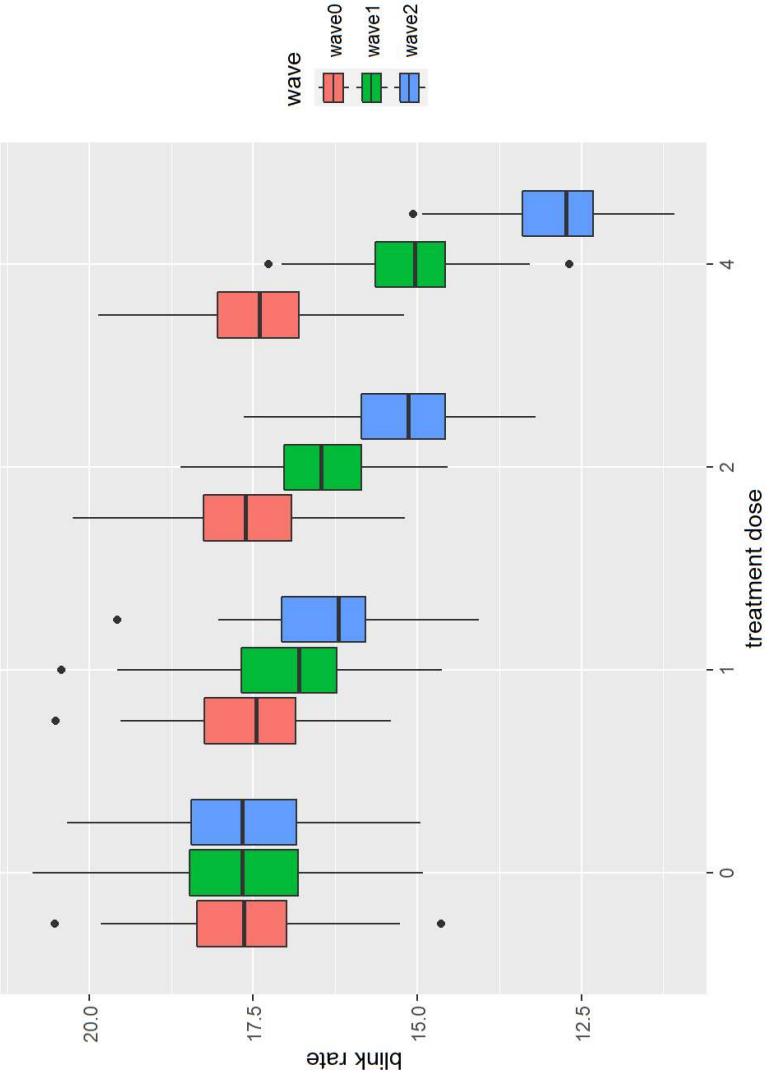
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We can visualise blink rate, treatment dose and time as follows:

1. pipe the data to `ggplot()`

2. tell `ggplot()` to show blink rates (y-axis) by dose (x-axis) and by wave



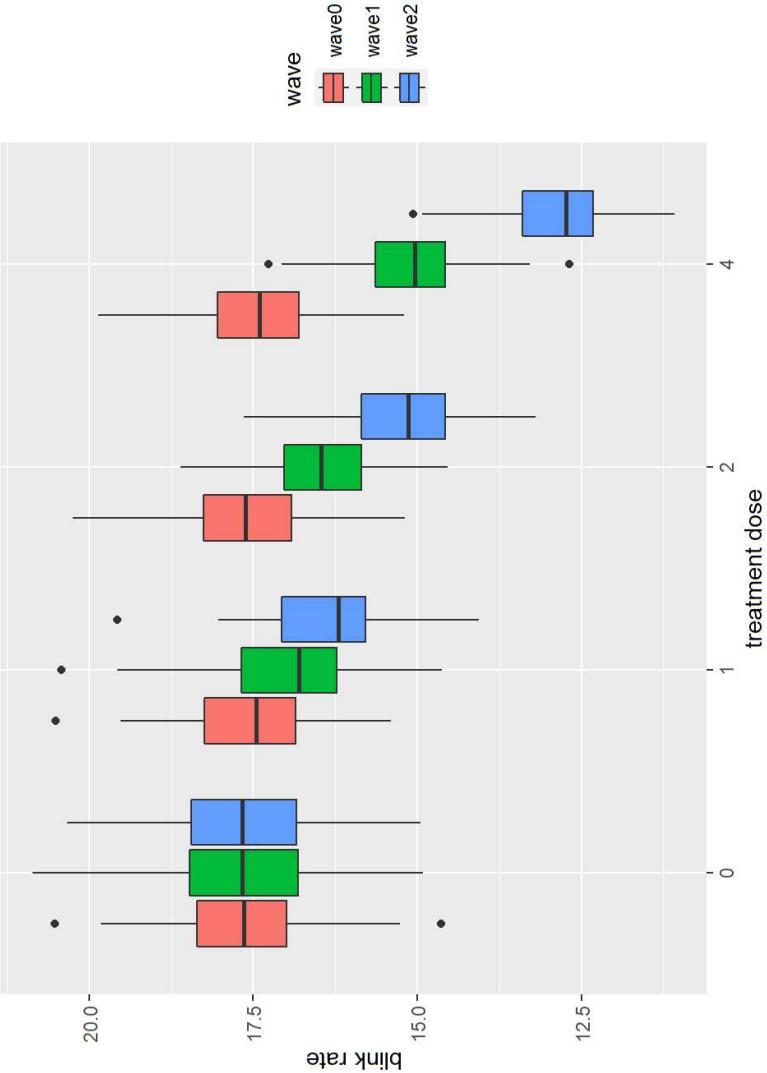
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3. tell `ggplot` that blink rate distributions will be displayed as box plots



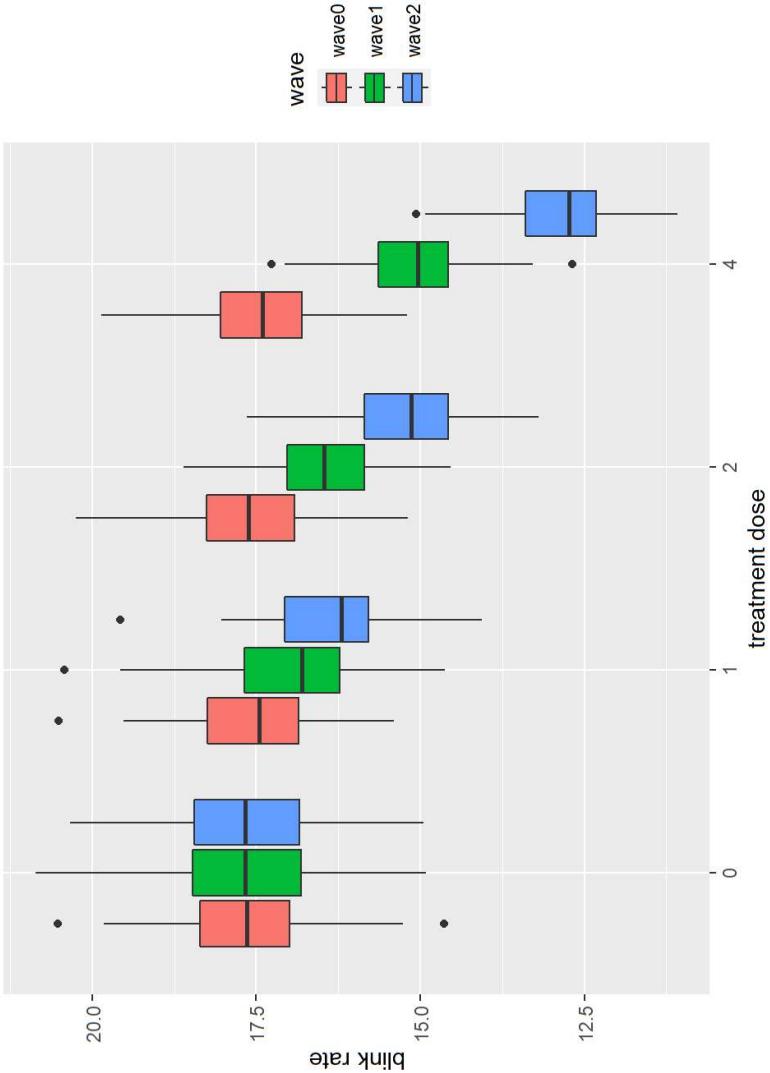
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3. tell `ggplot` that blink rate distributions will be displayed as box plots
4. label the x and y axes appropriately



```

## 1. pipe the data to `ggplot()`
visits %>%
  left_join(participants,by="participant") %>%
  left_join(arms,by="arm") %>%

## 2. tell `ggplot()` to show blink rates (y-axis)
## by dose (x-axis) and by wave
ggplot(aes(x=factor(dose),y=blink,fill=wave)) + 

## 3. tell `ggplot` that blink rate distributions
## will be displayed as box plots
geom_boxplot() + 

## 4. label the x and y axes appropriately
  xlab("treatment dose") +
  ylab("blink rate")

```



(without the comments)

```

visits %>%
  left_join(participants,by="participant") %>%
  left_join(arms,by="arm") %>%
  ggplot(aes(x=factor(dose),y=blink,fill=wave)) + 
  geom_boxplot() + 
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  ylab("blink rate")

```

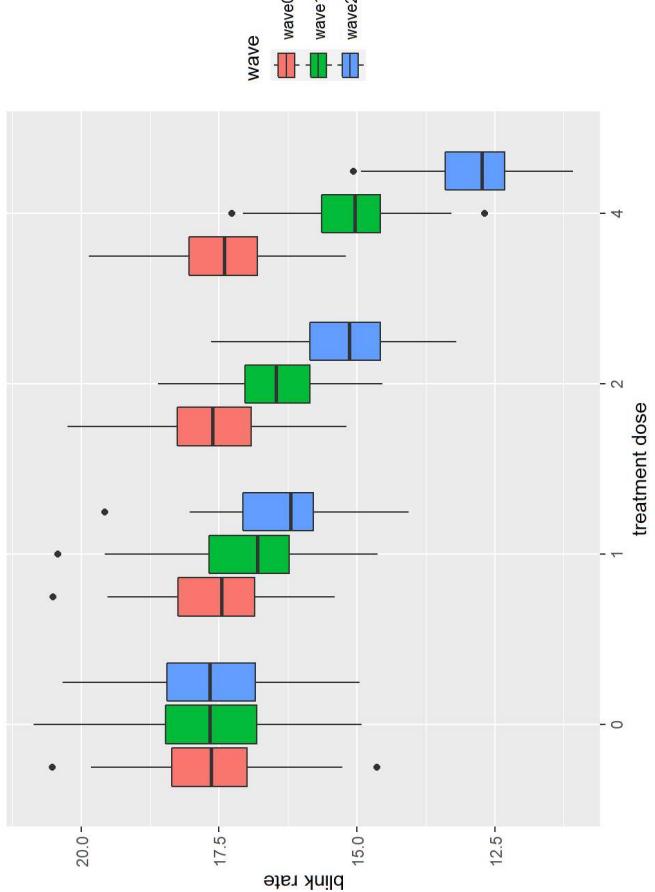
```

## 1. pipe the data to `ggplot()`
visits %>%
  left_join(participants,by="participant") %>%
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## 2. tell `ggplot()` to show blink rates (y-axis)
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```

Talking to ggplot

1. ggplot likes "long" data format. If your data is in "wide" format, use `pivot_longer()`.
2. Notice how the '+' is like '%>%'.
 - o We pipe *data* to functions with '%>%'.
 - o We pipe *instructions* to ggplot with '+'.

And just like pipes, we can refer to the plot with a variable.

```
p <- visits %>%
  left_join(participants, by = "participant") %>%
  left_join(arms, by = "arm") %>%
  ggplot(aes(x = factor(dose), y = blink, fill = wave)) +
  geom_boxplot() +
  xlab("treatment dose") +
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```

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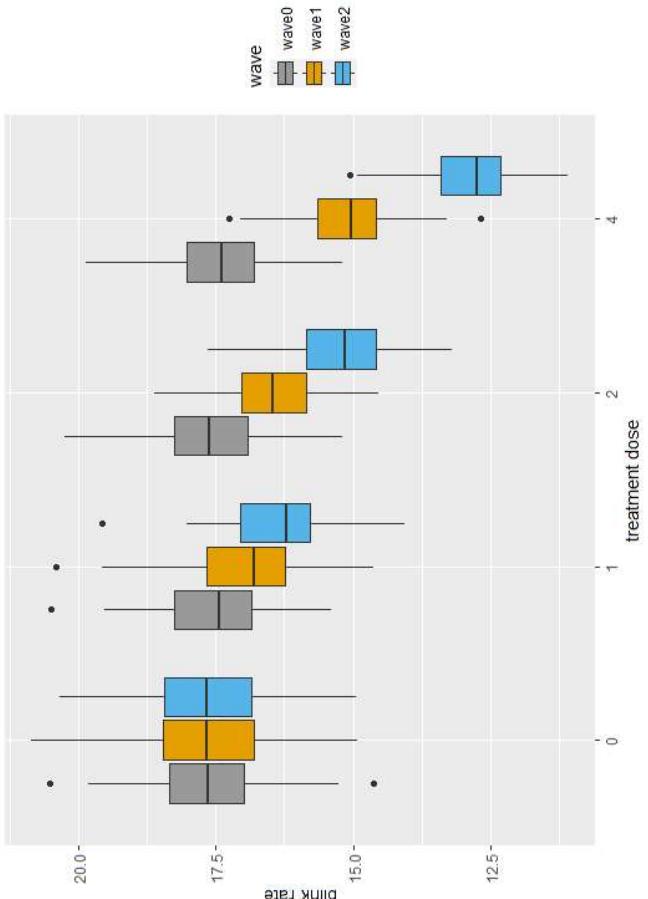
- o We pipe *instructions* to ggplot with '+'.

And just like pipes, we can refer to the plot with a variable.

```
p <- visits %>%
  left_join(participants, by = "participant") %>%
  left_join(arms, by = "arm") %>%
  ggplot(aes(x = factor(dose), y = blink, fill = wave)) +
  geom_boxplot() +
  xlab("treatment dose") +
  ylab("blink rate")
```

Later, we can add additional instructions about the plot, e.g. to change the boxplot colors

```
fill.cols <- c("#999999", "#E69F00", "#56B4E9")
p <- p + scale_fill_manual(values = fill.cols)
p
```



Challenge!

Change the plot to show HDL cholesterol instead of
blink rate.

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```
visits %>%
  left_join(participants, by="participant") %>%
  left_join(arms, by="arm") %>%
  ggplot(aes(x=factor(dose), y=hdl, fill=wave)) +
  geom_boxplot() +
  xlab("treatment dose") +
  ylab("HDL cholesterol")
```

Sorry! Not very exciting.

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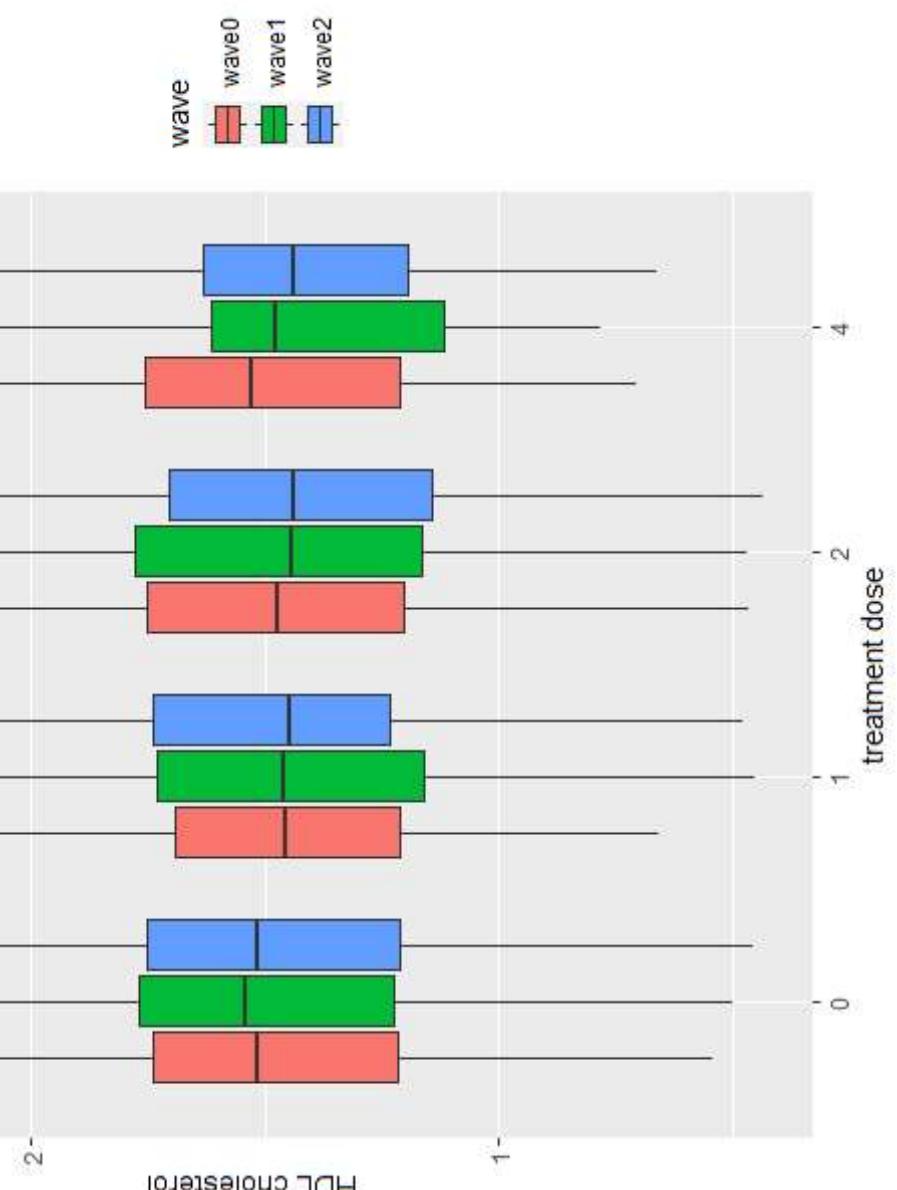
•

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Challenge!

Generate a plot showing HDL cholesterol vs BMI (baseline).

Hint: use `geom_point()`

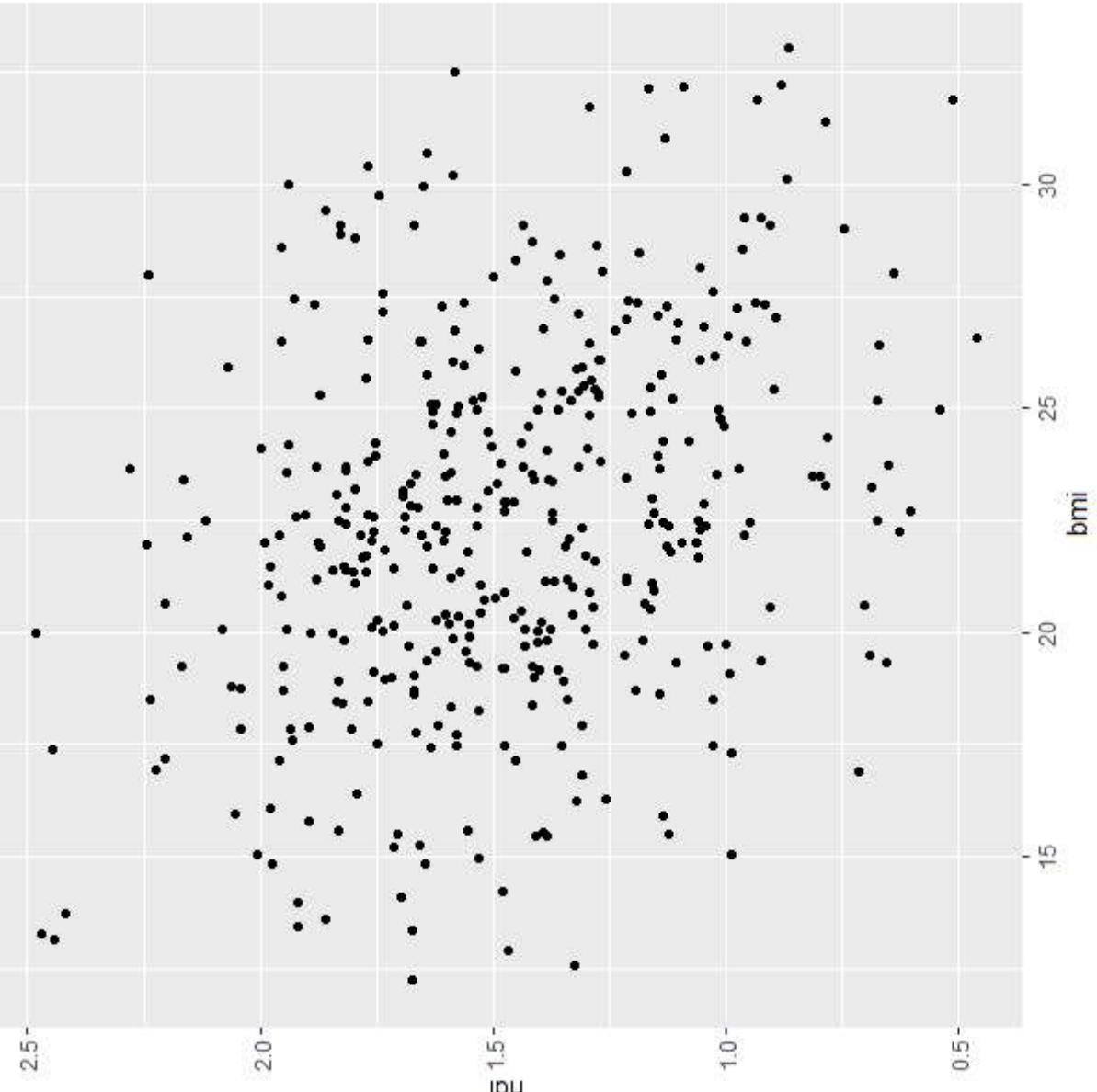
Challenge!

Generate a plot showing HDL cholesterol vs BMI

Hint: use geom_point()

```
p <- visits %>%
  filter(wave=="wave0") %>%
  ggplot(aes(x=bmi, y=hdl)) +
  geom_point()
```

(saving the plot so we make a modification)



Challenge!

Generate a plot showing HDL cholesterol vs B

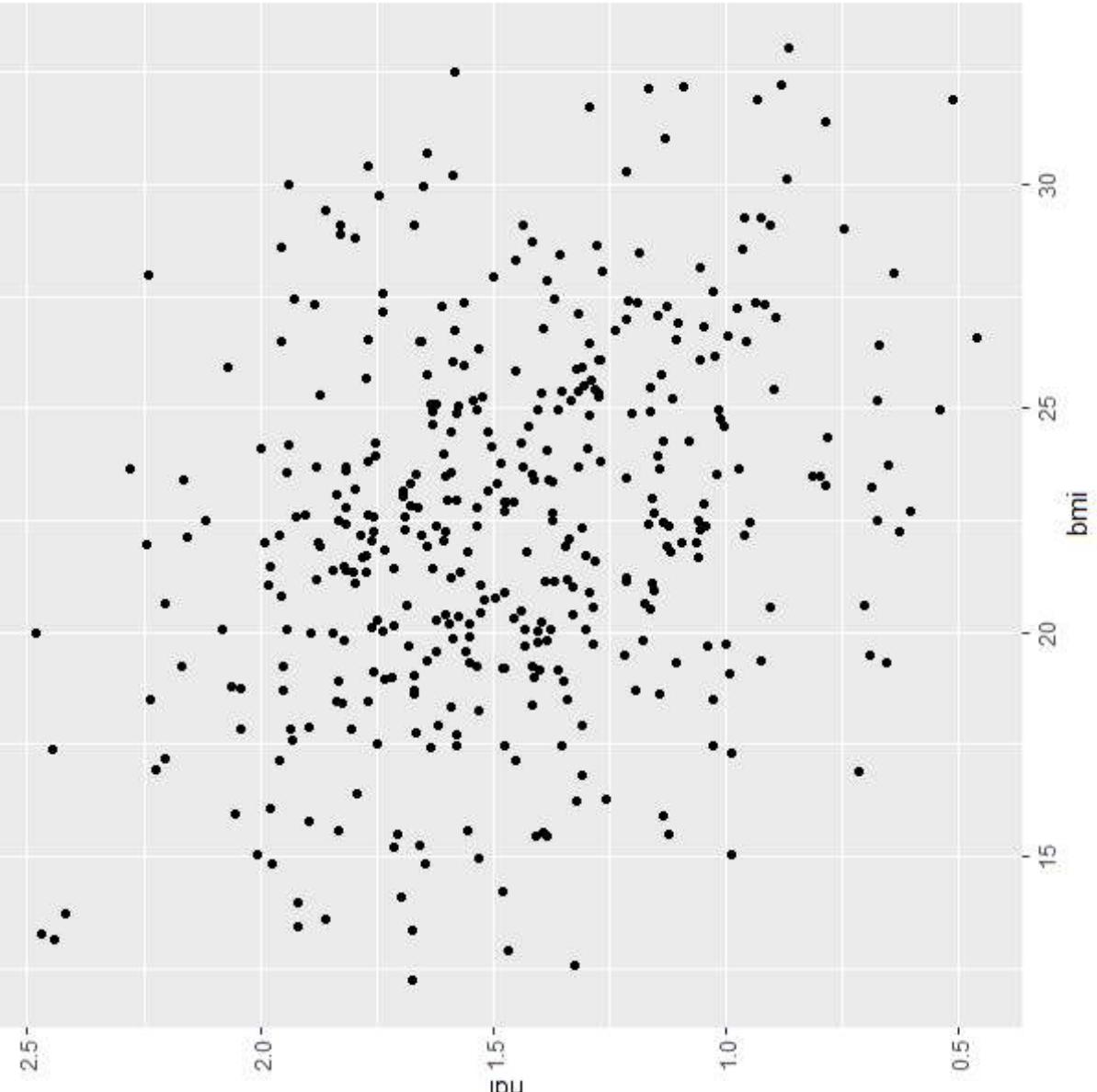
Hint: use geom_point()

```
p <- visits %>%
  filter(wave=="wave0") %>%
  ggplot(aes(x=bmi, y=hdl)) +
  geom_point()
```

(saving the plot so we make a modification)

Now add a regression line to the scatterplot.

Hint: add geom_smooth



Challenge!

Generate a plot showing HDL cholesterol vs BMI

Hint: use geom_point()

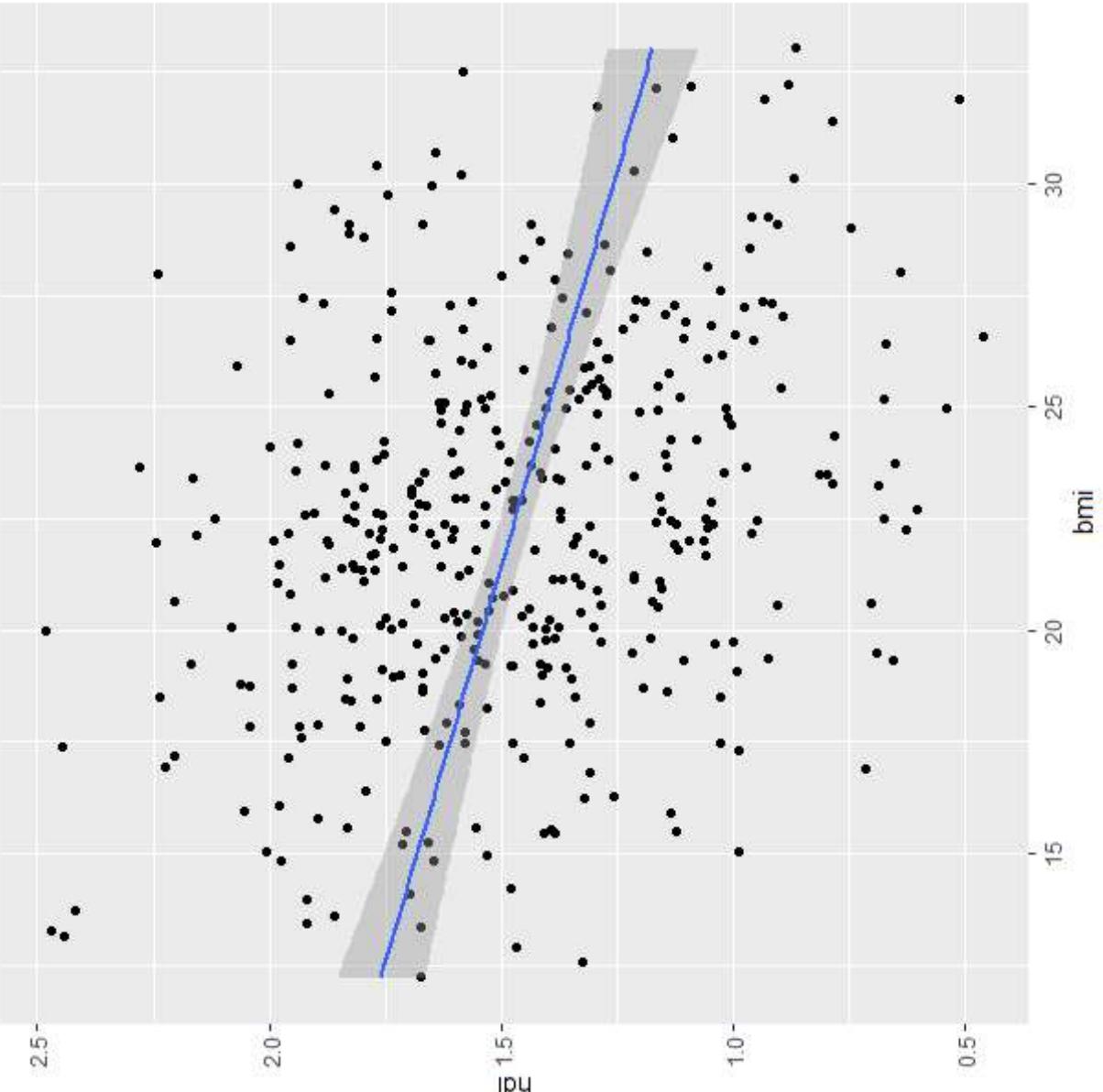
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p <- visits %>%
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  ggplot(aes(x=bmi, y=hdl)) +
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```

(saving the plot so we make a modification)

Now add a regression line to the scatterplot.

Hint: add geom_smooth

```
p <- p + geom_smooth(method=lm)
```



For more information about the tidyverse

<https://r4ds.had.co.nz/>

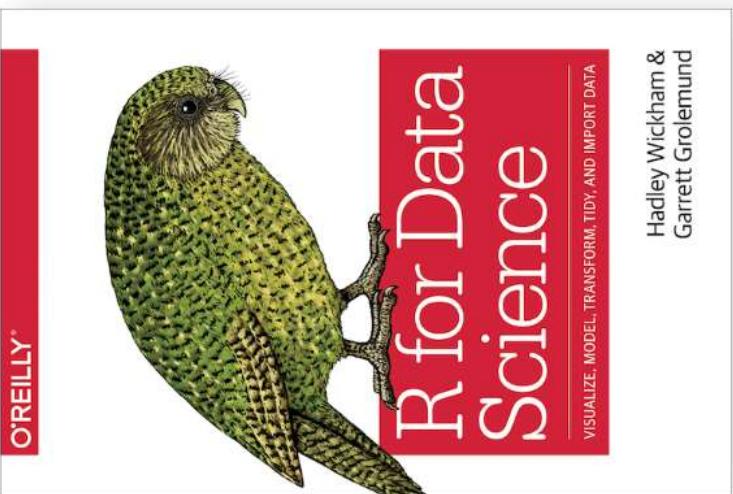
Welcome

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- 3 Data visualisation
- 4 Workflow: basics
- 5 Data transformation
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- 7 Exploratory Data Analysis
- 8 Workflow: projects
- Wrangle
- 9 Introduction

This is the website for “**R for Data Science**”. This book will teach you how to do data science with R: You’ll learn how to get your data into R, get it into the most useful structure, transform it, visualise it and model it. In this book, you will find a practicum of skills for data science. Just as a chemist learns how to clean test tubes and stock a lab, you’ll learn how to clean data and draw plots—and many other things besides. These are the skills that allow data science to happen, and here you will find the best practices for doing each of these things with R. You’ll learn how to use the grammar of graphics, literate programming, and reproducible research to save time. You’ll also learn how to manage



Converting between `base R` and `dplyr`

If you are familiar with `base R`, you might find it useful to see how `dplyr` commands map to `base R` commands.

<https://dplyr.tidyverse.org/articles/base.html>

e.g.

dplyr	base
<code>arrange(df, x)</code>	<code>df[order(x), , drop = FALSE]</code>
<code>distinct(df, x)</code>	<code>df[!duplicated(x), , drop = FALSE], unique()</code>
<code>filter(df, x)</code>	<code>df[which(x), , drop = FALSE], subset()</code>
<code>mutate(df, z = x + y)</code>	<code>df\$z <- df\$x + df\$y, transform()</code>
<code>pull(df, 1)</code>	<code>df[[1]]</code>
<code>pull(df, x)</code>	<code>df\$x</code>
<code>rename(df, y = x)</code>	<code>names(df)[names(df) == "x"] <- "y"</code>
	<code>...</code>

If you choose to enter the tidyverse ...

We've seen how tidyverse attempts to fix some problems in R.

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3. tidyverse functions can be difficult to debug
4. dplyr functions can be much slower than alternatives, e.g. data.table
5. the 'tidyverse way' can be confusing to new R users
(e.g. tidyverse does a lot 'behind the scenes magic' that can seem mysterious)

<https://github.com/matloff/TidyverseSkeptic>