Introduction to R for Data Analysis in the Health Sciences: Lecture 2

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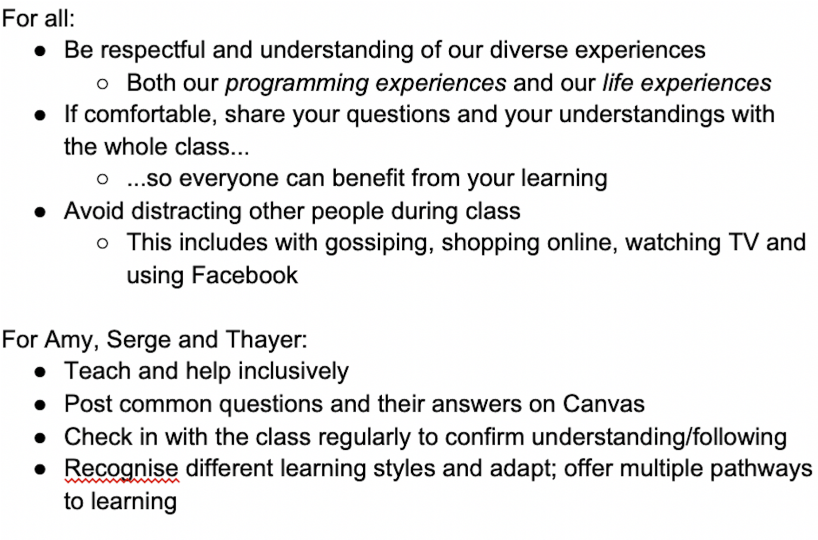
11 October, 2019

Welcome back

- Check out syllabus for *scope*, *grading*, *office hours*, *course policies* and *resources*
- Look at Lecture 1 slides for critical introductory material
- Congratulations on fantastic work on In-Class Exercise and Homework 1!

Norms and ground rules



For all:

- Be respectful and understanding of our diverse experiences
  - Both our *programming experiences* and our *life experiences*
- If comfortable, share your questions and your understandings with the whole class...
  - ...so everyone can benefit from your learning
- Avoid distracting other people during class
  - This includes with gossiping, shopping online, watching TV and using Facebook

For Amy, Serge and Thayer:

- Teach and help inclusively
- Post common questions and their answers on Canvas
- Check in with the class regularly to confirm understanding/following
- Recognise different learning styles and adapt; offer multiple pathways to learning

Normalising struggle

If this is your first time programming in `R`, it is likely that you will experience frustration and challenge in this course. Know that this is normal and a part of the learning process!

You can do it!

Outline of today plan

- Lecture (data manipulation)
  - Quick review of last week
  - New material: data manipulation
- Break
- In-class exercise

Recap

Last week we talked about the package tidyverse...

```r
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------- tidyverse 1
```

```
## v ggplot2 3.2.1     v purrr   0.3.2
## v tibble  2.1.3     v dplyr   0.8.3
## v tidyr   1.0.0     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.4.0
```

```
## -- Conflicts ------------------------------------- tidyverse_conflic
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

Recap

. . . and we talked about reading in and storing data. . .

```
fev_data <- "/Users/adwillis/teaching/19-509/datasets/fev.csv" %>%
    read_csv
```

```
## Parsed with column specification:
## cols(
##   seqnbr = col_double(),
##   subjid = col_double(),
##   age = col_double(),
##   fev = col_double(),
##   height = col_double(),
##   sex = col_double(),
##   smoke = col_double()
## )
```

Recap

. . . and we showed how we can filter data. . .

```r
is_tall <- fev_data$height > 72
fev_data[is_tall, ]
```

```
## # A tibble: 7 x 7
##   seqnbr subjid   age   fev height   sex smoke
##    <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1    401  18841    14  4.27   72.5     1     0
## 2    450  32741    13  4.22   74       1     0
## 3    464  37241    13  4.88   73       1     0
## 4    517  49541    13  5.08   74       1     0
## 5    550  59941    14  4.27   72.5     1     0
## 6    632  37441    17  5.63   73       1     0
## 7    636  44241    16  3.64   73.5     1     0
```

Recap

. . . and take some summary statistics

```r
mean(fev_data[is_tall, ]$fev)
```

```
## [1] 4.572429
```

```r
sd(fev_data[is_tall, ]$fev)
```

```
## [1] 0.6632754
```

Reminders

- The first line of any R script should be `library(tidyverse)`
- We refer to the rows and columns of a data frame using square brackets, e.g., `fev_data[is_tall, ]`
- We call functions using `function_name(input)` or `input %>% function_name`

Functions and arguments

Functions can have multiple arguments (inputs)

```
some_heights <- c(162, 170, 176, NA)
sd(some_heights)
```

```
## [1] NA
```

```
sd(some_heights, na.rm = TRUE)
```

```
## [1] 7.023769
```

Functions and arguments

Arguments can be referred to by name, or given in the canonical order. Find the canonical order by asking:

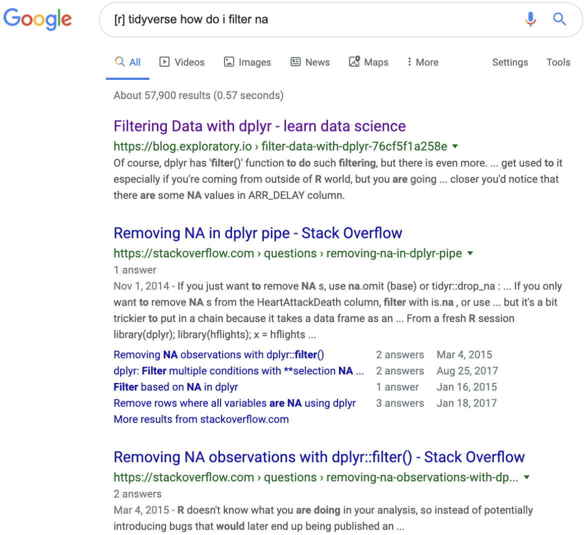
```
?sd
```

Getting help

Some functions are well documented and give helpful information. Others are not.

The internet is a fantastic resource!

Getting help



[r] tidyverse how do i filter na

About 57,900 results (0.57 seconds)

Filtering Data with dplyr - learn data science

https://blog.exploratory.io › filter-data-with-dplyr-76cf5f1a258e ▾

Of course, dplyr has '**filter**()' function **to do** such **filtering**, but there is even more. ... get used **to** it especially if you're coming from outside of **R** world, but you **are** going ... closer you'd notice that there **are** some **NA** values in ARR_DELAY column.

Removing NA in dplyr pipe - Stack Overflow

https://stackoverflow.com › questions › removing-na-in-dplyr-pipe ▾

1 answer

Nov 1, 2014 - If you just want **to** remove **NA** s, use **na**.omit (base) or tidyr::drop_na : ... If you only want **to** remove **NA** s from the HeartAttackDeath column, **filter** with is.**na** , or use ... but it's a bit trickier **to** put in a chain because it takes a data frame as an ... From a fresh **R** session library(dplyr); library(hflights); x = hflights ...

Removing **NA** observations with dplyr::**filter**()	2 answers	Mar 4, 2015
dplyr: **Filter** multiple conditions with **selection **NA** ...	2 answers	Aug 25, 2017
Filter based on **NA** in dplyr	1 answer	Jan 16, 2015
Remove rows where all variables **are NA** using dplyr	3 answers	Jan 18, 2017

More results from stackoverflow.com

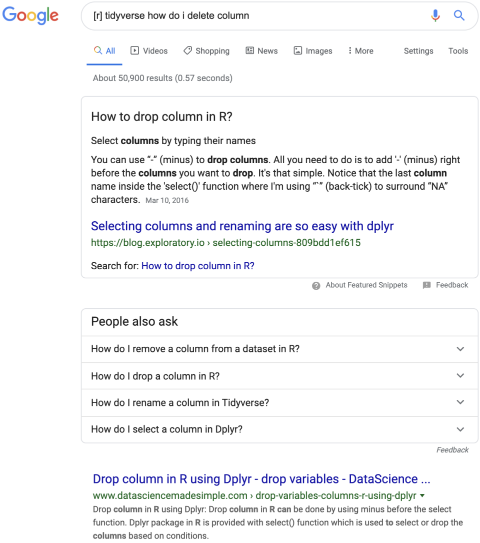
Removing NA observations with dplyr::filter() - Stack Overflow

https://stackoverflow.com › questions › removing-na-observations-with-dp... ▾

2 answers

Mar 4, 2015 - **R** doesn't know what you **are doing** in your analysis, so instead of potentially introducing bugs that **would** later end up being published an ...

Getting help



[r] tidyverse how do i delete column

About 50,900 results (0.57 seconds)

How to drop column in R?

Select **columns** by typing their names

You can use “-” (minus) to **drop columns**. All you need to do is to add '-' (minus) right before the **columns** you want to **drop**. It's that simple. Notice that the last **column** name inside the 'select()' function where I'm using “`” (back-tick) to surround “NA” characters. Mar 10, 2016

Selecting columns and renaming are so easy with dplyr
https://blog.exploratory.io › selecting-columns-809bdd1ef615

Search for: How to drop column in R?

People also ask

How do I remove a column from a dataset in R?

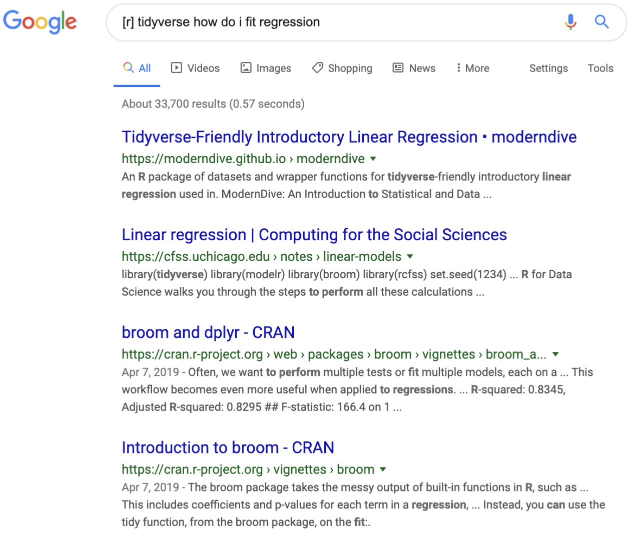
How do I drop a column in R?

How do I rename a column in Tidyverse?

How do I select a column in Dplyr?

Drop column in R using Dplyr - drop variables - DataScience ...
www.datasciencemadesimple.com › drop-variables-columns-r-using-dplyr ▾
Drop **column** in **R** using Dplyr: Drop **column** in **R can** be done by using minus before the select function. Dplyr package in **R** is provided with select() function which is used **to** select or drop the **columns** based on conditions.

Getting help



[r] tidyverse how do i fit regression

About 33,700 results (0.57 seconds)

Tidyverse-Friendly Introductory Linear Regression • moderndive
https://moderndive.github.io › moderndive ▾
An **R** package of datasets and wrapper functions for **tidyverse**-friendly introductory **linear regression** used in. ModernDive: An Introduction **to** Statistical and Data ...

Linear regression | Computing for the Social Sciences
https://cfss.uchicago.edu › notes › linear-models ▾
library(**tidyverse**) library(modelr) library(broom) library(rcfss) set.seed(1234) ... **R** for Data Science walks you through the steps **to perform** all these calculations ...

broom and dplyr - CRAN
https://cran.r-project.org › web › packages › broom › vignettes › broom_a... ▾
Apr 7, 2019 - Often, we want **to perform** multiple tests or **fit** multiple models, each on a ... This workflow becomes even more useful when applied **to regressions**. ... **R**-squared: 0.8345, Adjusted **R**-squared: 0.8295 ## F-statistic: 166.4 on 1 ...

Introduction to broom - CRAN
https://cran.r-project.org › vignettes › broom ▾
Apr 7, 2019 - The broom package takes the messy output of built-in functions in **R**, such as ... This includes coefficients and p-values for each term in a **regression**, ... Instead, you **can** use the tidy function, from the broom package, on the **fit**:.

Filtering data

We already know one way to filter data:

```
is_tall <- fev_data$height > 72
fev_data[is_tall, ]
```

```
## # A tibble: 7 x 7
##   seqnbr subjid   age   fev height   sex smoke
##    <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1    401  18841    14  4.27   72.5     1     0
## 2    450  32741    13  4.22   74       1     0
## 3    464  37241    13  4.88   73       1     0
## 4    517  49541    13  5.08   74       1     0
## 5    550  59941    14  4.27   72.5     1     0
## 6    632  37441    17  5.63   73       1     0
## 7    636  44241    16  3.64   73.5     1     0
```

Let's learn another way!

Filtering data

Why learn another way?

Easier to remember, faster to write, more robust to errors, highly scalable. . .

If you don't believe me by the end of the hour, let's chat about it after class!

Filtering data

```
fev_data %>%
  filter(height > 72)
```

```
## # A tibble: 7 x 7
##   seqnbr subjid   age   fev height   sex smoke
##    <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1    401  18841    14  4.27   72.5     1     0
## 2    450  32741    13  4.22   74       1     0
## 3    464  37241    13  4.88   73       1     0
## 4    517  49541    13  5.08   74       1     0
## 5    550  59941    14  4.27   72.5     1     0
## 6    632  37441    17  5.63   73       1     0
## 7    636  44241    16  3.64   73.5     1     0
```

Filtering data

```
fev_data %>%
  filter(age == 6)
```

```
## # A tibble: 37 x 7
##    seqnbr subjid   age   fev height   sex smoke
##     <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
##  1      7   1752     6  1.92   58       0     0
##  2      8   1753     6  1.42   56       0     0
##  3     11   1952     6  1.60   53       0     0
##  4     18   3551     6  1.88   53       0     0
##  5     49  10841     6  1.65   55       1     0
##  6     55  12241     6  1.63   54       1     0
##  7     63  14251     6  1.48   51       0     0
##  8     66  14541     6  1.75   57.5     1     0
##  9     80  16151     6  1.72   53       0     0
## 10     82  16252     6  1.70   53       0     0
## # ... with 27 more rows
```

Filtering data

```
fev_data %>%
  filter(age != 20)
```

```
## # A tibble: 654 x 7
##    seqnbr subjid   age   fev height   sex smoke
##     <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
##  1      1    301     9  1.71   57       0     0
##  2      2    451     8  1.72   67.5     0     0
##  3      3    501     7  1.72   54.5     0     0
##  4      4    642     9  1.56   53       1     0
##  5      5    901     9  1.90   57       1     0
##  6      6   1701     8  2.34   61       0     0
##  7      7   1752     6  1.92   58       0     0
##  8      8   1753     6  1.42   56       0     0
##  9      9   1901     8  1.99   58.5     0     0
## 10     10   1951     9  1.94   60       0     0
## # ... with 644 more rows
```

Filtering data

Syntax for filtering rules for continuous data:

- `age == 6`
- `age != 6`
- `fev > 2`
- `fev <= 1.5`: less than or equal to
- `is.na(age)`
- `!is.na(age)`

Filtering data

Syntax for filtering rules for categorical data:

- `sex == "F"` or `sex != "F"`
- `sex %in% c("M", "F")`

Filtering data

You can filter based on multiple criteria, too!

```
fev_data %>%
  filter(age == 14, smoke != 0)
```

```
## # A tibble: 7 x 7
##   seqnbr subjid   age   fev height   sex smoke
##    <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1    332   4952    14  2.24     66     0     1
## 2    358  10053    14  3.43     64     0     1
## 3    370  11642    14  3.96     72     1     1
## 4    384  15751    14  3.07     65     0     1
## 5    439  30042    14  4.31     69     1     1
## 6    556  61941    14  2.28     66     1     1
## 7    602  82743    14  4.76     68     1     1
```

Selecting columns

Now we know how to select rows. How do we select columns?

```
fev_data %>%
  select(fev, height, age)
```

```
## # A tibble: 654 x 3
##      fev height   age
##    <dbl>  <dbl> <dbl>
##  1  1.71   57       9
##  2  1.72   67.5     8
##  3  1.72   54.5     7
##  4  1.56   53       9
##  5  1.90   57       9
##  6  2.34   61       8
##  7  1.92   58       6
##  8  1.42   56       6
##  9  1.99   58.5     8
## 10  1.94   60       9
## # ... with 644 more rows
```

Selecting columns

We can also drop columns

```
fev_data %>%
  select(-seqnbr, -subjid)
```

```
## # A tibble: 654 x 5
##       age   fev height   sex smoke
##     <dbl> <dbl>  <dbl> <dbl> <dbl>
##  1     9  1.71   57        0     0
##  2     8  1.72   67.5      0     0
##  3     7  1.72   54.5      0     0
##  4     9  1.56   53        1     0
##  5     9  1.90   57        1     0
##  6     8  2.34   61        0     0
##  7     6  1.92   58        0     0
##  8     6  1.42   56        0     0
##  9     8  1.99   58.5      0     0
## 10     9  1.94   60        0     0
## # ... with 644 more rows
```

Summarising data

Now that we know how to subset our data, how do we summarize it?

```
fev_data %>%
  filter(age == 14, smoke != 0) %>%
  summarize(mean(fev))
```

```
## # A tibble: 1 x 1
##   `mean(fev)`
##         <dbl>
## 1        3.43
```

Summarising data

Now that we know how to subset our data, how do we summarize it?

```
fev_data %>%
  filter(age == 14, smoke != 0) %>%
  summarize(my_mean = mean(fev))
```

```
## # A tibble: 1 x 1
##   my_mean
##     <dbl>
## 1    3.43
```

You can give a summary variable a name, e.g., `my_mean`

Summarising data

We can summarize in multiple ways at once!

```r
fev_data %>%
  filter(age == 14, smoke != 0) %>%
  summarize(mean(fev), sd(fev))
```

```
## # A tibble: 1 x 2
##   `mean(fev)` `sd(fev)`
##         <dbl>     <dbl>
## 1        3.43     0.976
```

Both `summarise` and `summarize` work!

Summarising data

But what if I want the average FEV for both smokers and non-smokers? Do I have to repeat this?

No – I can create a grouping variable!

Summarising data

Create a grouping variable with group_by

```
fev_data %>%
  group_by(smoke)
```

```
## # A tibble: 654 x 7
## # Groups:   smoke [2]
##    seqnbr subjid   age   fev height   sex smoke
##     <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
##  1      1    301     9  1.71   57       0     0
##  2      2    451     8  1.72   67.5     0     0
##  3      3    501     7  1.72   54.5     0     0
##  4      4    642     9  1.56   53       1     0
##  5      5    901     9  1.90   57       1     0
##  6      6   1701     8  2.34   61       0     0
##  7      7   1752     6  1.92   58       0     0
##  8      8   1753     6  1.42   56       0     0
##  9      9   1901     8  1.99   58.5     0     0
## 10     10   1951     9  1.94   60       0     0
## # ... with 644 more rows
```

This doesn't change the dataset in any way (except the groups are listed)

Summarising data

Now when we go to `summarize` there is a summary for each group:

```
fev_data %>%
  group_by(smoke) %>%
  summarize(mean(fev), sd(fev))
```

```
## # A tibble: 2 x 3
##   smoke `mean(fev)` `sd(fev)`
##   <dbl>       <dbl>     <dbl>
## 1     0        2.57     0.851
## 2     1        3.28     0.750
```

Note: `smoke == 1` is smokers. Interesting. . .

Summarising data

It's hard to interpret differences in mean and standard deviation without knowledge of the sample size in each group!

```
fev_data %>%
  group_by(smoke) %>%
  summarize(mean(fev), sd(fev))
```

```
## # A tibble: 2 x 3
##   smoke `mean(fev)` `sd(fev)`
##   <dbl>       <dbl>     <dbl>
## 1     0        2.57     0.851
## 2     1        3.28     0.750
```

Summarising data

Use `n()` with `summarize` to get the number of observations in each group:

```
fev_data %>%
  group_by(smoke) %>%
  summarize(n = n(), mean = mean(fev), sd = sd(fev))
```

```
## # A tibble: 2 x 4
##   smoke     n  mean    sd
##   <dbl> <int> <dbl> <dbl>
## 1     0   589  2.57 0.851
## 2     1    65  3.28 0.750
```

Summarising data

You can also summarize based on your own variables!

```
fev_data %>%
  group_by(height < 60) %>%
  summarize(n(), mean(fev))
```

```
## # A tibble: 2 x 3
##   `height < 60` `n()` `mean(fev)`
##   <lgl>         <int>       <dbl>
## 1 FALSE           409        3.10
## 2 TRUE            245        1.86
```

Think-pair-share

```r
fev_data$sex %>% unique
```

```
## [1] 0 1
```

Suppose I was given this dataset without information about variable coding. We have 2 sexes observed in this dataset – most likely binary male and female. How could we figure out if `sex == 1` is male or female?

```r
fev_data %>%
  select(-seqnbr, -subjid) %>%
  names
```

```
## [1] "age"    "fev"    "height" "sex"    "smoke"
```

Discuss with a partner how you might investigate this (2 minutes).

Think-pair-share

[Live demo]

Final data analysis

Solving the smokers-have-better-lung-function paradox:

```
fev_data %>%
  group_by(smoke) %>%
  summarize(n(), mean(fev), sd(fev))
```

```
## # A tibble: 2 x 4
##   smoke `n()` `mean(fev)` `sd(fev)`
##   <dbl> <int>       <dbl>     <dbl>
## 1     0   589        2.57     0.851
## 2     1    65        3.28     0.750
```

This was surprising to me. What could be confounded with smoking status?

Final data analysis: smoking and lung function in children

```r
fev_data %>%
  group_by(smoke) %>%
  summarize(mean(age))
```

```
## # A tibble: 2 x 2
##   smoke `mean(age)`
##   <dbl>       <dbl>
## 1     0        9.53
## 2     1       13.5
```

Smokers are typically *older* than non-smokers!

Final data analysis: smoking and lung function in children

```
fev_data %>%
  group_by(age, smoke) %>%
  summarize(n(), mean(fev), sd(fev))
```

```
## # A tibble: 28 x 5
## # Groups:   age [17]
##      age smoke `n()` `mean(fev)` `sd(fev)`
##    <dbl> <dbl> <int>       <dbl>     <dbl>
##  1     3     0     2        1.24     0.235
##  2     4     0     9        1.28     0.353
##  3     5     0    28        1.55     0.308
##  4     6     0    37        1.66     0.223
##  5     7     0    54        1.87     0.335
##  6     8     0    85        2.12     0.391
##  7     9     0    93        2.44     0.478
##  8     9     1     1        1.95    NA
##  9    10     0    76        2.67     0.533
## 10    10     1     5        3.06     0.441
## # ... with 18 more rows
```

Sorting data

```r
fev_data %>%
  group_by(age, smoke) %>%
  summarize(n(), mean(fev), sd(fev)) %>%
  arrange(age) # arrange by increasing age
```

```
## # A tibble: 28 x 5
## # Groups:   age [17]
##      age smoke `n()` `mean(fev)` `sd(fev)`
##    <dbl> <dbl> <int>       <dbl>     <dbl>
##  1     3     0     2        1.24     0.235
##  2     4     0     9        1.28     0.353
##  3     5     0    28        1.55     0.308
##  4     6     0    37        1.66     0.223
##  5     7     0    54        1.87     0.335
##  6     8     0    85        2.12     0.391
##  7     9     0    93        2.44     0.478
##  8     9     1     1        1.95    NA
##  9    10     0    76        2.67     0.533
## 10    10     1     5        3.06     0.441
## # ... with 18 more rows
```

Putting it all together

```
fev_data %>%
  group_by(age, smoke) %>%
  summarize(n = n(), # name summary statistics columns...
            mean = mean(fev), sd = sd(fev)) %>%
  filter(n >= 5) %>% # ... so we can filter on them later
  arrange(desc(age)) # arrange by decreasing age
```

```
## # A tibble: 21 x 5
## # Groups:   age [14]
##      age smoke     n  mean    sd
##    <dbl> <dbl> <int> <dbl> <dbl>
##  1    17     0     6  4.65 0.871
##  2    16     0     6  3.75 0.567
##  3    16     1     7  3.60 0.858
##  4    15     0     9  3.92 0.960
##  5    15     1    10  3.09 0.766
##  6    14     0    18  3.64 0.627
##  7    14     1     7  3.43 0.976
##  8    13     0    30  3.53 0.717
##  9    13     1    13  3.38 0.776
## 10    12     0    50  3.24 0.733
## # ... with 11 more rows
```

Summary

Today we learnt 5 `tidyverse` functions that facilitate data analysis:

- `filter()` picks rows based on their valuess
- `select()` picks columns based on their names
- `summarize()` reduces multiple values to a single summary
- `group_by()` groups rows together (useful for `summarize`)
- `arrange()` changes the ordering of the rows

The plan

- 5 minute break
- In-class exercise available via Canvas and github.com/adw96/biost509
  - Designed to be completed by 3:20 p.m.
  - Due today 5 p.m.
  - Place a *yellow sticky note* on your computer to indicate you are stuck, or a *blue sticky note* to indicate you have a non-urgent question
- Homework due next week by 1 p.m. Friday

The TAs and I will walk around to help you; we will help *yellow stickies*, then *blue stickies*. Please put your sticky note high enough that we can see it!